(19) World Intellectual Property Organization International Bureau





(43) International Publication Date 31 October 2002 (31.10.2002)

PCT

(10) International Publication Number WO 02/086443 A2

- (51) International Patent Classification7:
- G01N
- (21) International Application Number: PCT/US02/12476
- (22) International Filing Date: 18 April 2002 (18.04.2002)
- (25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

60/284,770 18 April 2001 (18.04.2001) U 60/290,492 10 May 2001 (10.05.2001) U 60/339,245 9 November 2001 (09.11.2001) U 60/350,666 13 November 2001 (13.11.2001) U 60/374,370 29 November 2001 (29.11.2001) U 60/372,246 12 April 2002 (12.04.2002) U	12 April 2002 (12.04.2002) U
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- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:

of inventorship (Rule 4.17(iv)) for US only

Published:

 without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

//086443 A2

 $\textbf{(54) Title:} \ \, \text{METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER}$

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of lung cancer and similar pathologies. Also described herein are methods that can be used to identify modulators of lung cancer and similar pathologies.

METHODS OF DIAGNOSIS OF LUNG CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF LUNG CANCER

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application is related to USSN 60/284,770, filed April 18, 2001; USSN 60/290,492, filed May 10, 2001; USSN 60/334,370, filed November 29, 2001; USSN 60/339,245, filed November 9, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/xxx,xxx, filed April 12, 2002 (Docket OMNI-002P); each of which is incorporated herein by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in lung cancer; and to the use of such expression profiles and compositions in diagnosis and therapy of lung cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit lung cancer or related conditions.

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BACKGROUND OF THE INVENTION

Lung cancer is the second most commonly occurring cancer in the United States and is the leading cause of cancer-related death. It is estimated that there are over 160,000 new cases of lung cancer in the United States every year. Of those who are diagnosed with lung cancer, 86 percent will die within five years. Lung cancer is the most common visceral cancer in men and accounts for nearly one third of all cancer deaths in both men and women. In fact, lung cancer accounts for 7% of all deaths, due to any cause, in both men and women.

Smoking is the primary cause of lung cancer, with more than 80% of lung cancers resulting from smoking. About 400 to 500 separate gaseous substances are present in the smoke of a non-filter cigarette. The most noteworthy substances include nitrogen oxides, hydrogen cyanide, formaldehyde, benzene, and toluene. The particles present in cigarette smoke contain at least 3,500 individual compounds such as nicotine, tobacco alkaloids (nornicotine, anatabine, anabasine), polycyclic aromatic hydrocarbons (e.g., benzo(a)pyrene, B(a)P), naphthalenes, aromatic amines, phenols, and tobacco-specific nitrosamines.

Tobacco-specific nitrosamines are formed during tobacco curing and processing, and are suspected of causing lung cancer in humans. In rodent studies, regardless of the where or how it is applied, the tobacco-specific nitrosamine known as NNK produces lung adenomas and lung adenocarcinomas. The tobacco-specific nitrosamine known as NNAL also produces lung adenocarcinomas in rodents.

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Many of the chemicals found in cigarette smoke also affect the nonsmoker inhaling "secondhand" or sidestream smoke. Indeed, the smoke inhaled by non-smokers has a chemical composition similar to the smoke inhaled by smokers, but, importantly, the concentrations of the carcinogenic tobacco-specific nitrosamines are present in higher concentrations in second hand smoke. For this and other reasons, "passive smoking" is an important cause of lung cancer, causing as many as 3,000 lung cancer deaths in nonsmokers each year.

In addition to smoking, other factors thought to be causes of lung cancer include onthe-job exposure to carcinogens such as asbestos and uranium, exposure to chemical hazards such as radon, polycyclic aromatic hydrocarbons, chromium, nickel, and inorganic arsenic, genetic factors, and diet.

Histological classification of various lung cancers define the types of cancer that begin in the lung. See, e.g., Travis, et al. (1999) Histological Typing of Lung and Pleural Tumours (International Histological Classification of Tumours, No 1. Four major cell types make up more than 88% of all primary lung neoplasms. These are: squamous or epidermoid carcinoma, small cell (also called oat cell) carcinoma, adenocarcinoma, and large cell (also called large cell anaplastic) carcinoma. The remainder include undifferentiated carcinomas, carcinoids, bronchial gland tumors, and other rarer types. The various cell types have different natural histories and responses to therapy, and, thus, a correct histologic diagnosis is the first step of effective treatment.

Small cell lung cancer (SCLC) accounts for 18-25% of all lung cancers, and occurs less frequently than non-small cell lung cancers, and generally spread to distant organs more rapidly than non-small cell lung cancer. In general, at the time of presentation small cell lung cancers have already spread beyond the beyond the bounds where surgery and curative intent can be undertaken. Hoever, if identified early enough, these cancers are often responsive to chemotherapy and thoracic radiation treatment.

Non-small cell lung cancers (NSCLC) are the more frequently occurring form of lung cancer. They comprise squamous cell carcinoma, adenocarcinoma, and large cell carcinoma

and account for more than 75% of all lung cancers. Non-small cell tumors that are localized at the time of presentation can sometimes be cured with surgery and/or radiotherapy, but usually are not identified until significant metastasis has occurred, which are typically not very responsive to surgical, chemotherapy, or radiation treatment..

The screening of asymptomatic persons at high risk for lung cancer has often proven ineffective. In general, only 5 to 15 percent of lung cancer patients have their disease detected while they are asymptomatic. Of course, early detection and treatment are critical factors in the fight against lung cancer. The average survival rate is 49% for those whose cancer is detected early, before the cancer has spread from the lung. Lung cancer often spreads outside of the lung, and it may have spread to the bones or brain by the time it is diagnosed. While the prognosis may be better for lung cancers that are detected early, because of the lack of effective curative treatments, early detection does not necessarily alter the total death rate from lung cancer.

Thus, methods for diagnosis and prognosis of lung cancer and effective treatment of lung cancer would be desirable. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of lung cancer. Further provided are methods that can be used to screen candidate therapeutic agents for the ability to modulate, e.g., treat, lung cancer. Additionally, provided herein are molecular targets and compositions for therapeutic intervention in lung disease and other metastatic cancers.

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SUMMARY OF THE INVENTION

The present invention provides nucleotide sequences of genes that are up- and down-regulated in lung cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. The methods of detecting nucleic acids of the invention or their encoded proteins can be used for a number of purposes. Examples include early detection of lung cancers, monitoring and early detection of relapse following treatment of lung cancers, monitoring response to therapy of lung cancers, determining prognosis of lung cancers, directing therapy of lung cancers, selecting patients for postoperative chemotherapy or radiation therapy, selecting therapy, determining tumor prognosis, treatment, or response to treatment, and early detection of precancerous lesions of the lung. Examples of benign or precancerous lesions include: atelectasis, emphysema, brochitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis (HP), interstitial pulmonary fibrosis (IPF), asthma, and

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bronchiectasis. Other aspects of the invention will become apparent to the skilled artisan by
the following description of the invention.

In one aspect, the present invention provides a method of detecting a lung cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16. Alternatively, the sample may be contacted with a specific binding reagent, e.g., antibody.

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In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-16. In another embodiment, the polynucleotide comprises a sequence as shown in Tables 1A-16.

In one embodiment, the biological sample is a tissue sample, or a body fluid. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label. In one embodiment, the polynucleotide is immobilized on a solid surface. In one embodiment, the patient is undergoing a therapeutic regimen to treat lung cancer. In another embodiment, the patient is suspected of having lung cancer. In one embodiment, the patient is a primate, e.g., a human.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy. Or the sample may be evaluated for protein, e.g., contacting the sample with an antibody.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated transcript to a level of the lung cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. Or the sample may be evaluated for comparison of protein.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a

biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated antibody in the biological sample by contacting the biological sample with a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated antibody, thereby monitoring the efficacy of the therapy.

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In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated antibody to a level of the lung cancer-associated antibody in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of lung cancer, the method comprising the steps of: (i) providing a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a lung cancer-associated polypeptide in the biological sample by contacting the biological sample with an antibody, wherein the antibody specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16, thereby monitoring the efficacy of the therapy.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the lung cancer-associated polypeptide to a level of the lung cancer-associated polypeptide in a biological sample from the patient prior to, or earlier in, the therapeutic treatment. In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-16. In one embodiment, an expression vector or cell comprises the isolated nucleic acid. In one aspect, the present invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-16. In one embodiment, the antibody is conjugated to an effector component, e.g., a fluorescent label, a radioisotope or a cytotoxic chemical. In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting lung cancer in a a patient, the method comprising contacting a biological sample from the patient with an antibody or protein as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to a lung cancer gene in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprises a sequence from Tables 1A-16.

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In another aspect, the present invention provides a method for identifying a compound that modulates a lung cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a lung cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16; and (ii) determining the functional effect of the compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect. In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant. In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation or another critical process of a lung cancer-associated cell to treat lung cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound identified as described herein. In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having lung cancer or a cell isolated therefrom; (ii) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of lung cancer.

In one embodiment, the control is a mammal with lung cancer or a cell therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal, or a non-malignant lung disease.

In another aspect, the present invention provides a method for treating a mammal having lung cancer comprising administering a compound identified by the assay described herein.

In another aspect, the present invention provides a pharmaceutical composition for treating a mammal having lung cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

DETAILED DESCRIPTION OF THE INVENTION

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In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of lung disease or cancer, as well as methods for screening for compositions which modulate lung cancer. "Treatment, monitoring, detection or modulation of lung disease or cancer" includes treatment, monitoring, detection, or modulation of lung disease in those patients who have lung disease (whether malignant or non-malignant, e.g., emphysema, bronchitis, or fibrosis) as well as patients with lung cancers in which gene expression from a gene in Tables 1A-16 is increased or decreased, indicating that the subject is more likely to have disease. In particular, while these targets are identified primarily from lung cancer samples, these same targets are likely to be similarly found in analyses of other medical conditions. These other conditions may result from similar pathological processes which affect similar tissues, e.g., lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), interstitial pneumonitis, nonspecific idiopathic pneumonitis (NSIP)), chronic obstructive pulmonary disease (COPD, e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, and esophageal cancer. See, e.g., the NCI webpage and USSN 60/347,349 and USSN 60/xxx,xxx (docket LFBR-001-1P, filed March 29, 2002), each of which is incorporated herein by reference. The treatment may be of lung cancer or related condition itself, or treatment of metastasis.

In particular, identification of markers selectively expressed on these cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of lung diseases, which subsets may actually require

very different treatments. Moreover, the markers may also be important in related diseases to the specific cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 1A-16 provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in lung cancer samples. The tables also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster. In Table 1A, genes marked as "target 1" or "target 2" are particularly useful as therapeutic targets. Genes marked as "target 3" are particularly useful as diagnostic markers. Genes marked as "chron" are upregulated in chronically diseased lung (e.g., emphysema, bronchitis, fibrosis) relative to lung tumors and normal tissue. In certain analyses, the ratio for the "chron" category was determined using the 70th percentile of chronically diseases lung samples divided by the 90th percentile of lung tumor samples divided by the 90th percentile of lung tumor samples divided by the 90th percentile of normal lung samples.

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Definitions

The term "lung cancer protein" or "lung cancer polynucleotide" or "lung cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-16 and conservatively modified variants thereof; or (4)

have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a unigene cluster of Tables 1A-16. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "lung cancer polypeptide" and a "lung cancer polynucleotide," include both naturally occurring or recombinant forms.

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A "full length" lung cancer protein or nucleic acid refers to a lung cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains the elements normally contained in one or more naturally occurring, wild type lung cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a lung cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival materials, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or other mammal; or a bird; reptile; fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the

same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer

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Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see,

e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology.

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Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) <u>Proc. Nat'l. Acad. Sci. USA</u> 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between

two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

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An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant or component from the composition to be purified.

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In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymer.

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The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g., norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refer to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of

conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3^{rd} ed.) and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, 5 etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or Omethylphophoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford University Press); and peptide nucleic acid backbones and 10 linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, in Sanghui and Cook, eds. Carbohydrate Modifications in Antisense Research, ASC Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. 15 Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring 20 nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

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The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary

strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

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A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. Many methods known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth., 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; activatable moieties, a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method

WO 02/086443 PCT/US02/12476 using high affinity interactions may achieve the same results where one of a pair of binding

partners binds to the other, e.g., biotin, streptavidin.

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As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered

WO 02/086443 PCT/US02/12476 recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein

made using recombinant techniques, i.e., through the expression of a recombinant nucleic acid as depicted above.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

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A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to essentially no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in · 5 "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) 10 at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 15 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions are often: 50% formamide, 5x SSC, and 1% 20 SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32° C and 48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50° C 25 to about 65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C - 95° C for 0.5 - 2 min., an annealing phase lasting 0.5 - 2 min., and an extension phase of about 72° C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al.(1990) PCR Protocols, A Guide to Methods and 30 Applications.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This

occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., Ausubel, et al. (ed.) <u>Current Protocols in Molecular Biology</u> Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a lung cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the lung cancer protein or nucleic acid, e.g., a physiological, enzymatic, functional, physical, or chemical effect, such as the ability to decrease lung cancer. It includes ligand binding activity; cell viability, cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein expression in cells undergoing metastasis, and other characteristics of lung cancer cells. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a lung cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the lung cancer protein; measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation. Determination of the functional effect of a compound on lung cancer can also be performed using lung cancer assays known to those of skill in the art such as an *in vitro* assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis *in vivo*; mRNA and protein

expression in cells undergoing metastasis, and other characteristics of lung cancer cells. The functional effects can be evaluated by many means known to those skilled in the art, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for lung cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β-gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

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"Inhibitors", "activators", and "modulators" of lung cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of lung cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of lung cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate lung cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of lung cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the lung cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of lung cancer can also be identified by incubating lung cancer cells with the test compound and determining increases or decreases in the expression of 1 or more lung cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more lung cancer proteins, such as lung cancer proteins encoded by the sequences set out in Tables 1A-16.

Samples or assays comprising lung cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a lung cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more

WO 02/086443 PCT/US02/12476 preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics *in vitro* or *in vivo*, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., Freshney (1994) <u>Culture of Animal Cells a Manual of Basic Technique pp. 231-241</u> (3rd ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

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"Cancer cells," "transformed" cells, or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy (see, Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (3rd ed.)).

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul, Fundamental Immunology.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible

WO 02/086443 PCT/US02/12476 for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'₂, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'₂ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'₂ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985), pp. 77-96 in Monoclonal Antibodies and Cancer Therapy; Coligan (1991 and supplements) Current Protocols in Immunology; Harlow and Lane (1988) Antibodies, A Laboratory Manual; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.)). Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783).

A "chimeric antibody" is an antibody molecule in which, e.g, (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the

WO 02/086443 PCT/US02/12476 variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region

having a different or altered antigen specificity.

Identification of lung cancer-associated sequences

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In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different lung cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of lung cancer (chronic disease, adenocarcinoma, etc.)

The identification of sequences that are differentially expressed in lung cancer versus non-lung cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to downregulate lung cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant diseasemay be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of lung cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the lung cancer expression profile. This may be done by making biochips comprising sets of the important lung cancer genes, which can then be used in these screens. PCR methods may be applied with selected primer pairs, and analysis may be of RNA or of genomic sequences. These methods can also be done on the protein basis; that is, protein expression levels of the lung cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the lung cancer

nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the lung cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs or as protein or DNA vaccines.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in lung cancer relative to normal tissues and/or non-malignant lung disease, or in different types of lung disease, herein termed "lung cancer sequences." As outlined below, lung cancer sequences include those that are up-regulated (i.e., expressed at a higher level) in lung cancer, as well as those that are down-regulated (i.e., expressed at a lower level). In a preferred embodiment, the lung cancer sequences are from humans; however, as will be appreciated by those in the art, lung cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other lung cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (dogs, cats, etc.). Lung cancer sequences from other organisms may be obtained using the techniques outlined below.

Lung cancer sequences can include both nucleic acid and amino acid sequences. As will be appreciated by those in the art and is more fully outlined below, lung cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the lung cancer sequences can be generated.

A lung cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying lung cancer-associated sequences, the lung cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing lung cancer samples with metastatic cancer samples from other cancers, such as, breast, other gastrointestinal cancers, prostate, ovarian,

etc. Samples of, non metastatic disease tissue and tissue undergoing metastasis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

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In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal lung, but also including, and not limited to colon, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the lung cancer screen that are expressed in significant amounts in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible at a later stage of life). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs.

In a preferred embodiment, lung cancer sequences are those that are up-regulated in lung cancer; that is, the expression of these genes is higher in cancerous tissue than in normal lung or other tissue. "Up-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater. Another embodiment is directed to sequences up-regulated in nonmalignant conditions relative to normal. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al (1998) Nucleic Acids Research 26:1-7 and http://www.ncbi.nlm.nih.gov/. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH (Salamov and Solovyev (2000) Genome Res. 10:516-522). In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, lung cancer sequences are those that are downregulated in the lung cancer; that is, the expression of these genes is lower in cancerous tissue

or normal lung or other tissue. "Down-regulation" as used herein means, when the ratio is presented as a number greater than one, that the ratio is greater than one, preferably 1.5 or greater, more preferably 2.0 or greater, or, when the ratio is presented as a number less than one, that the ratio is less than one, preferably 0.5 or less, more preferably 0.25 or less.

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Informatics

The ability to identify genes that are over or under expressed in lung cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with lung cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (1998) Pharmaceutical Proteomics: Targets,

Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, ÇA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

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Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for assay data acquired using an assay of the invention.

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The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing lung cancer, i.e., the identification of lung cancer-associated sequences described herein, provide an abundance of information, which can be correlated with

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pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, genedisease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed

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An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multidimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics; Durbin, et al. (eds., 1999) <u>Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids</u> (; Baxevanis and Oeullette (eds., 1998) <u>Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins</u>); Rashidi and Buehler (1999) <u>Bioinformatics: Basic Applications in Biological Science and Medicine</u>; Setubal, et al. (eds 1997) <u>Introduction to Computational Molecular Biology</u>; Misener and Krawetz (eds, 2000) <u>Bioinformatics: Methods and Protocols</u>; Higgins and Taylor (eds., 2000) <u>Bioinformatics: Sequence, Structure, and Databanks: A Practical</u>

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Approach; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the

Internet; Han and Kamber (2000) Data Mining: Concepts and Techniques (2000); and

Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for lung cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may

be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

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The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC,

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MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain
molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a
data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM,
SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can
be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal
adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O
device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

15 Characteristics of lung cancer-associated proteins

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Lung cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the lung cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts (ed. 1994) Molecular Biology of the Cell (3d ed.). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2

domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden (see, e.g., Bateman, et al (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322).

In another embodiment, the lung cancer sequences are transmembrane proteins.

Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels, pumps, and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the

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localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site http://psort.nibb.ac.jp/).

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The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, hormones, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Lung cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for extracellular immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ or in histological analysis. Alternatively, antibodies can also label intracellular proteins, in which case analytical samples are typically permeablized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the lung cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit

signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, sax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Lung cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of lung cancer nucleic acids

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As described above, lung cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the lung cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The lung cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-16, can be fragments of larger genes, i.e., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the lung cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once a lung cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire lung cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant lung cancer nucleic acid can be further-used as a probe to identify and isolate

other lung cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant lung cancer nucleic acids and proteins.

The lung cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the lung cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, RNAi, vaccine, and/or antisense applications. Alternatively, the lung cancer nucleic acids that include coding regions of lung cancer proteins can be put into expression vectors for the expression of lung cancer proteins, again for screening purposes or for administration to a patient.

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In a preferred embodiment, nucleic acid probes to lung cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the lung cancer nucleic acids, i.e., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under appropriate reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally complements of ORFs or whole genes are not used. In some embodiments, nucleic acids of lengths up to hundreds of bases can be used.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

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particular target. The probes can be overlapping (i.e., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is typically meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to a biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often the substrate may contain discrete individual sites appropriate for ndivitual partitioning and identification. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in US application entitled Reusable Low Fluorescent Plastic Biochip, U.S.

WO 02/086443 PCT/US02/12476 Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

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In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or attachment may be via linkage to an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized *in situ*, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of lung cancer-associated sequences. These assays are typically performed in conjunction with

reverse transcription. In such assays, a lung cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of lung cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560, Landegren, et al. (1988) Science 241:1077, and Barringer, et al. (1990) Gene 89:117), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874), dot PCR, and linker adapter PCR, etc.

Expression of lung cancer proteins from nucleic acids

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In a preferred embodiment, lung cancer nucleic acids, e.g., encoding lung cancer proteins, are used to make a variety of expression vectors to express lung cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds 1999) Gene Expression Systems) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the lung cancer protein. The term "control sequences" refers to DNA

sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

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Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the lung cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating

vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez and Hoeffler, *supra*).

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

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The lung cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a lung cancer protein, under the appropriate conditions to induce or cause expression of the lung cancer protein. Conditions appropriate for lung cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the lung cancer proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived form SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

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In a preferred embodiment, lung cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the lung cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, lung cancer proteins are produced in insect cells. Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, lung cancer protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha,

Kluyveromyces fragilis and K. lactis, Pichia guillerimondii, and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The lung cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the lung cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the lung cancer protein may be made as a fusion protein to increase expression for affinity purification purposes, or for other reasons. For example, when the lung cancer protein is a lung cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression purposes.

In a preferred embodiment, the lung cancer protein is purified or isolated after expression. Lung cancer proteins may be isolated or purified in a variety of appropriate ways. Standard purification methods include electrophoretic, molecular, immunological and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the lung cancer protein may be purified using a standard anti-lung cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see Scopes (1982) Protein Purification. The degree of purification necessary will vary depending on the use of the lung cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the lung cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

25 Variants of lung cancer proteins

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In one embodiment, the lung cancer proteins are derivative or variant lung cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative lung cancer peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at a particular residue within the lung cancer peptide.

Also included within one embodiment of lung cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three

classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the lung cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant lung cancer protein fragments having up to about 100-150 residues may be prepared by *in vitro* synthesis. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the lung cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

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While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed lung cancer variants screened for the optimal combination of desired activity. Techniques exist for making substitution mutations at predetermined sites in DNA having a known sequence, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of lung cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be occasionally tolerated. Deletions generally range from about 1 to about 20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. Larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of a lung cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Variants typically exhibit essentially the same qualitative biological activity and will elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of lung cancer proteins as needed. Alternatively, the

variant may be designed or reorganized such that a biological activity of the lung cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

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Covalent modifications of lung cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a lung cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a lung cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking lung cancer polypeptides to a water-insoluble support matrix or surface for use in a method for purifying anti-lung cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl or tyrosyl residues, methylation of the γ-amino groups of lysine, arginine, and histidine side chains (Creighton (1983) Proteins: Structure and Molecular Properties, pp. 79-86), acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the lung cancer polypeptide encompassed by this invention is an altered native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended herein to mean adding to or deleting one or more carbohydrate moieties of a native sequence lung cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express lung cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to lung cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence lung cancer polypeptide (for O-linked glycosylation sites). The lung cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the lung cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the lung cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330, and in Aplin and Wriston (1981) CRC Crit. Rev. Biochem., pp. 259-306.

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Removal of carbohydrate moieties present on the lung cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al. (1987)

Arch. Biochem. Biophys., 259:52 and by Edge, et al. (1981) Anal. Biochem., 118:131.

Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura, et al. (1987) Meth.

Enzymol., 138:350.

Another type of covalent modification of lung cancer comprises linking the lung cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4.640.835; 4.496,689; 4.301,144; 4,670,417; 4,791,192, or 4,179,337.

Lung cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a lung cancer polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a lung cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the lung cancer polypeptide. The presence of such epitope-tagged forms of a lung cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the lung cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a lung cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known and examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies

WO 02/086443 PCT/US02/12476 thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes

Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) <u>Protein</u>

<u>Engineering</u> 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) <u>BioTechnology</u> 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) <u>Science</u>

255:192-194); tubulin epitope peptide (Skinner, et al. (1991) <u>J. Biol. Chem.</u> 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) <u>Proc. Nat'l</u>

Also included are other lung cancer proteins of the lung cancer family, and lung cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related lung cancer proteins from primates or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include unique areas of the lung cancer nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. PCR reaction conditions are well known in the art (e.g., Innis, PCR Protocols, *supra*).

Antibodies to lung cancer proteins

Acad. Sci. USA 87:6393-6397).

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In a preferred embodiment, when a lung cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the lung cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller lung cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are well known (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1A-16 or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal

being immunized. Immunogenic proteins include, e.g., keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Adjuvants include, e.g., Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if nonhuman mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding (1986) Monoclonal Antibodies: Principles and Practice, pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovin, or primate origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to lung cancer protein are capable of reducing or eliminating a biological function of a lung cancer protein, in a naked form or conjugated to an effector moiety. That is, the addition of anti-lung cancer protein antibodies (either polyclonal or preferably monoclonal) to lung cancer tissue (or cells containing lung cancer) may reduce or eliminate the lung cancer. Generally, at least a 25% decrease in activity, growth, size or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the lung cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. A humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human-like antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381; Marks, et al. (1991) J. Mol. Biol. 222:581). The techniques of Cole, et al. and Boerner, et al. are also available for the preparation of human monoclonal antibodies (Cole, et al. (1985) Monoclonal Antibodies and Cancer Therapy, p. 77 and Boerner, et al. (1991) J. Immunol. 5 147(1):86-95). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This 10 approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-51; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 15 13:65-93.

By immunotherapy is meant treatment of lung cancer with an antibody raised against a lung cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

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In a preferred embodiment the lung cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted lung cancer protein.

In another preferred embodiment, the lung cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the lung cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The

antibody may cause down-regulation of the transmembrane lung cancer protein. The antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the lung cancer protein. The antibody may be an antagonist of the lung cancer protein or may prevent activation of a transmembrane lung cancer protein, or may induce or suppress a particular cellular pathway. In some embodiments, when the antibody prevents the binding of other molecules to the lung cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-α, TNF-β, IL-1, INF-γ, and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, lung cancer may be treated by administering to a patient antibodies directed against the transmembrane lung cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a lung cancer protein. In another aspect the therapeutic moiety may modulate an activity of molecules associated with or in close proximity to a lung cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase activity associated with lung cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to lung cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with lung cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against lung cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane lung cancer proteins not only serves to increase the local concentration of therapeutic moiety in the lung cancer

WO 02/086443 PCT/US02/12476 afflicted area, but also serves to reduce deleterious side effects that may be associated with

the untargeted therapeutic moiety.

In another preferred embodiment, the lung cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein or other entity which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the lung cancer protein can be targeted within a cell, i.e., the nucleus, an antibody theretomay contain a signal for that target localization, i.e., a nuclear localization signal.

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The lung cancer antibodies of the invention specifically bind to lung cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related other sequences is also important.

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Detection of lung cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the lung cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing lung cancer), in lung cancer tissue (and in some cases, for varying severities of lung cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

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"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g.,

WO 02/086443 PCT/US02/12476 normal versus lung cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that 5 expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart (1996) Nature Biotechnology 14:1675-1680, hereby 10 expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is typically at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially 15 preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the lung cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to lung cancer genes, e.g., those identified as being important in a lung cancer or disease phenotype, can be evaluated in a lung cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes.

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The lung cancer nucleic acid probes may be attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In a preferred embodiment nucleic acids encoding the lung cancer protein are detected. Although DNA or RNA encoding the lung cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a lung cancer protein is detected.

Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed *in situ*. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a lung cancer protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

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In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, lung cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of lung cancer, e.g., for prognostic or diagnostic purposes. Detection of these proteins in putative lung cancer tissue allows for detection, prognosis, or diagnosis of lung cancer or similar disease, and perhaps for selection of therapeutic strategy. In one embodiment, antibodies are used to detect lung cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the lung cancer protein is detected, e.g., by immunoblotting with antibodies raised against the lung cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the lung cancer protein find use in *in situ* imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) Methods in Cell Biology:

Antibodies in Cell Biology, volume 37. In this method cells are contacted with from one to many antibodies to the lung cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label, e.g., multicolor fluorescence or confocal imaging. In another method the primary antibody to the lung cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of lung cancer proteins. Many other histological imaging techniques are also provided by the invention.

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In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing lung cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of lung cancer proteins. Antibodies can be used to detect a lung cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous lung cancer protein or vaccine.

In a preferred embodiment, in situ hybridization of labeled lung cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including lung cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to lung cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple

genes may be useful in various combinations. As above, lung cancer probes may be attached to biochips for the detection and quantification of lung cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

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Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing lung cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-8; Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the lung cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified lung cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the lung cancer phenotype or an identified physiological function of a lung cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

Having identified differentially expressed genes herein, a variety of assays may be performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene with altered regulation in lung cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the lung cancer protein. "Modulation" thus includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing lung cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in lung cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in lung

WO 02/086443 PCT/US02/12476 cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in

expression to be induced by the test compound.

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The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the lung cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene or protein expression monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein.

In this embodiment, the lung cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of lung cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the expression of one or more lung cancer-associated sequences, e.g., a polynucleotide sequence set out in the tables. Generally, in a preferred embodiment, a test compound is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate lung cancer, modulate lung cancer proteins, bind to a lung cancer protein, or interfere with the binding of a lung cancer protein and an antibody, substrate, or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the lung cancer phenotype or the expression of a lung cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles of nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a lung cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induces a lung cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of a lung cancer protein. By "neutralize" is meant that activity of a protein and the consequent effect on the cell is inhibited or blocked.

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In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a lung cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37(9):1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature, 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913), vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et

al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661), oligocarbamates (Cho, et al. (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993) C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices, with appropriate modification, are suitable for use with the present invention. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect modulation of lung cancer gene transcription, polypeptide expression, and polypeptide activity.

High throughput assays for evaluating the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins,

U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

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In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that the nucleic acid or peptide consists of essentially random sequences of nucleotides and amino acids, respectively. Since these random peptides (or nucleic acids, discussed below) are often chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. In a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc.

Modulators of lung cancer can also be nucleic acids, as defined above.

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As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After a candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence is analyzed. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

Nucleic acid assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos.

WO 02/086443 PCT/US02/12476 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of

which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

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A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the lung cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state,

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screens are performed to identify agents that bind and/or modulate the biological activity of the gene product, or evaluate genetic polymorphisms.

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Genes can be screened for those that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a lung cancer expression pattern leading to a normal expression pattern, or to modulate a single lung cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated lung cancer tissue reveals genes that are not expressed in normal tissue or lung cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for lung cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated lung cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of lung cancer cells, that have an associated lung cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., lung cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a lung cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on lung cancer activity. By defining such a signature for the lung cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of lung cancer polypeptide activity, or of lung cancer or the lung cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the metastatic polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of lung cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian lung cancer polypeptide is typically used, e.g., mouse, preferably human.

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Assays to identify compounds with modulating activity can be performed *in vitro*. For example, a lung cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the lung cancer polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the lung cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a lung cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed

genes are sometimes referred to herein as "lung cancer proteins." The lung cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

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In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the lung cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a lung cancer protein and a candidate compound, and determining the binding of the compound to the lung cancer protein. Preferred embodiments utilize the human lung cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative lung cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the lung cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation

sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the lung cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the lung cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the lung cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the lung cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ¹²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (i.e., a lung cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40° C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically

between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

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In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the lung cancer protein and thus is capable of binding to, and potentially modulating, the activity of the lung cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the lung cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the lung cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the lung cancer proteins. In one embodiment, the methods comprise combining a lung cancer protein and a competitor in a first sample. A second sample comprises a test compound, a lung cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the lung cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the lung cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native lung cancer protein, but cannot bind to modified lung cancer proteins. The structure of the lung cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a lung cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results.

Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

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A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a lung cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising lung cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a lung cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate lung cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the lung cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting lung cancer cell division is provided. The method comprises administration of a lung cancer inhibitor. In another embodiment, a method of inhibiting lung cancer is provided. The method may comprise administration of a lung cancer inhibitor. In a further embodiment, methods of treating cells or individuals with lung cancer are provided, e.g., comprising administration of a lung cancer inhibitor.

In one embodiment, a lung cancer inhibitor is an antibody as discussed above. In another embodiment, the lung cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

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Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of lung cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) <u>Culture of Animal Cells a Manual of Basic Technique</u> (3rd ed.), herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a lung cancer-associated sequence and are grown for 24 hours at saturation density in

PCT/US02/12476 WO 02/086443 non-limiting medium conditions. The percentage of cells labeling with (3H)-thymidine is

determined autoradiographically. See, Freshney (1994), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal

counterparts (see, e.g., Temin (1966) J. Natl. Cancer Insti. 37:167-175; Eagle, et al. (1970) J.

Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth

factors by the transformed cells. Growth factor or serum dependence of transformed host

cells can be compared with that of control.

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Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA)

is released from human glioma at a higher level than from normal brain cells (see, e.g.,

Gullino, "Angiogenesis, tumor vascularization, and potential interference with tumor growth"

in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184). Similarly, Tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal

counterparts. See, e.g., Folkman (1992) "Angiogenesis and Cancer" in Sem Cancer Biol.).

Various techniques which measure the release of these factors are described in

Freshney (1994), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305;

Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer

42:305-312; Gullino, "Angiogenesis, tumor vascularization, and potential interference with

tumor growth" in Mihich (ed. 1985) Biological Responses in Cancer, pp. 178-184; Freshney

Anticancer Res. 5:111-130 (1985).

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Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate lung cancerassociated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ¹²⁵I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

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Effects of lung cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the lung cancer gene is disrupted or in which a lung cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous lung cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous lung cancer gene with a mutated version of the lung cancer gene, or by mutating the endogenous lung cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, Cold Spring Harbor Laboratory and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) <u>J. Natl. Cancer Inst.</u> 52:921), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) <u>Br. J. Cancer</u> 38:263; Selby, et al. (1980) <u>Br. J. Cancer</u> 41:52) can be used as a host. Transplantable tumor cells (typically about 10⁶ cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a lung cancer-associated sequences are injected subcutaneously. After a suitable length of time,

preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

5 Polynucleotide modulators of lung cancer

Antisense and RNAi Polynucleotides

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In certain embodiments, the activity of a lung cancer-associated protein is downregulated, or entirely inhibited, by the use of antisense or an inhibitory polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a lung cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or intersugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the lung cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the antisense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for lung cancer molecules. A preferred antisense molecule is for a lung cancer sequence in the tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein

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is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659 and van der Krol, et al.
(1988) BioTechniques 6:958).

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) <u>Sciencexpress</u> (21March2002); Sharp (1999) <u>Genes Dev.</u> 13:139-141; and Cathew (2001) <u>Curr. Op. Cell Biol.</u> 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) <u>Nature</u> 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

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Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of lung cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126).

Polynucleotide modulators of lung cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of lung cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by

formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

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Thus, in one embodiment, methods of modulating lung cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-lung cancer antibody that reduces or eliminates the biological activity of an endogenous lung cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a lung cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the lung cancer sequence is down-regulated in lung cancer, such state may be reversed by increasing the amount of lung cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous lung cancer gene or administering a gene encoding the lung cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety.

Alternatively, e.g., when the lung cancer sequence is up-regulated in lung cancer, the activity of the endogenous lung cancer gene is decreased, e.g., by the administration of a lung cancer antisense or RNAi nucleic acid.

In one embodiment, the lung cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to lung cancer proteins. Similarly, the lung cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify lung cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a lung cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The lung cancer antibodies may be coupled to standard affinity chromatography columns and used to purify lung cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the lung cancer protein.

Methods of identifying variant lung cancer-associated sequences

Without being bound by theory, expression of various lung cancer sequences is correlated with lung cancer. Accordingly, disorders based on mutant or variant lung cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant lung cancer genes, e.g., determining all or part of the sequence of at least one endogenous lung cancer genes in a cell. In a preferred embodiment, the invention provides methods of identifying the lung cancer genotype of an individual, e.g., determining all or part of the sequence of at least one lung cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced lung cancer gene to a known lung cancer gene, i.e., a wild-type gene.

The sequence of all or part of the lung cancer gene can then be compared to the sequence of a known lung cancer gene to determine if any differences exist. This can be done using known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the lung cancer gene of the patient and the known lung cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the lung cancer genes are used as probes to determine the number of copies of the lung cancer gene in the genome.

In another preferred embodiment, the lung cancer genes are used as probes to determine the chromosomal localization of the lung cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the lung cancer gene locus.

Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of a lung cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel, et al. (1992) Pharmaceutical Dosage Forms and Drug Delivery; Lieberman, Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding; and Pickar (1999) Dosage Calculations). Adjustments for lung cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration,

drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

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The administration of the lung cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the lung cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a lung cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose,

lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

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The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that lung cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a lung cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman, et al. (eds. 1996) Goodman and Gilman: The Pharmacologial Basis of Therapeutics).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman, The Pharmacologial Basis of Therapeutics, supra.

The compositions containing modulators of lung cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

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It will be appreciated that the present lung cancer protein-modulating compounds can be administered alone or in combination with additional lung cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the tables, such as antisense or RNAi polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of lung cancer-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo*, or *in vivo* (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g.,

Berger and Kimmel, <u>Guide to Molecular Cloning Techniques</u>, <u>Methods in Enzymology</u> volume 152 (Berger), Ausubel, et al. (eds. 1999) <u>Current Protocols</u> (supplemented through 1999), and Sambrook, et al. (1989) <u>Molecular Cloning - A Laboratory Manual</u> (2nd ed., Vol. 1-3).

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In a preferred embodiment, lung cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, lung cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the lung cancer coding regions) can be administered in a gene therapy application. These lung cancer genes can include antisense or inhibitory applications, e.g., as inhibitory RNA or gene therapy (e.g., for incorporation into the genome) or as antisense compositions.

Lung cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p. 379 In: Kaufmann (ed. 1996) Concepts in vaccine development; Chakrabarti, et al. (1986) Nature 320:535; Hu, et al. (1986) Nature 320:537; Kieny, et al. (1986) AIDS Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148; Chanda, et al. (1990) Virology 175:535), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25; Eldridge, et al. (1993) Sem. Hematol. 30:16; Falo, et al. (1995) Nature Med. 7:649), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369; Gupta, et al. (1993) Vaccine 11:293), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585; Rock (1996) Immunol. Today 17:131), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745; Robinson, et al. (1993) Vaccine 11:957; Shiver, et al., p. 423 In: Kaufmann (ed. 1996) Concepts in vaccine development; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923 and Eldridge, et al. (1993) Sem. Hematol. 30:16). Toxin-targeted

delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

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Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bortadella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et. al. (1990) Science 247:1465 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode lung cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the

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To will be apparent to those skilled in the art from the description herein (see e.g. Shata e.g.

like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85).

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Methods for the use of genes as DNA vaccines are well known, and include placing a lung cancer gene or portion of a lung cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a lung cancer patient. The lung cancer gene used for DNA vaccines can encode full-length lung cancer proteins, but more preferably encodes portions of the lung cancer proteins including peptides derived from the lung cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a lung cancer gene. For example, lung cancer-associated genes or sequence encoding subfragments of a lung cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the lung cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment lung cancer genes find use in generating animal models of lung cancer. When the lung cancer gene identified is repressed or diminished in metastatic tissue, gene therapy technology, e.g., wherein antisense or inhibitory RNA directed to the lung cancer gene will also diminish or repress expression of the gene. Animal models of lung cancer find use in screening for modulators of a lung cancer-associated sequence or modulators of lung cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the lung cancer protein. When desired, tissue-specific expression or knockout of the lung cancer protein may be necessary.

It is also possible that the lung cancer protein is overexpressed in lung cancer. As such, transgenic animals can be generated that overexpress the lung cancer protein.

Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene.

Animals generated by such methods will find use as animal models of lung cancer and are additionally useful in screening for modulators to treat lung cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications such kits may include at least one of the following: assay reagents, buffers, lung cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, RNAi, dominant negative lung cancer polypeptides or polynucleotides, small molecule inhibitors of lung cancer-associated sequences, etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of lung cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a lung cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing lung cancer-associated activity. Optionally, the kit contains biologically active lung cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes typically will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

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Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Tables 1A and 1B were previously filed on April 18, 2001 in USSN 60/284,770 (18501-001500US) and on November 29, 2001 in USSN 60/334,370 (18501-001520US)

5	Table 1A					
•	Pkey	ExAccn	UnigenelD	Unigene Title	70% chron/90% NL	70% SQAD/90% NL
	100134	D13264	Hs.49	macrophage scavenger receptor 1	1.61	0.74
	100780	HG3731-HT4001		mmunoglobulin Heavy Chain, Vdjrc Reg	2.68	3.28
10	100971 101088	J02874 L05568	Hs.83213 Hs.553	fatty acid binding protein 4; adipocyte solute carrier family 6 (neurotransmitte	1.96 0.79	0.14 0.07
10	101102	L07594	Hs.79059	transforming growth factor; beta recepto	2.55	1
	101168	L15388	Hs.211569	G protein-coupled receptor kinase 5	0.88	0.27
	101277	L38486	Hs.118223	microfibrillar-associated protein 4	0.89	0.26
15	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do FBJ murine osteosarcoma viral oncogene h	0.59 1.15	0.29 0.41
13	101336 101345	L49169 L76380	Hs.75678 Hs.152175	calcitonin receptor-like	0.81	0.31
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	1.31	0.77
	101764	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	1.44	0.82
20	101771	M81750 M93221	Hs.153837	myeloid cell nuclear differentiation ant	0.96 1.27	0.45 0.37
20	101842 102283	W33221 U31384	Hs.75182 Hs.83381	mannose receptor, C type 1 quanine nucleotide binding protein 11	1.04	0.3
	102363	U39447	Hs.198241	amine oxidase; copper containing 3 (vasc	0.96	0.26
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel; s	2.81	3.45
25	102698	U75272	Hs.1867	progastricsin (pepsinogen C)	0.95 1.62	0.23 0.21
23	103025 103280	X54131 X79981	Hs.123641 Hs.76206	protein tyrosine phosphatase; receptor t cadherin 5; VE-cadherin (vascular epithe	0.9	0.41
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2	1.27	0.49
	103541	Z11697	Hs.79197	CD83 antigen (activated B lymphocytes; I	1.86	1
30	103554	Z18951	Hs.74034	caveolin 1; caveolae protein; 22kD	1.27 1.17	0.47 0.16
30	104212 104691	AB002298 AA011176	Hs.173035 Hs.37744	KIAA0300 protein ESTs	1.08	0.35
	104825	AA035613	Hs.141883	ESTs	0.75	0.27
	104857	AA043219	Hs.19058	ESTs	2.6	3.3
35	104865	AA045136	Hs.22575	ESTs	1.23 0.63	Q.49 Q.32
33	104989 105729	AA102098 AA292694	Hs.118615 Hs.3807	ESTs ESTs; Weakly similar to PHOSPHOLEMMAN PR	0.86	0.34
	105847	AA398606	Hs.32241	ESTs	1.32	0.4
	105894	AA400979	Hs.25691	calcitonin receptor-like receptor activi	0.78	0.28
40	106490	AA451861	Hs.115537	ESTs; Weakly similar to dipeptidase prec	1.2 0.82	0.47 0.15
40	106536 106605	AA453997 AA457718	Hs.23804 Hs.21103	ESTs Homo sapiens mRNA; cDNA DKFZp564B076 (fr	0.99	0.07
	106667	AA461086	Hs.16578	ESTs	1.17	0.4
	106773	AA478109	Hs.188833	ESTs	1.46	0.43
45	106797	AA478962	Hs.169943	ESTS	1.18 0.98	0.32 0.51
45	106844 106870	AA485055 AA487576	Hs.158213 Hs.26530	sperm associated artigen 6 serum deprivation response (phosphatidy)	1.05	0.14
	106954	AA496980	Hs.204038	ESTs	1.25	0.33
	107054	AA600150	Hs.14366	ESTs	1.11	0.4
50	107292 107994	T30407 AA036811	Hs.4789 Hs.165030	ESTs; Weakly similar to oxidative-stress ESTs	1.07 0.7	2.58 0.21
50	107997	AA037388	Hs.82223	Human DNA sequence from clone 141H5 on c	1.02	0.48
	108041	AA041552	Hs.61957	ESTs	1.44	0.51
	108087	AA045709	Hs.40545	ESTs	1.98 1.52	1 0.72
55	108382 108435	AA074885 AA078787	Hs.67726 Hs.194101	macrophage receptor with collagenous str ESTs	2.53	1.53
55	108480	AA081093	Hs.68055	ESTs	1.56	0.48
	109252	AA194830	Hs.85944	ESTs .	2.69	3.18
	109550	F01534	Hs.26981	ESTs	1.19 1.01	0.65 0.29
60	109613 109837	F03031 H00656	Hs.27519 Hs.29792	ESTs ESTs	0.81	0.25
00	109893	H04768	Hs.30484	ESTs	1.44	0.32
	109984	H09594	Hs.10299	ESTs	0.62	0.14
	110099	H16568 N30796	Hs.23748	ESTs ESTs; Weakly similar to semaphorin F [H.	1.01 1.1	0.28 0.22
65	110837 111247	N69825	Hs.17424 Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.26	0.26
00	111341	N80935	Hs.22483	ESTs	1.57	0.52
	111510	R07856	Hs.16355	ESTs	3.96	1
	111737	R25410	Hs.9218	ESTs "yc20g11.s1 Stratagene lung (#937210) .	0.97 1.22	0.24 0.35
70	113195 113238	T57112 T62979	Hs.189813	ESTs	2.27	0.45
	113540	T90496	Hs.16757	ESTs	1.06 -	0.22
	113552	T90889	Hs.16026	ESTs	1.16	0.42
	113606	T93093	Hs.17125	ESTs	1.48 1.54	0.7 0.28
75	113695 113946	T96965 W84753	Hs.17948 Hs.37896	ESTs ESTs	1.79	0.26
	114251	Z39898	Hs.21948	ESTs	1.95	0.25
	114359	Z41589	Hs.153483	ESTs; Moderately similar to H1 chloride	1.42	0.13
	115230	AA278300 AA279760	Hs.182980 Hs.63671	ESTs ESTs	2.62 1.79	0.42 0.91
80	115279 115566	AA398083	Hs.43977	ESTs ESTs	0.86	0.2
	115965	AA446661	Hs.173233	ESTs	0.79	0.04
	116166	AA461556	Hs.202949	KIAA1102 protein	2.29	0.68
	116279	AA486073 H88157	Hs.57362 Hs.41105	ESTs ESTs	2.27 1.36	0.78 · 0.16
	117023	.100101	110171100	20.0	****	

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	117209	H99959	Hs.42768	ESTs	1.46	0.48 1	
	118901 118981	N90719 N93839	Hs.94445 Hs.39288	ESTs ESTs	1.51 1.34	0.48	
_	119073	R32894	Hs.45514	v-ets avian erythroblastosis virus E26 o	1.14	0.27	
5	119221	R98105		""yr30g11.s1 Soares fetal liver spleen	1.32	0.53	
	119824 119861	W74538	Hs.184	advanced glycosylation end product-spect ESTs; Moderately similar to !!!! ALU SUB	1 1.83	0.19 0.45	
	120041	W80715 W92775	Hs.59368	ESTs	1.23	0.55	
10	120132	Z38839	Hs.125019	ESTs; Highly similar to KIAA0886 protein	0.91	0.37	
10	120467	AA251579	Hs.187628	ESTs	1.87 1.3	1.91 0.31	
	121314 121643	AA402799 AA417078	Hs.182538 Hs.193767	ESTs ESTs	2.31	0.68	
	121690	AA418074	Hs.110286	ESTs	1.47	0.51	
15	122633	AA454080	Hs.34853	inhibitor of DNA binding 4; dominant neg	1.31 1.52	0.63 0.32	
15	123978 124214	C20653 H58608	Hs.170278 Hs.151323	ESTs ESTs	0.93	0.35	
	124357	N22401	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	""yw37g07.s1 Morton Fetal Cochlea Homo	1.29	1	
	124438	N40188	Hs.102550	ESTs	1.36 1.46	0.7 0.69	
20	125167 125174	W45560 W51835	Hs.102541 Hs.231082	ESTS EST	3.07	3.76	
20	125422	AA903229	Hs.153717	ESTs	1.34	0.3	
	125561	Al417667	Hs.22978	ESTs	1.89	0.63 0.36	
	125831 127002	D60988 R35380	Hs.24979	***HUM145809B Clontech human fetal brain ESTs	0.94 3.02	4.06	
25	127307	AA369367	Hs.126712	ESTs; Weakly similar to plL2 hypothetica	1.01	0.69	
	127609	AA622559	Hs.150318	ESTs	1.21	0.32	
	127959 128458	Al302471 D52193	Hs.124292 Hs.56340	ESTs ESTs	2.5 1.13	1 0.33	
	128624	AA479209	Hs.102647	ESTs	1.45	0.58	
30	128789	AA486567	Hs.105695	ESTs	1.1	0.34	
	128798	AF014958 R51076	Hs.105938 Hs.107361	chemokine (C-C motif) receptor-like 2 ESTs; Highly similar to Rap2 interacting	1.16 2.04	0.55 2.4	
	128952 129057	X62466	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	1.77	0.73	
2.5	129210	AA401654	Hs.202949	KIAA1102 protein	1,11	0.36	
35	129240	W24360	Hs.237868	Interleukin 7 receptor ""yc21g01.s1 Stratagene lung (#937210)	0.91 1.36	0.41 0.43	
	129402 129565	T63781 X77777	Hs.198726	vasoactive intestinal peptide receptor 1	0.67	0.08	
	129593	AA487015	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	1.3	0.42	
40	129626	AA447410	Hs.11712 Hs.12017	ESTs; Weakly similar to !!!! ALU SUBFAM! KIAA0439 protein; homolog of yeast ubiqu	1.28 1.58	0.46 1	
40	129699 129898	AA458578 N48595	Hs.13256	ESTs	1.13	0.53	
	129958	L20591	Hs.1378	annexin A3	0.81	0.31	
	130273	U59914	Hs.153863	MAD (mothers against decapentaplegic; Dr	0.59 1.44	0.22 0.76	
45	130655 130657	N92934 T94452	Hs.17409 Hs.201591	cysteine-rich protein 1 (Intestinal) ESTs	0.96	0.42	
	131061	N64328	Hs.22567	ESTs; Moderately similar to HYPOTHETICAL	1.51	0.45	
	131066	F09006	Hs.22588 Hs.24950	ESTs regulator of G-protein signalling 5	0.97 2.34	0.37 2.82	
	131263 131589	R38334 U52100	Hs.29191	epithelial membrane protein 2	1.2	0.62	
50	131686	AA157428	Hs.30687	Grb2-associated binder 2	0.95	0.38	
	131751	H18335	Hs.31562 Hs.258675	ESTS EST	1.47 1.86	0.52 2.09	
	132430 132476	T23630 N67192	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	1.73	0.58	
	132836	F09557	Hs.57929	slit (Drosophila) homolog 3	0.91	0.29	
55	133120	X64559	Hs.65424 Hs.74120	tetranectin (plasminogen-binding protein adipose specific 2	0.82 1.29	0.2 0.48	
	133488 133565	D45370 H57056	Hs.204831	ESTs	2.25	0.57	
	133651	U97105	Hs.173381	dihydropyrimidinase-like 2	1.65	0.62	
60	133835	AA059489	Hs.76640	ESTs; Highly similar to RGC-32 [R.norveg transcription factor 21	1.16 0.79	0.34 0.27	
UU	133978 133985	W73859 L34657	Hs.78061 Hs.78146	platelet/endothellal cell adhesion molec	0.99	0.28	
	134299	AA487558	Hs.8135	ESTs	1.02	0.46	
	134300	U81984 AA028976	Hs.166082 Hs.8175	endothelial PAS domain protein 1. Homo saplens mRNA; cDNA DKFZp564M0763 (f	0.86 1.19	0.42 0.27	
65	134323 134343	D50683	Hs.82028	transforming growth factor, beta recepto	1.21	0.67	
	134417	D87969	Hs.82921	solute carrier family 35 (CMP-stalic aci	1.28	1	
	134561	U76421	Hs.85302 Hs.8700	adenosine dearninase; RNA-specific; B1 (h deleted in liver cancer 1	2.12 2.35	0.55 2.74	
	134624 134696	W67147 H88354	Hs.8861	ESTs	1.35	0.33	
70	134749	L10955	Hs.89485	carbonic anhydrase IV	0.89	0.2	
	134786	L06139	Hs.89640	TEK tyrosine kinase; endothelial (venous ESTs; Moderately similar to IIII ALU SUB	0.48 2.14	0.21 2.64	
	134869 135346	T35288 M21056	Hs.90421 Hs.992	phospholipase A2; group (B (pancreas)	0.63	0.13	
a -	100113	D00591	Hs.84746	Chromosome condensation 1	1	2.15	
75	100147	D13666	Hs.136348	Homo sapiens mRNA for osteoblast specifi	0.5 1.02	2 1.39	
	100280 100335	D42085 D63391	Hs.155314 Hs.6793	KIAA0095 gene product platelet-activating factor acetylhydrola	1.02	5.58	
	100360	D78335	Hs.75939	Uridine monophosphate kinase	0.91	2.04	
80	100372	D79997	Hs.184339	KIAA0175 gene product TIGR: ras-like protein TC4	0.75 1.09	2.03 1.93	
ou	100486 100559	HG1112-HT11 HG2197-HT22		"collagen, type VII, alpha 1"	0.97	3.6	
	100576	HG2290-HT23	86	"calcitonin/alpha-CGRP, all. transcript	1	1	
	100668	HG2981-HT393		*TIGR: CD44 (apican, alt. transcript 12 Guanosine 5-Monophosphate Synthase	0.85 1.18	1.9 2.29	
85	100906 100930	HG4716-HT51: HG721-HT482		"TIGR: placental protein 14, endometrial	1	1.45	
-				•			

	W	O 02/086	443			
	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	0.84	2.6
	101031	J05070	Hs.151738	*Matrix metalloproteinase 9 (gelatinase	0.77	1.52
	101111	L08424	Hs.1619	Achaete-scute complex (Drosophila) homol	1	1
	101124	L10343	Hs.112341	*Protease Inhibitor 3, skin-derived (SKA	0.62	2.67
5	101175	L18920	Hs.36980	"Melanoma antigen, family A, 2"	1	1
	101204		Hs.82237		0.74	4.1
	101431	L24203		Ataxia-telangiectasia group D-associated		
		M19888	Hs.1076	Small proline-rich protein 1B (cornifin)	0.85	2.51
	101448	M21389	Hs.195850	keratin 5 (epidermolysis bullosa simplex	. 0.61	8.83
10	101511	M27826	Hs.267319	Endogenous retroviral protease	1.03	1.13
10	101526	M29540	Hs.220529	Carcinoembryonic antigen-related cell ad	1.07	4.61
	101548	M31328	Hs.71642	*Guanine nucleotide binding protein (G p	0.97	1.13
	101625	M57293		"Human parathyroid hormone-related pepti	1	1
	101649	M60047	Hs.1690	Heparin-binding growth factor binding pr	1	2.7
	101724	M69225	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	1	8.98
15	101748	M76482	Hs.1925	Desmoglein 3 (pemphigus vulgaris antigen	1	2.78
	101759	M80244	Hs.184601	"Solute carrier family 7 (cationic amino	1.07	2.45
	101804	M86699	Hs.169840	TTK protein kinase	1	1
	101806	MB6757	Hs.112408	S100 calcium-binding protein A7 (psorias	0.74	1.76
			113.112400	"Homo sapiens connexin 26 (GJB2) mRNA, c		7
20	101809	M86849	11. 20002		1	í
20	101845	M93426	Hs.78867	"Protein tyrosine phosphatase, receptor-	1	
	101851	M94250	Hs.82045	Midkine (neurite growth-promoting factor	1.13	2.6
	102083	U10323	Hs.75117	"Interleukin enhancer binding factor 2,	1.03	1.61
	102154	U17760	Hs.75517	"Laminin, beta 3 (nicein (125kD), kalini	0.94	3.62
~~	102193	U20758	Hs.313	secreted phosphoprotein 1 (osteopontin;	0.34	4.59
25	102305	U33286	Hs.90073	chromosome segregation 1 (yeast homolog)	1.45	2.97
	102348	U37519	Hs.87539	Aldehyde dehydrogenase 8	0.52	2.25
	102581	U61145	Hs.77256	Enhancer of zeste (Drosophila) homolog 2	0.91	2.46
	102610	U65011	Hs.30743	Preferentially expressed antigen in mela	1	3.88
	102623	U66083	Hs.37110	"Melanoma antigen, family A, 9 (MAGE-9)"	i	1
30	102669	U71207	Hs.29279	Eyes absent (Drosophila) homolog 2	Í	1
	102696	U74612	Hs.239	Forkhead box M1	1.06	2.77
	102829	U91618	Hs.80962	Neurotensin	1	1
	102888		Hs.76118	Ubiquitin carboxyl-terminal esterase L1	1.13	2.59
		X04741				4.72
35	102913	X07696	Hs.80342	keratin 15	0.7	
33	102915	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin	1.15	3.35
	102963	X15943	Hs.37058	"Calcitonin/calcitonin-related polypepti	1	1
	103021	X53587	Hs.85266	"Integrin, beta 4"	1.38	2.34
	103036	X54925	Hs.83169	Matrix metalloprotease 1 (interstitial c	1	14.93
40	103058	X57348	Hs.184510	Stratifin	1.25	4.17
40	103060	X57766	Hs.155324	matrix metalloproteinase 11 (stromelysin	1	1.72
	103119	X63629	Hs.2877	"Cadherin 3, P-cadherin (placental)"	1.16	7.38
	103206	X72755	Hs.77367	monokine induced by gamma interferon	0.71	1.48
	103242	X76342	Hs.389	*Alcohol dehydrogenase 7 (class IV), mu	1	1
	103312	X82693	Hs.3185	"Lymphocyte antigen 6 complex, locus D;	0.92	1.28
45	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	1.05	5.81
	103558	Z19574	Hs.2785	keratin 17	0.65	6.68
	103576	Z26317	Hs.2631	Desmoglein 2	0.79	1.73
	103587	Z29083 .	Hs.82128	5T4 Oncofetal antigen	1	3.93
	103594				0.71	7.23
50		Z31560	Hs.816	"SRY (sex determining region Y)-box 2, p		
50	103768	AA089997	11. 0407	ESTs, Highly similar to integral membra	0.99	1.8
	104158	AA454908	Hs.8127	KIAA0144 gene product	0.96	1.29
	104558	R56678	Hs.88959	Human DNA sequence from clone 967N21 on	1.23	7.23
	104689	AA010665		ESTs	0.96	2.11
e e	104733	AA019498	Hs.23071	ESTs	1.18	1.88
55	104906	AA055809	Hs.26802	Protein kinase domains containing protei	1.11	3.15
	104978	AA088458	Hs.19322	ESTs; Weakly similar to !!!! ALU SUBFAM!	1.64	2,89
	105012	AA116036	Hs.9329	"Homo sapiens mRNA for fls353, complete	1.19	3.91
	105175	AA186804	Hs.25740	ESTs; Weakly similar to unknown (S.cerev	0.9	4.63
	105263	AA227926	Hs.6682	ESTs	0.95	2.87
60	105298	AA233459	Hs.26369	ESTs	1	1.13
	105312	AA233854	Hs.23348	S-phase kinase-associated protein 2 (p45	1.32	3.01
	105719	AA291644	Hs.36793	Hypothetical protein FLJ23188	1.28	2.31
	105743	AA293300	Hs.9598	ESTs	1	1
		AA411621	Hs.8895	ESTs; same as BFH6?	0.94	2.04
65			Hs.38002		1.04	1.5
05	106231	AA429571		KIAA1355 protein		
	106540	AA454607	Hs.38114	Hypothetical protein FLJ11100	1.26	2.26
	106575	AA456039	Hs.105421	ESTs	1	2
	105632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	0.87	1.32
~^	106727	AA465342	Hs.34045	Hypothetical protein FLJ20764	0.87	1.59
70	106906	AA490237	Hs.222024	Transcription factor BMAL2 (cycle-like f	0.61	1.6
	107059	AA608545	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	0.48	2.67
	107104	AA609786	Hs.15243	Nucleolar protein 1 (120kD)	1.01	1.44
	107151	AA621169	Hs.8687	ESTs; procollagen I-N proteinase	0.97	2.89
	107284	S74039	Hs.291904	Accessory proteins BAP31/BAP29	1.15	3.65
75	107901	AA026418	Hs.91539	ESTs	0.72	3.44
	107922	AA028028	Hs.61460	lg superfamily receptor LNIR precursor	1	2.48
	107932				i	1
		AA029317	Hs.18878	Hypothetical protein FLJ21620	0.91	
	108695	AA121315	Hs.70823	KIAA1077 protein		3.53
QΛ	108857	AA133250	Hs.62180	ESTS	1	1 70
80	108860	AA133334	Hs.129911	ESTs	0.73	7.3
	108990	AA152296	Hs.72045	ESTs	1	1
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	1	4.55
	109424	AA227919	Hs.85962	Hyaluronan synthase 3	1	1.28
	109665	F05012	Hs.27027	Hypothetical protein DKFZp762H1311	1.42	2
85	109970	H09281	Hs.13234	ESTs	1.13	2.16

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	110015	H10998		A disintegrin and metalloproteinase doma	0.84 0.94	1.95 1.41		
	110156 110561	H18957 H59617	Hs.4213 Hs.5199	ESTs HSPC150 protein similar to ubiquitin-con	0.91	3.18		
_	111223	N68921	Hs.34806	ESTs; Weakly similar to neogenin [H.sapi	0.91	3.13		
5	111345	N89820	Hs.14559	Hypothetical protein FLJ 10540	1 0.83	1.25 1.27		
	111876 111902	R38239 R39191	Hs.293246 Hs.109445	*ESTs, Weakly similar to putative p150 [KIAA1020 protein	0.03	0.91		
	112244	R51309	Hs.70823	KIAA1077 protein	0.77	3.01		
10	112973	T17271		*cDNA FLJ13308 fis, clone OVARC1001436,	1	1 1.03		
10	112989 113047	T23482 T25867	Hs.89981 Hs.7549	"Diacylglycerol kinase, zeta (104kD)" ESTs	0.55 0.87	2		
	113047	T40920	Hs.126733	ESTs	1	1		
	113531	T90345	Hs.16740	Hypothetical protein FLJ11036	0.42	1.44		
15	113970	W86748	Hs.8109 Hs.130489	ESTs *ATPase, aminophospholipid transporter-I	1.17 0.86	1.73 0.82		
13	114346 114407	Z41450 AA010188	Hs.103305	ESTs	0.8	1.88		
	114471	AA028074	Hs.104613	RP42 homolog	1.06	1.34		
	114509	AA043551	Hs.101799	*Gap junction protein, beta 5 (connexin	1.82 0.79	2.32 1.49		
20	115060 115091	AA253214 AA255900	Hs.198249 Hs.184523	KIAA0965 protein	0.72	1.92		
	115123	AA256642	Hs.236894	*ESTs, High sim to LRP1_hu low density I	0.59	1.97		
	115291	AA279943	Hs.122579	ESTs Hypothetical protein KIAA1335	1 1.15	1.25 1.48		
	115506 115522	AA292537 AA331393	Hs.45207 Hs.47378	ESTs	0.5	3.29		
25	115536	AA347193	Hs.62180	ESTs	1	1		
	115697	AA411502	Hs.63325	Homo sapiens type II membrane serine pro	1	6.53 6.98		
	115909 115978	AA436666 AA447522	Hs.59761 Hs.69517	ESTs Differentially expressed in Fanconi anem	i	2.31		
	116028	AA452112	Hs.42644	thioredoxin-like	0.99	1.68		
30	116107	AA456968	Hs.92030	ESTs	1.14 1.11	1.8 1.86		
	116134 116157	AA460246 AA461063	Hs.50441 Hs.44298	CGI-04 protein Hypothetical protein	0.99	1.9		
	116158	AA461187	Hs.61762	Hypoxia-inducible protein 2	0.44	0.86		
25	116335	AA495830	Hs.87013	"Homo sapiens cDNA FLJ10238 fis, clone H	0.62 1.04	3.89 2.36		
35	116483 117320	C14092 N23239	Hs.76118 Hs.211092	Ubiquitin carboxyl-terminal esterase L1 LUNX protein; PLUNC(palate lung & nasal	0.51	0.64		
	117557	N33920	Hs.44532	Diubiquitin	1.11	2.63		
	117693	N40939	Hs.112110	PTD007 protein	0.98 1	1.79 1.43		
40	117881 118368	N50073 N64339	Hs.260622 Hs.48956	Butyrate-induced transcript 1 ESTs	0.67	2.86		
-10	118566	N68558	Hs.42824	Hypothetical protein FLJ10718	1.21	0.83		
	118695	N71781	Hs.50081	KIAA1199 see CVA7.doc	0.88 1	1.63 1		
	119780 119845	W72967 W79920	Hs.191381 Hs.58561	ESTs; Weakly similar to hypothetical pro G protein-coupled receptor 87	i	i		
45	120102	W95428	Hs.132927	"ESTs, Moderately similar to p53 regulat	1	1		
	120104	W95477	Hs.180479	ESTs Tumor protein 63 kDa with strong homolog	0.69 1.08	3.07 12.05		
	120486 120859	AA253400 AA350158	Hs.137569 Hs.1619	Achaele-scute complex (Drosophila) homo!	1	1		
~ ^	120880	AA360240	Hs.97019	EST	1	1		
50	120948	AA397822	Hs.104650	Hypothetical protein FLJ10292 EST	1.04 1	2.15 1		
	120983 121362	AA398209 AA405500	Hs.97587 Hs.97932	Chondromodulin I precursor	i	i		
	121369	AA405657	Hs.128791	CGI-09 protein	1	1.8		
55	121791	AA423978	Hs.293317	"ESTs, Weakly similar to JM27 (H.sapiens ESTs	1	1		
22	123005 123044	AA479726 AA481549	Hs.105577 Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	0.95	1.88		
	123160	AA488687	Hs.284235	ESTs	1.59	4.98		
	123479	AA599469	Hs.135056	clone RP5-850E9 on chromosome 20	1.19 1.03	1.64 1.14		
60	123571 123829	AA608956 AA620697	Hs.112619 Hs.112208	"ESTs, Weakly similar to PQ0109 Purkinje XAGE-1 prolein-	1.39	2.2		
•	124006	D60302	Hs.108977	ESTs	1	4.85		
	124059	F13673	Hs.99769	ESTs Selzure related gene 6 (mouse)-like	1.49 0.76	- 8.62 0.77		
	124960 125218	T15386 W73561	Hs.194766 Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33	1.77		
65	125453	R06041	Hs.18048	"Melanoma antigen, family A, 10"	0.8	1.42		
	125759	AA425587	Hs.82226	Glycoprotein (transmembrane) nmb "ESTs, Highly similar to unnamed protein	1.52 1.05	2.26 2.48		
	125972 125994	AA434562 H55782	Hs.35406 Hs.270799	EST	1	1.95		
~ 0	126395	N70192	Hs.278956	Hypothetical protein FLJ12929 .	1	1.35		
70	126645	Al167942	Hs.61635 Hs.72365	STEAP1 (Homo sapiens BAC clone RG041D11 ESTs	1 0.73	2.23 3.27		
	127221 127479	Al354332 AA513722	Hs.179729	collagen; type X; alpha 1 (Schmid metaph	0.51	1.94		
	128192	A1204246		KIAA1085 protein	1.8	3.16		
75	128610	L38608	Hs.10247 Hs.10526	activated leucocyte cell adhesion molecu Cysteine and glycine-rich protein 2	0.89 1	0.97 1		
13	128777 128924	U46006 AA234962	Hs.10526 Hs.26557	Plakophilin 3	1.3	2.97		
	129041	H58873	Hs.169902	"Solute carrier family 2 (facilitated gl	0.84	2.04		
	129099	H50398	Hs.108660	*ATP-binding cassette, sub-family C (CFT	0.87 1	1.04 1		
80	129404 129466	AA172056 L42583	Hs.111128	ESTs "Genbank Homo sapiens keratin 6 Isoform	0.72	12.67		
	129605	S72493	Hs.115947	Keratin 16 (focal non-epidermolytic palm	0.92	1.5		
	129628	U26727	Hs.1174 Hs.239600	*Cyclin-dependent kinase inhibitor 2A (m Calmodulin-like 3	0.85 0.84	1.93 1.22		
	130023 130080	X13461 X14850	Hs.147097	"H2A histone family, member X"	0.98	1.96		
85	130385		Hs.155223	stanniocalcin 2	1	1		

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	130410	V01514	Hs.155421	Alpha-fetoprotein	0.63	0.63		
	130441 130482	U35835 L32866	Hs.301387 Hs.1578	"Human DNA-PK mRNA, partial cds" Baculoviral IAP repeat-containing 5 (sur	1.15 1	3.65 1.88		
_	130553	AA430032	Hs.252587	Pituitary tumor-transforming 1	0.92	1.96		
5	130577	M35410	Hs.162	Insulin-like growth factor binding prote	1.17	4.7		
	130627 130800	L23808	Hs.1695 Hs.19574	Matrix metalloproteinase 12 (macrophage	0.69 1.13	4.05 2.41		
	130939	AA223386 AA598689	Hs.21400	ESTs; Weakly similar to katanin p80 subu	0.8	0.89		
10	131046	X02530	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN PRECURS	0.8	1.15		
10	131244	D38076	Hs.24763	RAN binding protein 1	1.13	1.85		
	131877 131927	J04088 AA461549	Hs.156346 Hs.34780	Topoisomerase (DNA) II alpha (170kD) "Doublecortex; lissencephaly, X-linked (1 0.81	1 0.62		
	131965	W90146	Hs.35962	ESTs	0.74	3.27		
15	131978	D80008	Hs.36232	KIAA0186 gene product	1	1		
15	132354 132543	L05187 AA417152	Hs.211913 Hs.5101	Small proline-rich protein 1A ESTs; Highly similar to protein regulati	0.69 0.79	1.43 4.27		
	132632	N59764	Hs.5398	guanine-monophosphate synthetase	1	1.08		
	132653	U31201	Hs.54451	"taminin gamma2 chain gene (LAMC2), exon	1	1		
20	132659 132710	Z75190 W93726	Hs.54481 Hs.55279	"Low density lipoprotein receptor-relate "Serine (or cysteine) proteinase inhibit	0.89 0.64	0.89 4.41		
20	132758	W52432	Hs.56105	"ESTs, Weakly similar to WDNM RAT WDNM1	1.55	2.08		
	132767	L05188	Hs.231622	Small proline-rich protein 2B	0.83	1.66		
	132816 132990	M74542	Hs.575 Hs.18387	Aldehyde dehydrogenase 3	0.55 1	0.55 3.53		
25	133070	AA458761 U69611	Hs.64311	transcription factor AP-2 alpha (activat "A disintegrin and metalloprotetnase dom	1.16	2		
	133282	U52960	Hs.286145	"SRB7 (suppressor of RNA polymerase B, y	1	2.7		
	133317	AA215299	Hs.70830	U6 snRNA-associated Sm-like protein LSm7 Homo saplens mRNA; cDNA DKFZp564l1922	0.95 1.12	1.42 2.55		
	133370 133391	AA156897 X57579	Hs.72157 Hs.727	H.sapiens activin beta-A subunit (exon 2	1.65	1.76		
30	133832	H03387	Hs.241305	estrogen-responsive B box protein (EBBP)	1.02	1.39		
	134032	Z81326	Hs.78589	"Serine (or cysteine) proteinase Inhibit	1 0.95	1 1.53		
	134168 134218	AA398908 AA227480	Hs.181634 Hs.80205	"Homo sapiens cDNA: FLJ23602 fis, clone Pim-2 oncogene	1.36	2.48		
~ -	134405	R67275	Hs.82772	collagen, type XI, alpha 1***	0.76	2.86		
35	134453	X70683	Hs.83484	SRY (sex determining region Y)-box 4	1.89	3.78		
	134470 134645	X54942 U87459	Hs.83758 Hs.167379	CDC28 protein kinase 2 "Cancer/testis antigen (NY-ESO-1, CTAG1,	1.82 0.82	4.11 0.83		
	134781	M17183	Hs.89626	Parathyrold hormone-like hormone	1	1		
40	135002	U19147	Hs.272484	Gantigen 6	1	1		
40	100040 101201	M97935 L22524	Hs.2256	AFFX control: STAT1 matrix metalloproteinase 7 (matrilysin;	0.92 2.92	1.25 8.5		
	101664	M60752	Hs.121017	H2A histone family; member A	1	1		
	102025	U03911	Hs.78934	mutS (E. coli) homolog 2 (colon cancer;	0.8	1.61		
45	102031 102221	U04898 U24576	Hs.2156	RAR-related orphan receptor A LIM domain only 4	1	1		
	102270	U30255	Hs.75888	phosphogluconate dehydrogenase	1.08	1.43		
	102339	U37022	Hs.95577	cyclin-dependent kinase 4	0.88	1.32		
	102391 103000	U41668 X51956	Hs.77494 Hs.146580	deoxyguanosine kinase enolase 2; (gamma; neuronal)	1.07 0.91	1.58 1.49		
50	103395	X94754	Hs.119503		0.89	1.32		
	105638	AA281599	Hs.20418		0.91	1.25		
	105726 114841	AA292328 AA234722	Hs.9754 Hs.55408	activating transcription factor 5 ESTs; Moderately similar to CALCIUM-DEPE	0.94 0.78	1.48 1.56		
~ ~	115206	AA262491	Hs.186572	ESTs	1	1		
55	115906	AA436616	Hs.82302	ESTs ATP-binding cassette; sub-family 8 (MDR/	0.74 1.1	2.52 1.51		
	119132 124163	R49046 H30539	Hs.107911 Hs.189838	ESTs	1	1.51		
	126487	AA482505	Hs.184601	solute carrier family 7 (cationic amino	1.01	1.46		
60	127141	AA307960 AA905754	Hs.75478 Hs.75103	KIAA0956 protein tyrosine 3-monooxygenase/tryptophan 5-mo	0.85 1	1.4 1.18		
00	128034 128609	AA234365	Hs.102456	survival of motor neuron protein interac	i	1.5		
	128895	R37753	Hs.106985	ESTs	1.7	2		
	130199	Z48579 U89995	Hs.172028 Hs.159234	a disintegrin and metalloprotease domain forthead box E1	1 1	1		
65	130524 133000	U24152	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast	i	i		
	133658	M25756	Hs.75426	secretogranin II (chromogranin C)	1	1		
	135047	AA460466	Hs.93597	ESTs AFFX control: 28S ribosomal RNA	1 0.88	1 1.53		
	100053 100114	M27830 D00596	Hs.82962	thymidylate synthetase	0.68	1.86		
70	100128	D11094	Hs.61153	proteasome (prosome; macropain) 26S subu	1.29	2.03		
	100154	D14657	Hs.81892		0.71	4.26		
	100161 100168	D14694 D14874	Hs.77329 Hs.394	phosphatidylserine synthase 1 adrenomedullin	1.02 0.46	1.56 1.17		
a c	100187	D17793	Hs.78183	aldo-keto reductase family 1; member C3	1	1		
75	100188	D21063	Hs.57101		0.97	1.4		
	100217 100220	D26600 D28364	Hs.89545	proteasome (prosome; macropain) subunit; ****Human mRNA for annexin II, 5'UTR (seq	1.13 1.11	1.9 1.53		
	100287	D43950	Hs.1600	chaperonin containing TCP1; subunit 5 (e	1.13	2.09		
80	100297	D49489	Hs.182429		0.92	1.78		
80	100330 100355	D55716 D78129	Hs.77152	minichromosome maintenance deficient (S. ""Homo sapiens mRNA for squalene epoxid	1.07 0.96	1.61 1.87		
	100364	D78586	Hs.154868	cerbamoyl-phosphate synthetase 2; aspart	1.49	2.46		
	100368	D79987	Hs.153479	extra spindle poles; S. cerevisiae; homo	0.59	1.32		
85	100398 100438	D84557 D87448	Hs.155462 Hs.91417	minichromosome maintenance deficient (mi topoisomerase (DNA) II binding protein	1.08 1	1.9 2.15		
				• • • • • • • • • • • • • • • • • • • •				

WO 02/086443 Hs.75789 N-myc downstream regulated 1.48 100455 D87953 0.91 HG1153-HT1153 100491 Nucleoside Diphosphate Kinase Nm23-H2s 0.99 1.41 3.17 100518 HG174-HT174 Desmoplakin i 1 28 "Nexin, Glia-Derived" 0.68 100528 HG1828-HT1857 1.9 5 HG2874-HT3018 Ribosomal Protein L39 Homolog 100661 100667 HG2981-HT3127 ""Epican, Alt. Splice 11"" 8.0 1.97 100830 HG4074-HT4344 Rad2 1.01 2.12 glucose phosphate isomerase splicing factor, arginine/serine-rich 3 1.79 101061 Hs 944 K03515 0.91 L10838 Hs.167460 1.23 1.87 101131 10 101162 L14595 Hs.174203 solute carrier family 1 (glutamate/neutr 1.35 2.73 macrophage migration inhibitory factor (H2A histone family; member O cyclin-dependent kinase inhibitor 3 (CDK 101181 L19686 Hs.73798 1.03 1.78 0.57 1.3 101183 1.19779 Hs.795 101216 Hs.84113 L25876 L27706 Hs.82916 chaperonin containing TCP1; subunit 6A (0.99 1.99 101228 15 sorbitol dehydrogenase glycogen synthase kinase 3 beta 101233 L29008 Hs.878 0.82 2.11 Hs.78802 1.91 101247 1.33801 1.2 "Homo sapiens (cell line HL-6) alpha t 0.69 101332 2.78 L47276 Hs.182018 interleukin-1 receptor-associated kinase 1.84 101342 L76191 101396 M15796 Hs.78996 proliferating cell nuclear antigen 0.95 3.55 20 101423 101445 M18391 M21259 Hs.89839 FnhA1 1.5 small nuclear ribonucleoprotein polypept 1.21 1.96 Hs.1066 asparagine synthetase eukaryotic translation initiation factor casein kinase 2; beta polypeptide 0.93 101505 M27396 Hs.75692 M29536 M30448 Hs.12163 1.19 1.93 101525 1.42 101535 Hs 251669 0.9625 CD9 antigen (p24) ""Human alpha-1 collagen type I gene, 3 M38690 Hs.1244 1.11 1.25 101607 M55998 1.98 101624 1.17 101758 M77836 Hs.79217 pyrroline-5-carboxylate reductase 1 1 77 3.45 1.45 membrane component; chromosomal 4; surfa 0.71 101839 M93036 Hs.692 M94362 101853 Hs.76084 0.84 1.19 30 putative Rab5-interacting protein (cl 0.89 1.9 101977 S83364 1.46 Hs.77597 Hs.82643 polo (Drosophia)-like kinase protein tyrosine kinase 9 101992 U01038 0.66 3.35 1.23 102009 U02680 Hs.118400 singed (Drosophila)-like (sea urchin fas 1.88 U03057 102012 102039 U05861 Hs.201967 aldo-keto reductase family 1; member C1 0.93 2.32 35 centromere protein A (17kD) small nuclear ribonucleoprotein D3 polyp ALL1-fused gene from chromosome 1q 4.28 102123 U14518 Hs.1594 0.89 1.42 102130 102148 1115009 Hs 1575 U16954 2.95 Hs.75823 102210 U23028 Hs.2437 eukaryotic translation initiation factor 1.01 1.34 lysyl oxidase-like 1 karyopherin alpha 2 (RAG cohort 1; Impor Hs.65436 2.34 102220 U24389 1.15 40 U28386 2.69 Hs.159557 102260 chromobox homolog 1 (Drosophila HP1 beta small nuclear RNA activating complex; po discoldin domain receptor family; member 102330 U35451 Hs.77254 1.05 1.7 2.99 102423 U44754 U48705 Hs.179312 1.14 2.01 1.05 102455 Hs.75562 ATPase; Na+/K+ transporting; beta 3 poly 1.92 102499 U51478 Hs.76941 45 solute carrier family 1 (neutral amino a 102522 U53347 Hs.183556 0.84 1.31 "Homo saplens enterocyte differentiati 1.11 1.6 102590 U82136 2.17 Hs.12045 putative protein U72514 102676 Hs.93002 ubiquitin carrier protein E2-C 0.86 2.28 102687 U73379 BRCA1 associated RING domain 1 ""Human HIV-1 Net Interacting protein (102704 U76638 Hs.54089 1.12 1.63 1.39 50 102781 102784 0.9 U83843 U85658 Hs.61796 transcription factor AP-2 gamma (activat 2.16 chaperonin containing TCP1; subunit 2 (b small nuclear ribonucleoprotein polypept 102827 U91327 Hs.6456 0.96 1.62 1.21 1.25 102935 X13482 Hs.80506 4.2 2.32 annexin A8 102972 X16662 Hs.87268 55 non-metastatic cells 1; protein (NM23A) 1.03 1.83 102983 X17620 Hs.118638 multifunctional polypeptide similar to S CDC28 protein kinase 1 ribonucleolide reductase M1 polypeptide 5.44 3.79 103023 Hs.117950 1.58 X53793 1.32 103038 X54941 Hs.77550 Hs.2934 Hs.2704 1.11 2.58 103075 X59543 glutathione peroxidase 2 (gastrointestin 3.05 103168 X68314 60 103185 X69910 Hs.74368 transmembrane protein (63kD); endoplasmi 1.01 1.97 phosphorylase kinase; alpha 1 (muscle) chaperonin containing TCP1; subunit 3 (g X73874 X74801 Hs.2393 Hs.1708 1.72 103212 0.950.97 1.77 103223 X78416 Hs.3155 casein; alpha 103260 hexabrachion (tenascin C; cytotactin) small nuclear ribonucleoprotein polypept Hs.204133 Hs.77496 1 23 3.09 103262 X78565 65 103330 103364 1.12 2.25 X85373 SULT1C sulfotransferase X90872 Hs.75854 2.85 4.62 103375 X91868 Hs.54416 sine oculis homeobox (Drosophila) homolo 2.48 103391 X94453 Hs.114366 pyrroline-5-carboxylate synthetase (glut 1.53 proteasome (prosome; macropain) subunit; M-phase phosphoprotein 11 1.53 0.92 103404 103437 X95586 Hs.78596 70 X98260 Hs.82254 1.54 0.92 M-priase prices proportion (1) Ipocalin 2 (oncogene 24p3) cadherin 1; E-cadherin (epithelial) junction plakoglobin collagen; type 1; alpha 1 ESTs; Weakly similar to R07G3.8 [C.elega 0.55 0.96 2.51 103448 X99133 Hs.204238 Z35402 Z68228 103605 Hs.194657 1.28 0.88 Hs.2340 103646 Hs.172928 2.98 Z74615 103658 75 103774 AA092898 Hs.92918 1.88 4 66 2.17 RNA polymerase I subunit ESTs: Weakly similar to R27090_2 (H.sapi 0.87 104261 AF008442 Hs.5409 1.4 2.49 Hs.85222 104276 C02193 104289 C16281 Hs.75478 KIAA0956 protein 1.68 collagen; type VII; alpha 1 (epidermolys cystalin SN 104434 L02870 Hs.1640 1.04 1.49 80 104453 104611 Hs.123114 Hs.125845 0.38 0.76 M19169 ribulose-5-phosphate-3-epimerase ESTs; Wealthy similar to ACYL-COA DEHYDRO R98280 1.08 2.25 Hs.7010 1.65 104758 AA024661 105114 AA156532 Hs.11801 adenosine A2b receptor pseudogene 0.91 1.38 1.7 105132 105174 AA159501 AA186613 Hs.247280 Hs.34744 **HBV** associated factor 1 08 85 0.95 2.05 **ESTs**

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	105280	AA232215	Hs.14600	ESTs	1 0.72	1.4		
	105344 105516	AA235303 AA257971	Hs.8645 Hs.21214	ESTs ESTs	0.72 1.35	2.02 3.56		
_	105621	AA280865	Hs.6375	Homo sapiens mRNA; cDNA DKFZp564K0222 (f	1.23	1.82		
5	105698	AA287393	Hs.15202	ESTs; Weakly similar to oligodendrocyte-	0.98 0.92	1.28 1.32		
	105705 105724	AA290767 AA292098	Hs.101282 Hs.22934	Homo saplens mRNA; cDNA DKFZp434B102 (fr ESTs; Weakly similar to ZINC FINGER PROT	0.99	1.41		
	105782	AA350215	Hs.21580	ESTs	1	1		
10	105799 105807	AA372018	Hs.24743 Hs.16869	ESTs ESTs: Moderately similar to COLLAGEN ALP	1.08 0.95	1.78 1.34		
10	105891	AA393803 AA400768	Hs.26662	ESTs; Weakly similar to tumor necrosis f	0.87	2.25		
	105936	AA404338	11-00000	ESTs	1.14 1	1.46 1		
	106069 106103	AA417741 AA421104	Hs.29899 Hs.12094	ESTs; Weakly similar to ZINC FINGER PROT ESTs	1.04	1.44		
15	106140	AA424524	Hs.14912	KIAA0286 protein	1.23	2.11		
	106149	AA424881	Hs.256301 Hs.6994	ESTs ESTs	0.83 0.77	1.48 2.05		
	106154 106182	AA425304 AA426609	Hs.10862	ESTs	0.74	2.23		
20	106220	AA428582	Hs.32196	ESTs; Moderately similar to metargidin p	0.97 0.99	1.99 1.54		
20	106228 106318	AA429290 AA436570	Hs.17719 Hs.9605	ESTs pre-mRNA cleavage factor Im (25kD)	0.95	2.09		
	106341	AA441798	Hs.5243	ESTs; Moderately similar to piL2 hypothe	0.98	2.66		
	106432	AA448850	Hs.17138 Hs.42484	ESTs Homo sapiens mRNA; cDNA DKFZp564C053 (fr	0.95 1	1.93 1		
25	106474 106483	AA450212 AA451676	Hs.30299	IGF-II mRNA-binding protein 2	1.4	2.29		
-	106599	AA457235	Hs.12842	ESTs; Moderately similar to non-function	1 1.49	1.82 2.78		
	106611 106654	AA458904 AA460449	Hs.26267 Hs.3784	ESTs; Weakly similar to torsinA [H.sapie ESTs; Highly similar to phosphoserine am	1.45	1.4		
••	107076	AA609145	Hs.21143	ESTs; Weakly similar to fos39554_1 [H.sa	1.11	1.49		
30	107115	AA610108	Hs.27693 Hs.4756	ESTs; Highly similar to CGI-124 protein flap structure-specific endonuclease 1	1 1.13	1.03 3.63		
	107129 107159	AA620553 AA621340	Hs.10600	ESTs; Weakly similar to ORF YKR081c [S.c	1.05	2.09		
	107444	W28391	Hs.5181	proliferation-associated 2G4; 38kD	1.18 0.99	1.9 2.74		
35	107481 107516	W58247 X56597	Hs.27437 Hs.99853	Homo sapiens kinesin superfamily motor K fibrillarin	0.94	1.77		
55	107529	Y12065	Hs.5092	nucleolar protein (KKE/D repeat)	1.05	2.29		
	107531	Y13936	Hs.17883 Hs.173100	protein phosphatase 1G (formerly 2C); ma ESTs	1.06 1.03	1.62 1.4		
	107801 107957	AA019433 AA031948	Hs.57548	ESTs	0.95	1.46		
40	108565	AA085342	Hs.1526	ATPase; Ca++ transporting; cardiac muscl	0.59 1	1.35 7.63		
	108780 108828	AA128561 AA131584	Hs.117938 Hs.71435	collagen; type XVII; alpha 1 DKFZP56400463 protein	1.33	2.56		
	109060	AA160879	Hs.241551	chloride channel; calcium activated; fam	0.67	1.42		
45	109112 109344	AA169379 AA213696	Hs.72865 Hs.86559	ESTs poly(A)-binding protein-like 1	1.03 0.97	2.31 1.55		
73	109344	AA227145	Hs.209473	ESTs; Weakly similar to REGULATOR OF MIT	0.76	1.87		
	110780	N23174	Hs.22891	solute carrier family 7 (cationic amino	0.9 1.17	0.95 2.26		
	110958 111018	N50550 N54067	Hs.24587 Hs.3628	signal transduction protein (SH3 contain mitogen-activated protein kinase kinase	1.21	1.85		
50	111337	N79612	Hs.16607	ESTs; Highly similar to Myosin heavy cha	1	1.45		
	112305 112401	R54822 R61279	Hs.26244 Hs.237536	ESTs ESTs; Wealdy similar to F25B5.3 [C.elega	1 1.24	1 1.64		
	112853	T02843	Hs.4351	EST	1.56	1.96		
55	112869	T03313 T23513	Hs.4747 Hs.7147	dyskeratosis congenita 1; dyskerin ESTs	1.03 1	1.57 1		
55	112992 113048	T25895	Hs.184008	ESTs; Weakly similar to RNA-binding prot	1.37	2.26		
	113063	T32438	Hs.5027	ESTS	1 1.33	1 2.7		
	113179 113573	T55182 T91166	Hs.152571 Hs.15990	ESTs; Highly similar to IGF-II mRNA-bind ESTs	0.76	1.47		
60	113811	W44928	Hs.4878	ESTs	0.79	1.51		
	114086	Z38266 AA070827	Hs.12770 Hs.180320	Homo saplens PAC clone DJ0777023 from 7p ESTs; Wealtly similar to GOLGI 4-TRANSMEM	0.9 1.02	1.34 1.76		
	114587 114846	AA234929	Hs.44343	ESTs	1.32	2.36		
65	114964	AA243873	Hs.82184	ring finger protein 3	1.1 1.01	1.84 2.36		
65	115047 115166	AA252627 AA258409	Hs.22554 Hs.198907	homeo box 85 myelin protein zero-like 1	1.05	2.31		
	115167	AA258421	Hs.43728	hypothetical protein	1.52	2.52		
	115239 115278	AA278650 AA279757	Hs.73291 Hs.67466	ESTs; Weakly similar to similar to the b ESTs; Weakly similar to BACN32G11.d [D.m	0.7 1.14	2.57 2.12		
70	115652	AA405098	Hs.38178	ESTS	0.82	4.67		
	115875	AA433943	Hs.43946	ESTs; Weakly similar to Weak similarity ESTs; Highly similar to small zinc finge	1.2 0.96	1.98 1.31		
	116004 116121	AA449122 AA459254	Hs.76086 Hs.48855	ESTs	0.97	1.55		
	116129	AA459956	Hs.49163	ESTs; Highly similar to putative ribonuc	1.08	2.73		
75	116190 116312	AA464963 AA490494	Hs.67776 Hs.65403	ESTs ESTs	0.8 1.37	1.57 2.65		
	116732	F13779	Hs.165909	ESTs	0.92	1.8		
	117602	N35020	Hs.44685	ESTs; Weakly similar to GOLIATH PROTEIN	1.15 1.04	1.84 2.36		
80	117950 117992	N51394 N52000	Hs.75478 Hs.172089	KIAA0956 protein Homo sapiens mRNA; cDNA DKFZp586B0222 (f	0.62	1.29		
- •	118785	N75386	Hs.111867	GLI-Kruppel family member GLI2	1	1		
	119717 119814	W69134 W74069	Hs.57987 Hs.58350	ESTs ESTs	1 0.78	1.4 1.77		
0.5	120128	Z38499	Hs.91448	MKP-1 like protein tyrosine phosphatase	0.86	1.46		
85	120242	Z98443	Hs.86366	ESTs	0.83	2.01		

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	120483	AA252994	Hs.1578	apoptosis inhibitor 4 (survivin)	0.74	1.64	
	121054 121326	AA398604 AA404246	Hs.97387 Hs.97031	ESTs ESTs; Weakly similar to Similar to phyto	1.05 0.98	1.93 1.3	
_	121376	AA405699	Hs.166232	ESTs; Moderately similar to SODIUM- AND	0.91	1.83	
5	121457	AA411448	Hs.208985	ESTs	0.91	1.59	
	121780 121781	AA422086 AA422150	Hs.124660 Hs.98370	ESTs cytochrome P540 family member predicted	0.46 1.07	0.55 1.54	
	121844	AA422130 AA425732	Hs.98485	gap junction protein; beta 2; 26kD (conn	0.94	1.4	
10	122059	AA431737	Hs.98749	EST	1.93	2.33	
10	122338	AA443311	Hs.98998	ESTs ESTs	1 0.88	1 1.39	
	122354 122591	AA443772 AA453265	Hs.186692 Hs.99311	ESTs; Weakly similar to MRJ [H.saplens]	2.28	2.93	
	122790	AA460156	Hs.99556	ESTs	0.88	1.3	
15	123398	AA521265	Hs.105514	ESTs ·	1 .	1.93 1	
13	123518 123673	AA608531 AA609471	Hs.170313 Hs.112712	ESTs	i	1.15	
	124000	D57317	Hs.74861	activated RNA polymerase II transcriptio	0.74	1.12	
	124367	N24006	Hs.99348	distal-less homeo box 5 Homo saplens mRNA; cDNA DKFZp586L141 (fr	0.67 1.19	1.1 1.7	
20	124447 125756	N48000 W25498	Hs.140945 Hs.81634	ATP synthase; H+ transporting; mitochond	0.93	1.59	
	125769	Al382972	Hs.82128	5T4 oncofetal trophoblast glycoprotein	1.65	6.76	
	125852	H09290	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	0.72 1.22	2.26 2.25	
	125924 126037	AA526849 M85772	Hs.82109 Hs.6066	syndecan 1 KIAA1112 protein	1.36	1.63	
25	126214	N29455	Hs.74316	desmoplakin (DPI; DPII)	1.93	3.55	
	126414	N78770	Hs.223439 Hs.62741	ESTs ESTs	1.21 1	1.66 1	
	126737 126743	AA488132 AA179253	Hs.172182	poly(A)-binding protein; cytoptasmic 1	1.3	2.16	
20	126926	AA179546	Hs.832	ESTs; Highly similar to INTEGRIN BETA-8	2.53	2.8	
30	127432	AA501734	Hs.170311 Hs.99189	heterogeneous nuclear ribonucleoprotein ESTs; Moderately similar to recombinatio	1.57 1.24	2.12 2.09	
	128218 128527	H02682 M31523	Hs.101047	transcription factor 3 (E2A immunoglobul	1.08	1.78	
	128568	X60673	Hs.247568	adenylate kinase 3	1.23	3.48	
35	128584	M11433	Hs.101850	retinal-binding protein 1; cellular	0.87 1.22	2.42 1.9	
33	128628 128691	C14037 W27939	Hs.251978 Hs.103834	EST ESTs	1.1	1.73	
	128714	V00599	Hs.179661	Homo sapiens clone 24703 beta-tubulin mR	0.92	1.17	
	128733	AA328993 X85372	Hs.104558 Hs.105465	ESTs small nuclear ribonucleoprotein polypept	1.34 0.9	1.94 1.34	
40	128781 129052	AA496297	Hs.182740	ribosomal protein S11	2.59	3.19	
	129095	L12350	Hs.108623	thrombospondin 2	1.04	3.2	
	129241 129665	AA435665 M88458	Hs.109706 Hs.118778	ESTs; Moderately similar to HN1 [M.muscu KDEL (Lys-Asp-Giu-Leu) endoplasmic retic	0.95 1.28	1.61 2.63	
	129703	AA401348	Hs.179999	ESTs	0.97	1.63	
45	129720	AA476582	Hs.12152	ESTs; Moderately similar to SIGNAL RECOG	1.09	1.79 1.68	
	129850 129896	N20593 AA043021	Hs.56845 Hs.13225	GDP dissociation inhibitor 2 UDP-Gat:betaGlcNAc beta 1;4- galactosylt	0.74 1.43	4.19	
	130069	AA055896	Hs.146428	collagen; type V; alpha 1	1.17	1.98	
50	130405	H88359	Hs.155396	nuclear factor (erythroid-derived 2)-lik	1.26 1	1.79 1	
50	130541 130599	X05608 M91670	Hs.211584 Hs.174070	neurofilament; light polypeptide (68kD) ubiquilin carrier protein	1.07	1.66	
	130867	J04093	Hs.2056	UDP glycosyltransferase 1	1	4.8	
	131009	AA063596	Hs.22142	ESTs; Weakly similar to NADH-CYTOCHROME	0.93 1	1.05 1.23	
55	131028 131083	U20240 U66661	Hs.2227 Hs.22785	CCAAT/enhancer binding protein (C/EBP); gamma-aminobutyric acid (GABA) A recepto	1.1	1.8	
55	131091	T35341	Hs.22880	ESTs; Highly similar to dipeptidyl pepti	1.28	1.98	
•	131144	C14412	Hs.23528	ESTs; Highly similar to HSPC038 protein ESTs	1.43 0.88	2.06 3.38	
	131148 131164	C00038 Y00503	Hs.23579 Hs.182265	keratin 19	1.19	2.77	
60	131185	M25753	Hs.23960	cyclin B1	0.86	3.84	
	131219	C00476	Hs.24395 Hs.2699	small inducible cytokine subfamily B (Cy	0.66 0.99	2.96 1.54	
	131454 131687	AA455896 L11066	Hs.3069	glypican 1 heat shock 70kD protein 9B (mortalin-2)	1	1.18	
~~	131689	AA599653	Hs.30696	transcription factor-like 5 (basic helix	1	1.95	
65	131692	D50914 AA135554	Hs.30736 Hs.32125	KIAA0124 protein ESTs	1.55 1	2.39 1.33	
	131786 131843	AA195893	Hs.184062	ESTs; Moderately similar to putative Rab	0.83	1.63	
•	131860	U02082	Hs.334	Oncogene TIM	1.08	2.2 1.24	
70	131884 131903	H90124 AA481723	Hs.3463 Hs.3436	ribosomal protein S23 deleted in oral cancer (mouse; homolog)	1.23 0.91	1.18	
70	131945	M87339	Hs.35120	replication factor C (activator 1) 4 (37	1	2.8	
	131958	AA093998	Hs.3566	ESTs; Highly similar to phosphorylation	0.87	1.36 1.25	
	131964	W42508 J00277	Hs:3593 Hs:37003	ESTs v-Ha-ras Harvey rat sarcoma viral oncoge	1 1.12	1.43	
75	132001 132040	AA146843	Hs.172894	BH3 Interacting domain death agonist	1	1. 5 5	
	132065	D82226	Hs.211594	proteasome (prosome; macropain) 26S subu	0.89 1	1.27 1.05	
	132109 132112	AA599801 AA150661	Hs.40098 Hs.40154	ESTs jumonji (mouse) homolog	0.99	1.44	
	132123	AA447123	Hs.250705	ESTs	1.06	2.46	
80	132162	H89551	Hs.41241	ESTs	1.08 1.02	2.46 4.56	
	132180 132309	AA405569 AA460917	Hs.418 Hs.2780	fibroblast activation protein; alpha; se Jun D proto-oncogene	1.16	1.8	
	132371	AA235448	Hs.46677	ESTs	0.8	1.26	
85	132618	AA253330	Hs.5344	adaptor-related protein complex 1; gamma MAD (mothers against decapentaplegic; Dr	0.5 1.21	1.49 1.81	
93	132736	U68019	Hs.211578	MAN Interes affairst resobstrationalist re	****	,,,,,	

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	132771	AA488432	Hs.56407	phosphoserine phosphatase	1	1.3		
	132833	U78525	Hs.57783	eukaryotic translation initiation factor	0.91	1.43		
	132922		Hs.6066	KIAA1112 protein	1.16	1.53		
	132959	AA028103	Hs.61472	ESTs; Weakly similar to unknown [S.cerev	1.02	1.88		
5		AA505133	Hs.7594	solute carrier family 2 (facilitated glu	0.72	2.97		
•	133005	C21400	Hs.103329	KIAA0970 protein	0.88	1.34		
	133065	X62535	Hs.172690	diacylglycerol kinase; alpha (80kD)	0.93	1.23		
	133083	N70633	Hs.6456	chaperonin containing TCP1; subunit 2 (b	1.14	1.76		
	133086	L17131	Hs.139800	high-mobility group (nonhistone chromoso	0.97	1.43		
10	133134	T89703	Hs.65648	RNA binding motif protein 8	1.1	1.8		
	133195	AA350744	Hs.181409	KIAA1007 protein	2.29	2.69		
	133313	AA249427	Hs.70704	ESTs	1.07	1.68		
	133331	T62039	Hs.158675	ribosomal protein L14	0.85	1.18		
	133438	D13370	Hs.73722	APEX nuclease (multifunctional DNA repai	0.91	1.45		
15	133445	T99303	Hs.73797	guanine nucleotide binding protein (G pr	0.94	1.68		
	133483	X52426	Hs.74070	keratin 13	0.85	1.14		
	133492	L40397	Hs.74137	transmembrane trafficking protein	1.1	1.69		
	133504	W95070	Hs.74316	desmoplakin (DPI; DPII)	0.7	6.21		
	133517		Hs.74471	gap junction protein; alpha 1; 43kD (con	0.95	1.3		
20	133540	D78151	Hs.74619	proteasome (prosome; macropain) 26S subu	0.91	1.25		
	133594	L07758	Hs, 172589	nuclear phosphoprotein similar to S. cer	0.84	1.29		
	133627	U09587	Hs.75280	glycyl-tRNA synthetase	1.09	1.99		
	133671	T25747	Hs.75471	zinc finger protein 146	1.02	1.5		
	133859	U86782	Hs.178761	26S proteasome-associated pad1 homolog	1.11	3.33		
25	133865	F09315	Hs.170290	discs; large (Drosophila) homolog 5	1.84	6.7		
	133913	W84712	Hs.7753	calumenin	1.15	1.86		
	133963	L34587	Hs.184693	transcription elongation factor B (SIII)	1.3	1.91		
	133982	U47621	Hs.207251	nucleolar autoantigen (55kD) similar to	1.3	1.99		
• •	134100	L07540	Hs.171075	replication factor C (activator 1) 5 (36	0.72	1.65		
30	134110	U41060	Hs.79136	LIV-1 protein; estrogen regulated	1.04	1.62		
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	1	1.55		
	134161	U97188	Hs.79440	IGF-II mRNA-binding protein 3	0.82	1.95		
	134193	F09570	Hs.7980	ESTs	0.98	1.48		
25	134367	X54199	Hs.82285	phosphoribosylglycinamide formyltransfer	1	2.8		
35	134402	U25165	Hs.82712	fragile X mental retardation; autosomal	1.26	2	!	
	134457	D86963	Hs.174044	dishevelled 3 (homologous to Drosophila	1 0.94	1.47		
	134469	X17567	Hs.83753	small nuclear ribonucleoprotein polypept		1.57 2.64		
	134498	M63180	Hs.84131	threonyl-tRNA synthetase	1.2 0.84	1.36		
40	134501	W84870	Hs.211568	eukaryotic translation initiation factor	1.7	2.93		
40	134507	M63488	Hs.84318	replication protein A1 (70kD)	1.7	2.73		
	134548	U41515	Hs.85215	Deleted in split-hand/split-foot 1 regio	1.36	2.22		
	134599	X99226	Hs.86297	Fanconi anemia; complementation group A a disintegrin and metalloproteinase doma	0.77	1.64		
	134692	R73567 N70361	Hs.8850 Hs.8854	ESTs	1.09	1.82		
45	134693	Z49099	Hs.89718	spermine synthase	0.98	1.35		
40	134806	Z34974	Hs.198382	plakophilin 1 (ectodermal dysplasia/skin	0.99	1.4		
	134821 134864	Y08999	Hs.90370	actin related protein 2/3 complex; subun	0.95	1.42		
	134914	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.16	1.29		
	134953	L10678	Hs.91747	profilin 2	0.95	1.76		
50	134993	AA282343	Hs.9242	purine-rich element binding protein B	0.98	1.73		
•	135051	C15324	Hs.93668	ESTs	1.35	2.11		
	135158	U51711	. 10.0000	Human desmocollin-2 mRNA; 3' UTR	0.86	1.16		
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Table 1B shows the accession numbers for those pkeys in Table 1A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the Accession column.

60	Pkey: CAT numb Accession:	er: Gene cluste:	probeset Identifier number r number cession numbers
	Pkey	CAT	Accessions
65	100661 100667	23182_1 26401_3	BE623001 L05096 AA383604 AW966416 N53295 AA460213 AW571519 AA603655 L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE089717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA332714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20368 N44163 BE546944 T69231 AW3777441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700
70			ALS98974 AIBS3855 AA77489 AW7130675 AIS950833 AA146687 H99482 X55150 BE005414 BE005339 N28294 AI673068 AI887890 AW804171 AI675961 AW804172 AA778841 AL048050 AI127757 AI095568 AW204965 AW468978 W31898 AI052595 AI278771 BE464018 AI081503 AI824196 AA513211 AA411062 AW084376 N48752 AA703209 N35580 AW059918 AA054563 AI280942 T27619 BE621435 N66010 AW589527 AI160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565671 C00444 AA054555
75	100668	26401_3	AUG4933 L05424 X56794 S66400 X55150 W60071 AW351820 X55938 M83326 BE005289 BE070059 M83324 BE005248 BE069717 BE181648 BE069700 AW606203 BE069721 AW382138 AW803776 BE463954 BE005334 BE005274 T27386 AA932714 AA972695 AW377728 AI632506 T29066 AI783934 AW377727 BE163715 AL047291 AA279047 AA523003 BE008048 BE440141 W23614 BE090519 BE092193 N29181 N20358 N44153 BE546944 T69231 AW377441 AA907406 H50799 AW051416 AI420712 BE620922 AI279161 AA992549 W47198 BE005241 AI342696 H50700 AI969974 AI863855 AA374490 AW130675 AI950633 AA146687 H99482 X55180 BE005414 BE005339 N28294 AI673068 AI887890 AW804171
80			A1675961 AW804172 AA778841 AL048050 A1127757 A1990535 AA746867 H99402 A55130 BEU03414 BE005339 N26294 N107306 A1067650 AN064177 A1675961 AW804172 AA778841 AL048050 A1127757 A1095568 AW204965 AW468978 W31898 A1052595 A1278771 BE464018 A1081503 A1824196 AA513211 AA411062 AW084376 N48762 AA703209 N35580 AW059918 AA054563 A1280942 T27619 BE621435 N66010 AW589527 A1160414 AA283090 AA962536 H82726 W52115 W45432 W60433 AA577548 AA146714 BE150994 AA054615 AW796025 AW382768 BE565571 C00444 AA054555
85	101332	25130_1	J04088 NM_001067 AF071747 AJ011741 N85424 AL042407 AA218572 BE296748 BE083981 AL040877 AW499918 AW675045 H17813 BE081283 AA670403 AW504327 BE094229 AA104024 AI471482 AI970337 AA737616 AI827444 AW003286 AI742333 AI344044 AI765634

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AA026221 AA316774 AA486908 AI500094 AA096362 AW983742 BE586422 BE6186583 R70203 AA731732 AA345048 BE562720 T28342
NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789
AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 75 100518 13165_1 AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 PE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI95935 AW747871 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365155 AW365157 AW365154 AW068840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159846 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 80 R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264

AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467

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	wo	02/08644	PCT/US02/12476
5			AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798589 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AA056527 AI471874 AI304772 AW617828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070
10			A494069 Al911702 AA149191 AA026864 Al830049 Al887258 AW780435 Al910434 Al819984 Al858282 Al078449 Al025932 Al860584 Al635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782068 AW243815 AW150038 AW268383 AW004633 Al927207 AA782109 AW473233 Al804485 AW169216 Al572669 AA602182 AW015480 AW771865 Al270027 AA961816 AA283207 Al076962 Al498487 Al348053 Al783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 Al905927 AA022701 W38382 R20795 T77861 AW860878
15	100528	45979_1	BE386801 AU077299 AA143755 BE302747 AA853375 U30162 BE274163 BE277479 BE408180 BE274874 C15000 AA047476 N27099 Al359165 Al638794 Al151283 Al863925 AW444977 Al207392 AA931263 AA43112 R40138 AW068638 AA351008 AA676972 R62503 AA916492 AW001865 H42334 H38280 AA121497 AA114137 Al750938 M17783 AA388786 BE274462 Al753182 C05975 AA347404 AW069298 Al754351 Al754044 AA188808 AA188879 AA565243 AL040655 AA456177 Al750722 AA045756 AA213580 C16936 AW578747 AW753731 H41632 N44761 R58560 R61260 AA039902 N59721 AW992543 R68380 AA149686 T29017 H03739 BE383822 BE387105 BE408251 BE410425 H41560 AA247591
20	100559	2260_1	BE389677 A1752233 A1566195 AA868004 A1424523 AW753720 AA852159 BE386803 NM_000094 L02870 D13694 S61236 M96984 AW946290 M56158 A1285422 D29523 AL119886 AW630655 L06862 A1884355 AW168737 T29085 AW797005 AW801340 A1355504 AW079048 AW801337 A1690455 A1972063 AW268565 W68588 AA587326 AA883498 A1033523 AW510356 AW591998 H98463 AL043852 A1150055 A1566239 A1624803 AA844717 H40670 AA922334 A1864424 AW615094 AW451233 A1302203 F31221 A1872170 W68589 AA904478 A1917631 AW014208 AW450759 AA847625 A1284033 AA848176 AA5998507
25	100576 124357 101624 101625 135158	9986_1 genbank_N224 entrez_M5599 entrez_M5729 57963_1	8 M55998

Tables 2A-8C were previously filed on November 9, 2001 in USSN 60/339,245 (18501-004100US)

Table 2A shows 504 genes down-regulated in lung tumors relative to normal lung and chronically diseased lung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene 5 expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number ExAccn: UnigenelD: Unigene number 10 Unigene Title: Unigene gene title 90th percentile of AI for normal lung samples divided by the 80th percentile of AI for adenocarcinoma and squamous cell carcinoma lung tumor R1: median of Al for normal lung samples divided by 90th percentile of Al for adenocarcinoma and squamous cell carcinoma lung tumor samples. median of Al for normal lung samples minus the 15th percentile of Al for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of Al for adenocarcinoma and squamous cell carcinoma lung tumor samples minus the 15th percentile of Al for all normal R2: R3: 15 lung, chronically diseased lung and tumor samples. average of Al for normal lung samples divided by average Al for squamous cell carcinoma and adenocarcinoma lung turnors. R4: median of Al for normal lung samples divided by the 90th percentile of Al for adenocarcinomas.

median of Al for normal lung samples minus the 15th percentile of Al for all normal lung, chronically diseased lung and lumor samples divided by the 90th R5: R6: percentile of AI for adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples. 20 average of Al for normal tung samples divided by the 90th percentile of Al for squamous cell carcinomas. R7: median of Al for normal lung samples minus the 15th percentile of Al for all normal lung, chronically diseased lung and turnor samples divided by the 90th R8: percentile of AI for squamous cell carcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples. 25 R1 R2 **R3** R4 **R5 R6** R7 **R8** Pkey ExAcen UnigenelD Unigene Title 40.20 Z97171 NM 002084 Hs.78454 myocilin; trabecular meshwork inducible 100095 glutathione peroxidase 3 (plasma) 3.46 100115 Hs.336920 2.30 100138 U83508 Hs.2463 angiopoietin 1 11.00 30 growth differentiation factor 10 transcription elongation factor A (SII); 100299 D49493 Hs.2171 3.06 100306 U86749 Hs.80598 100447 KIAA0275 gene product 3.16 NM 014767 Hs.74583 100458 S74019 Hs.247979 42.40 Vpre-8 4.13 100862 AA005247 Hs.285754 Hepatocyte Growth Factor Receptor 125.60 35 actin; alpha; cardiac muscle 100959 AA359129 Hs.118127 BE206854 phosphoglycerate mutase 2 (muscle) 101032 Hs.46039 36.40 34.60 AF047347 Hs.4880 armylold beta (A4) precursor protein-bind 101081 solute carrier family 6 (neurotransmitte transmembrane 4 superfamily member 2 193,20 101088 X70697 Hs.553 3.10 AJ250562 Hs.82749 101125 54 86 40 U11874 Hs.846 interleukin 8 receptor; beta 101180 "Homo saplens core 2 beta-1,6-N-acetylgi enhancer of filamentation 1 (cas-like do 101308 L41390 33.20 36.40 101330 L43821 NM_005795 Hs.80261 Calcitonin receptor-like 2.29 Hs.152175 101345 70.55 hydroxyprostaglandin dehydrogenase 15-{N 101346 A1738616 Hs.77348 45 3.54 lipoprotein lipase 101397 M26380 Hs.180878 3.81 complement component 8; beta polypeptide actin; alpha 1; skeletal muscle NM_000066 NM_001100 101414 Hs.38069 34.60 Hs.1288 101435 37.60 X16896 Hs.82112 interteukin 1 receptor; type I 101507 4.25 cytochrome P450; subfamily IIB (phenobar M29874 Hs.1360 101530 50 zinc finger protein; Y-linked 2.54 101537 A1469059 Hs.184915 NM 000102 Hs.1363 cytochrome P450; subfamily XVII (steroid 5.50 101542 EDG1; endothelial differentiation, sphin thyroid stimulating hormone receptor Intercellular adhesion molecule 2, exon BE246154 Hs.154210 39 40 101545 13.00 101554 BE207611 Hs.123078 3.38 Hs.83733 101560 AW958272 4.37 55 protein kinase; cAMP-dependent; catalyti 101574 M34182 Hs.158029 3.80 101605 M37984 Hs.118845 troponin C; slow guanylate binding protein 1; interferon-Sjogren syndrome antigen A1 (52kD; ribon 30.20 101621 RF391804 Hs.62661 Hs.1042 2.75 AA299330 101680 3.37 solute carrier family 8 (sodium/calcium 101829 AW452398 Hs.129763 38.20 60 M93221 AW004056 101842 Hs.75182 mannose receptor; C type 1 "Hs-TBX2=T-box gene (T-box region) [huma 2.32 Hs.168357 101961 6.85 T92248 Hs.2240 uteroglobin 101994 2.45 AU077315 Hs.154970 transcription factor CP2 102020 6.75 aldehyde dehydrogenase 7 102091 BF280901 Hs.83155 54.60 65 AW025430 forkhead box F1 Hs.155591 102112 3.98 AA723157 Hs.73769 folate receptor 1 (adult) 102190 3.62 NM_000507 102202 Hs.574 fructose-bisphosphatase 1 2.32 102241 NM_007351 Hs.268107 U33839 Multimerin 7.00 Accession not listed in Genbank 102310 Human sodium cotransporter RKST1 mRNA 29.40 70 U41898 102397 3.75 "Homo sapiens skeletal muscle LIM-protei Human clone W2-6 mRNA from chromosome X 102571 U60115 Hs.239069 3.07 102620 AA976427 Hs.121513 Human ataxia-telanglectasia locus prote 2.40 102636 U67092 solute carrier family 21 (prostaglandin 3.15 U70867 Hs.83974 102667 75 3.56 U72512 Hs.7771 Human B-cell receptor associated protei 102675 4.51

37.40

28.80

6.00

2 47

2.69

12.00

13.00

10.00

2.16

progastricsin (pepsinogen C) opiold-binding protein/cell adhesion mol corticotropin releasing hormone

thyroid and eye muscle autoantigen D1 (6

pregnancy-zone protein Human mRNA for T cell receptor; clone IG

Cadherin 5, VE-cadherin (vascular epithe

H.sapiens MAL gene exon 4

keratio: hair; acidic: 5

102698

102727

102852

103026

103028

103098

103117

103241 103280

103360

80

85

M18667

1179251

V00571

X54162

X54380

M86361 X63578

X76223

U84722

Y16791

Hs.1867

Hs.99902

Hs.75294

Hs.79386

Hs.74094

Hs 295449

Hs.76206

Hs.73082

parvalbumin

	w	O 02/080	5443							PCT/	US02/1	2476
	103496	Y09267	Hs.132821	flavin containing monooxygenase 2							0002/1	5.97
	103508 103561	Y10141 NM_001843	Un 142424	"H.sapiens DAT1 gene, parlial, VNTR" contactin 1			2.40			3.27		
	103569	NM_001643		glycoprotein A repetitions predominant			2.99					
5	103575	Z26256		*H.sapiens isoform 1 gene for L-type cal						4.18		
	103627 103767	Z48513 BE244667	Hs.296155	H.sapiens XG mRNA (clone PEP6) CGI-100 protein						3.44	2.25	
	103/6/	AA187101	Hs.213194	Hypothetical protein MGC10895; sim to SR				46.55			2.20	
10	104078	AA402801	Hs.303276	ESTs						3.05 3.54		
10	104326 104352	AW732858 BE219898	Hs.143067 Hs.173135	ESTs dual-specificity tyrosine-(Y)-phosphoryl						3.16		
	104398	AI423930	Hs.36790	ESTs; Weakly similar to putative p150 [H	64.80							2 20
	104473 104493	A1904823 AW960427	Hs.31297 Hs.79059	ESTs ESTs: Moderately similar to TGF-BETA REC			2.47					3.38
15	104495	AW975687	Hs.292979	ESTs	28.60					- 14		
	104595	A1799603	Hs.271568	ESTs ESTs; Weakly similar to Slit-1 protein [6.00				3.42		
	104597 104659	Al364504 AW969769	Hs.93967 Hs.105201	ESTs	34.00	0.00						
20	104686	AA010539	Hs.18912	ESTs	50.00	11.00						
20	104691 104764	U29690 Al039243	Hs.37744 Hs.278585	ESTs; Beta-1-adrenergic receptor ESTs	56.80			60.40				
	104776	AA026349	110.2.1 0000	ESTs	34.20							
	104825	AA035613 T79340	Hs.141883 Hs.22575	ESTs Homo sapiens cDNA: FLJ21042 fis, clone C	41.20		3.03					
25	104865 104942	NM_016348		ESTs	41.20							3.27
	104989	R65998	Hs.285243	ESTs				40.00				3.20
	105062 105101	AW954355 H63202	Hs.36529 Hs.38163	ESTs ESTs	34.20							3.20
20	105173	U54617	Hs.8364	ESTs		40.00						4.17
30	105194 105226	R06780 R58958	Hs.19800 Hs.26608	ESTs ESTs		16.00	2.34					
	105256	AA430650	Hs.16529	transmembrane 4 superfamily member (tetr			2.72					
	105394	BE245812	Hs.8941	ESTs	33.60		2.61					
35	105647 105789	Y09306 AF106941	Hs.30148 Hs.18142	homeodomain-interacting protein kinase 3 arrestin; beta 2	33.00							3.59
-	105817	AA397825		synaptopodin				05.40		4.46		. *
	105847 105894	AW964490 Al904740	Hs.32241 Hs.25691	ESTs calcitonin receptor-like receptor activi			3.43	35.40				
	105999	BE268786	Hs.21543	ESTs		7.00						
40	106075	AA045290	Hs.25930	ESTs	34.80			42.60				
	106178 106381	AL049935 AB040916	Hs.301763 Hs.24106	KIAA0554 protein ESTs	J-4.00				12.00		•	
	106467	AA450040	Hs.154162	ADP-ribosylation factor-like 2				96.40		3.69		
45	106536 106569	AA329648 R20909	Hs.23804 Hs.300741	ESTs sorcin				47.20		•		
	106605	AW772298	Hs.21103	Homo saplens mRNA; cDNA DKFZp564B076 (fr			0.55	220.40				
	106842 106844	AF124251 AA485055	Hs.26054 Hs.158213	novel SH2-containing protein 3 sperm associated antigen 6	39.20		2.55					
~ 0	106870	AI983730	Hs.26530	serum deprivation response (phosphatidy)	30.25		2.28					4.00
50	106943	AW888222	Hs.9973 Hs.204038	ESTs ESTs								4.28 4.32
	106954 107106	AF128847 AA862496	Hs.28482	ESTs					10.45			
	107163	AF233588	Hs.27018	ESTs			2.57			3.84		
55	107201 107238	D20378 D59362	Hs.30731 Hs.330777	EST EST		8.00				0.04		
	107376	U90545	Hs.327179	solute carrier family 17 (sodium phospha		10.67	0.20					
	107530 107688	Y13622 AW082221	Hs.85087 Hs.60536	latent transforming growth factor bela b ESTs			2.32	34.60				
	107706	AA015579	Hs.29276	ESTs	28.40					0.00		
60	107723 107727	AA015967 AA149707	Hs.173091	EST DKFZP434K151 protein				80.80		3.29		
	107750	AA017291	Hs.60781	ESTs				51.40				
	107751	AA017301	Hs.235390	ESTs		9.00				3.14		
65	107873 107899	AK000520 BE019261	Hs.143811 Hs.83869	ESTs ESTs; Weakly similar to !!!! ALU SUBFAMI		5.00				3.65		
•••	107994	AA036811	Hs.48469	ESTs				44.60				
	107997 108041	AL049176 AW204712	Hs.82223 Hs.61957	Hurnan DNA sequence from clone 141H5 on c ESTs				32.00 30.80				
5 0	108048	A1797341	Hs.165195	ESTs							4.75	
70	108338 108434	AA070773 AA078899		"zm53g11.s1 Stratagene fibroblast (#9372 "zm94b1.s1 Stratagene colon HT29 (#93722			2.33				2.92	
	108447	AA079126		"zm92a11.s1 Stratagene ovarian cancer (#						3.06		
	108480	AL133092	Hs.68055	ESTS				34.00	•			3.36
75	108499 108535	AA083103 R13949	Hs.226440	"zn1b12.s1 Stratagene hNT neuron (#93723 Homo sapiens clone 24881 mRNA sequence					19.00			5.55
	108550	AA084867		"zn11f6.s1 Stratagene hNT neuron (#93723			222		12.00			
	108604 108625	AA934589 AW972330	Hs.49696 Hs.283022	ESTs ESTs			2.33					5.82
00	108629	AA102425		"zn24c6.s1 Stratagene neuroepithelium NT							3.42	
80	108655 108756	AA099960 AA127221	Hs.117037	"zm65c6.s1 Stratagene fibroblast (#93721 Homo saplens mRNA; cDNA DKFZp564N1164 (f		7.00 6.05						
	108864	Al733852	Hs.199957	ESTs	28.80	00						
	108895	AL138272	Hs.62713	ESTs	32.80			57.80				
85	108921 108967	Al568801 AA142989	Hs.71721 Hs.71730	ESTs ESTs	28.80			01.00				
												

	W	O 02/086	443							PCT/I	US02/1	2476
	109001	Al056548	Hs.72116	ESTs, Moderately similar to hedgehog-int			2.57			2. 0 271		2470
	109003	AA147497	Hs.71825	ESTs		r co					2.11	
	109004 109065	AA156235 AA161125	Hs.139077 Hs.252739	EST EST		5.60			10.00			
5	109250	H83784	Hs.62113	ESTs; Weakly similar to PHOSPHATIDYLETHA							3.44	
	109490	AA233416	Hs.139202	ESTs			0.40				2.92	
	109510 109578	A1798863 F02208	Hs.87191 Hs.27214	ESTs ESTs		10.00	2.40					
	109601	F02695	Hs.311662	EST		10.00		40.80				
10	109613	H47315	Hs.27519	ESTs				54.40				
	109650	R31770	Hs.23540 Hs.22869	ESTs ESTs	31.20	8.40						
	109682 109724	H18017 D59899	Hs.127842	ESTs		0.40		29.40				
1.5	109782	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene					8.00			
15	109833	R79864	Hs.29889	ESTs ESTs		10.00	6.49					
	109837 109977	H00656 T64183	Hs.29792 Hs.282982	ESTs			0.10				2.75	
	109984	A1796320	Hs.10299	ESTs				107.00				
20	110146	H41324	Hs.31581	ESTs; Moderately similar to SYNTAXIN 1B						3.48	2.22	
20	110271 110280	H28985 AW874263	Hs.31330 Hs.32468	ESTs ESTs	44.20					3.40		
	110420	R93141	Hs.184261	ESTs				32.00				
	110578	T62507	Hs.11038	ESTs	28.40				20.00			
25	110634 110726	R98905 AW961818	Hs.35992 Hs.24379	ESTs potassium voltage-gated channel; shaker-					20.00			4.15
20	110837	H03109	Hs.108920	ESTs; Wealdy similar to semaphorin F [H.				56.80				
	110875	N35070	Hs.26401	tumor necrosis factor (ligand) superfami		5.33	3.13					•
	110894 110971	R92356 A1760098	Hs.66881 Hs.21411	ESTs; Moderately similar to cytoplasmic ESTs		3.33		44.60				
30	111023	AV655386	Hs.7645	ESTs	32.40							
	111057	T79639	Hs.14629	ESTs					17.14		4.58	
	111247 111330	AW058350 BE247767	Hs.16762 Hs.18166	Homo sapiens mRNA; cDNA DKFZp564B2062 (f KIAA0870 protein							4.00	3.42
	111374	BE250726	Hs.283724	ESTs; Moderately similar to HYA22 [H.sap								3.91
35	111442	AW449573	Hs.181003	ESTs				33.20 53.00				
	111737 111747	H04607 Al741471	Hs.9218 Hs.23666	ESTs ESTs	46.20			55.00				
	111807	R33508	Hs.18827	ESTs	10120	16.00						
40	111862	R37472	Hs.21559	EST						3.91	2.74	
40	112045 112057	Al372588 R43713	Hs.8022 Hs.22945	TU3A protein EST							4.92	
	112214	AW148652	Hs.167398	ESTs					13.00			
	112263	R52393	Hs.25917	ESTs		9.00	2.43					
45 ·	112314 112324	AW206093 R55965	Hs.748 Hs.26479	ESTs Ilmbic system-associated membrane protei		5.00			14.00			
-10	112362	AW300887	Hs.26638	ESTs; Weakly similar to CD20 receptor [H			2.49					
	112380	H63010	Hs.5740	ESTS		8.00	2.34					
	112425 112473	AA324998 R65993	Hs.321677 Hs.279798	ESTs; Weakly similar to IIII ALU SUBFAMI pregnancy specific beta-1-glycoprotein 9		0.00				4.53		
50	112492	N51620	Hs.28694	ESTs				29.80				
	112541	AF038392	Hs.116674	ESTs			2.37			3.62		
	112620 112623	R80552 AW373104	Hs.29040 Hs.25094	ESTs ESTs			2.26					
~ ~	112867	T03254	Hs.167393	ESTs					12.00			
55	112894	T08188	Hs.3770	ESTs ESTs		6.50 7.00						
	112954 113029	AA928953 AW081710	Hs.6655 Hs.7369	ESTs; Weakly similar to !!!! ALU SUBFAMi		·						4.39
	113086	AA346839	Hs.209100	DKFZP434C171 protein					40.00			4.47
60	113140 113252	T50405 NM_004469	Hs.175967	ESTs c-fos Induced growth factor (vascular en		14.00			10.00			
00	113257	AI821378	Hs.159367	ESTs		14.00				3.72		
	113394	T81473	Hs.177894	ESTs	00.00					3.60		
	113437 113454	T85349 Al022166	Hs.15923 Hs.16188	EST ESTs	35.00	6.00						
65	113454	T89130	ns.10100	ESTs	39.60	0.00						
	113552	AI654223	Hs.16026	ESTs							2.00	3.88
	113645	T95358	Hs.333181 Hs.17932	ESTs EST				38.20		_	2.58	
	113691 113706	T96935 AA004693	Hs.269192	ESTs						3.09		
70	113883	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro			2.31					
	113924	8E178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	30.40				13.00		-	
	114035 114058	W92798 AK002016	Hs.269181 Hs.114727	ESTs ESTs					10.00			5.00
7.5	114084	AA708035	Hs.12248	ESTs			0.04	40.60				
75	114121	H05785	Hs.25425	ESTs		7.00	2.31					
	114124 114275	W57554 AW515443	Hs.125019 Hs.306117	Human tymphoid nuclear protein (LAF-4) Interleukin 13 receptor; alpha 1		6.00						
	114297	AA149707	Hs.173091	DKFZP434K151 protein				48.80		0.15		
80	114427	AA017176	Hs.33532	ESTs; Highly similar to Miz-1 protein [H *ze63b11.s1 Soares retina N2b4HR Homo sa					10.00	3.45		•
au	114449 114452	AA020736 Al369275	Hs.243010	ESTs, Moderately similar to RTCO_HUMAN G		14.00						
	114609	AA079505		"zm97a5.s1 Stratagene colon HT29 (#93722				05.40		3.13		
	114648	AA101056	Un 1FFCF4	zn25b3.s1 Stratagene neuroepithelium NT Homo sapiens HNF-3beta mRNA for hepatocy				35.40				3.42
85	114731 114762	BE094291 AA146979	Hs.155651 Hs.288464	ESTs	33.00							
-			•									

	W	O 02/086	6443							PCT/	US02/1	2476
	114776	AA151719	Hs.95834	ESTs	34.40							
	115009	AA251561	Hs.48689	ESTs ESTs: Weakly similar to hypothetical L1	30.20 32.60							
	115272 115279	AW015947 AW964897	Hs.290825	ESTs	32.00	6.00						
5	115302	AL109719	Hs.47578	ESTs					12.00			
	115365	AW976252	Hs.268391	ESTs				48.00		3.32		
	115559 115566	AL079707 Al142336	Hs.207443 Hs.43977	ESTs ESTs				56.20				
10	115683	AF255910	Hs.54650	ESTs, Weakly similar to (defline not ava	31.40							
10	115744	AA418538	Hs.43945	ESTs; Highly similar to dJ1178H5.3 [H.sa Endomucin 2				33.60 74.40				
	115819 115949	AA486620 Al478427	Hs.41135 Hs.43125	ESTs			3.18	14.40				
	115965	AA001732	Hs.173233	ESTs				388.80				
15	116035	AA621405 AA454033	Hs.184664 Hs.41644	ESTs .				33.20 45.80				
13	116049 116081	AJ190071	Hs.55278	ESTs				10.00		3.57		
	116082	AB029496	Hs.59729	ESTs	50.00		3.06					
	116213 116228	AA292105 Al767947	Hs.326740 Hs.50841	leucine rich repeat (in FLII) Interactin ESTs; Weakly similar to tuftelln [M.musc	50.60		3.85					
20	116250	N76712	Hs.44829	ESTs		6.00						
	116419	A1613480	Hs.47152	ESTs; Weakly similar to testicular tekti			2.27	30.00				
	116617 116784	D80761 AB007979	Hs.45220 Hs.301281	EST tenascin R (restrictin; janusin)	47.20		2.21					
0.5	116835	N39230	Hs.38218	ESTs				41.20	44.00			
25	116970 117023	AB023179 AW070211	Hs.9059 Hs.102415	KIAA0962 protein ESTs				91.00	11.00			
	117023	AW085208	Hs.130093	ESTs	49.40							
	117036	H88908	Hs.41192	EST		0.67		32.60				
30	117110 117209	AA160079 W03011	Hs.172932 Hs.306881	ESTs .		8.67		30.60				
50	117325	N23599	Hs.43396	ESTs					9.29	0.40		
	117454	N29569	Hs.44055	ESTs	44.00					3.19		
	117475 117543	N30205 BE219453	Hs.93740 Hs.42722	ESTs ESTs	44.00	16.00						
35	117567	AW444761	Hs.44565	ESTs					12.00			
	117570 117600	N48649 N34963	Hs.44583 Hs.44676	ESTs EST					11.00	3.74		
	117730	N45513	Hs.46608	ESTs		6.00						
40	117791	N48325	Hs.93956	EST		9.00		29.20				
40	117929 117990	N51075 AA446167	Hs.47191 Hs.47385	ESTs ESTs		8.00		23.20				
	118224	N62275	Hs.48503	EST	31.40							
	118244 118357	N62516 AL109667	Hs.48556 Hs.124154	ESTs Homo sapiens mRNA full length Insert cDN	32.80		2.40					
45	118446	N66361	Hs.269121	ESTs			2.28					
	118447	N66399	Hs.49193	EST	30.80					3.10		
	118530 118549	N67900 N68163	Hs.118446 Hs.322954	ESTs EST						3.41		
50	118823	W03754	Hs.50813	ESTs; Weakly similar to long chain fatty			3.94			2 00		
50	118862 118935	W17065 Al979247	Hs.54522 Hs.247043	ESTs KIAA0525 protein				33.00		3.58		
	118944	A1734233	Hs.226142	ESTs; Weakly similar to !!!! ALU SUBFAMI				00.00	11.43			
	118995	N94591	Hs.323056	ESTs		14.00		52.60				
55	119073 119268	BE245360 T16335	Hs.279477 Hs.65325	ERG-2/ERG-1; V-els avian erythroblastosi EST	31.40			52.00				
	119514	W37937		Accession not listed in Genbank						3.50		
	119824	W74536	Hs.184 Hs.58419	advanced glycosylation end product-speci DKFZP586L2024 protein			2.75					3.21
	119831 119861	AL117664 W78816	Hs.49943	ESTs; Moderately similar to IIII ALU SUB				33.80				
60	119889	W84346	Hs.58671	ESTs	20.00			30.03				
	119921 120082	W86192 H80286	Hs.58815 Hs.40111	ESTs ESTs	29.00					3.80		
	120094	AA811339	Hs.124049	ESTs		6.00						
65	120132	W57554	Hs.125019	Human lymphoid nuclear protein (LAF-4)		12.00		36.60				
65	120378 120404	AA223249 AB023230	Hs.285728 Hs.96427	ESTs KIAA1013 protein	39.40	12.00						
	120504	AA256837		ESTs	•••				8.00			
	120512 120667	N55761 AA287740	Hs.194718 Hs.78335	ESTs microtubule-associated protein; RP/EB fa	33.00							4.18
70	120777	AA287702	Hs.10031	KIAA0955 protein				46.60				
	121082	AA398722	11- 404447	ESTs	41 60			39.00				
	121191 121248	AA400205 AA400914	Hs.104447 Hs.97827	ESTs EST	41.60						5.08	
	121363	Al287280	Hs.97933	ESTs					12.00			
75	121366	A1743515 A1660332	He SESTA	ESTs ESTs; Moderately similar to putative sev					20.00	3.32		
	121483 121518	AR000332 AA412155	Hs.25274	ESTs Moderatery strings to potative sev				30.20				
	121545	AA412442	Hs.98132	ESTs			2.29					
80	121622 121665	AA416931 AA416556	Hs.126065 Hs.98234	ESTs ESTs		9.00		34.80				
00	121709	Al338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	34.80							•
	121730	Al140683	Hs.98328	ESTs	38.80	7.00						
	121740 121772	AA421138 Al590770	Hs.98334 Hs.110347	EST Homo saplens mRNA for alpha integrin bin	36.20	7.00						
85	121821	AL040235	Hs.3346	ESTs								3.61

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	121835	AB033030	Hs.300670	ESTs			2.34					
	121841	AA427794	Hs.104864	ESTs			2.61				0.05	
	121885	AA934883	Hs.98467	ESTs							2.25 2.92	
5	121888 121938	AA426429 AA428659	Hs.98463 Hs.98610	ESTs ESTs				46.80			2.32	
_	121950	AA429515	10.50010	EST				31.40				
	122030	AA431310	Hs.98724	ESTs	34.40							
	122054	AA431725	Hs.98746	EST	40.40						3.58	
10	122211 122233	AA300900 AA436455	Hs.98849 Hs.98872	ESTs; Moderately similar to bithoraxoid- EST	49.40 29.80							
10	122233	AA436455 AA436676	Hs.98890	EST	25.00			39.80				
	122253	AA436703	Hs.104936	ESTs; Weakly similar to hypothetical pro		9.00		-				•
	122266	AA436840	Hs.98907	EST						3.60		
15	122285	AA436981	Hs.121602	EST	30.80					3.14		
13	122409 122485	AA446830 AA524547	Hs.99081 Hs.160318	ESTs phospholemman	30.00		2.65					
	122697	AA420683	Hs.98321	Homo saplens cDNA FLJ14103 fis, clone MA		15.00						
	122772	AW117452	Hs.99489	ESTs		6.67						
20	122831	AI857570	Hs.5120	ESTs				22.20		3.37		
20	122913	A1638774	Hs.105328	ESTs ESTs				32.20 41.80				
	123049 123076	BE047680 Al345569	Hs.211869 Hs.190046	ESTs	35.80			41.00		•		
	123136	AW451999	Hs.194024	ESTs			•				2.58	
0.5	123309	N52937	Hs.102679	ESTs					19.00			
25	123455	AA353113	Hs.112497	ESTs				82.80		3.95		
	123691 123756	AA609579 AA609971	Hs.112724 Hs.112795	ESTs EST	35.40				•	3.53		
	123802	AA620448	13.112130	Homo sapiens clone 24760 mRNA sequence	58.00							
	123837	AI807243	Hs.112893	ESTs				32.40				
30	123844	AA938905	Hs.120017	olfactory receptor, family 7; subfamily	20.00		2.63					
	123936	NM_004673		ESTS ESTS Mandaly similar to CLUCOSE TRANSPOR	29.00			70.60				
	123987 124013	C21171 Al521936	Hs.95497 Hs.107149	ESTs; Weakly similar to GLUCOSE TRANSPOR ESTs; Weakly similar to PTB-ASSOCIATED S	28.40			70.00				
	124160	R40290	Hs.124685	ESTs					13.00			
35	124205	H77570	Hs.108135	ESTs						4.74		
	124226	AA618527	Hs.190266	ESTs			2.35	20.40				
	124246 124348	H67680 Al796320	Hs.270962 Hs.10299	ESTs ESTs		17.00		29.40				
	124348	AW070211	Hs.102415	*yw35g11.s1 Morton Fetal Cochlea Homo sa		11.00	3.07					
40	124409	Al814166	Hs.107197	ESTs						3.14		
	124442	AW663632	Hs.285625	TATA box binding protein (TBP)-associate			2.48	20.00				
	124468	N51413	Hs.109284	ESTs calcium channel; voltage-dependent; alph				30.80				6.03
	124479 124519	AB011130 Al670056	Hs.127436 Hs.137274	ESTs; Weakly similar to SPLICEOSOME ASSO			2.50					4.00
45	124711	NM_004657		serum deprivation response (phosphatidy)	59.20							
	124866	AI768289	Hs.304389	ESTs		8.00		07.00				
	124874	BE550182	Hs.127826	ESTs ESTs				37.60	10.00			
	125097 125179	AW576389 AW206468	Hs.335774 Hs.103118	ESTs					10.00	3.12		
50	125200	AW836591	Hs.103156	ESTs							2.79	
	125299	T32982	Hs.102720	ESTs				34.20				
	125400	AL110151	Hs.128797	DKFZP586D0824 protein	29.00							
	125810 126176	H00083 BE242256	Hs.2441	aryl hydrocarbon receptor-interacting pr KIAA0022 gene product	32.20	12.00						
55	126303	D78841	110.2771	HUM525A05B Human placenta polyA+ (TFuji				33.60				
	126403	AW629054	Hs.125976	ESTs; Weakly similar to metalloprotease/	35.80							
	126507	AL040137	Hs.23964	ESTs; Weakly similar to HC1 ORF (M.muscu	20.50			29.80				
	126773	AA648284 AW962712	Hs.187584 Hs.126712	ESTs ESTs; Weakly similar to pIL2 hypothetica	39.60 28.80							
60	127307 127462	AA760776	Hs.293977	ea59b04.s1 NCL_CGAP_GCB1 Homo saplens c	20.00			34.40				
	127486	AW002846	Hs.105468	ESTs		9.00						
	127572	AA594027	Hs.191788	ESTs			2.36	00.40				
	127609	X80031	Hs.530	ESTs				29.40 37.20				•
65	127832 127898	AW976035 AA774725	Hs.292396 Hs.128970	ESTs ESTs				37.20			4.42	
UJ	128073	AW340720	Hs.125983	ESTs				38.40				
	128101	AA905730	Hs.128254	ESTs		7.33						
	128149	NM_012214		mannosyl (alpha-1;3-)-glycoprotein beta-			3.09				2.58	
70	128212 128333	W27411 W68800	Hs.336920 Hs.12126	glutathione peroxidase 3 (plasma) ESTs; Weakly similar to LR8 [H.sapiens]			3.05	34.40				
70	128364	N76462	Hs.269152	ESTs; Weakly similar to ZINC FINGER PROT		10.00		•				
	128426	Al265784	Hs.145197	ESTs							4.31	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel; s	31.20			44.00				
75	128634	AA464918	II- 99707	ESTs; Moderately similar to IIII ALU SUB				41.60 87.00				
75	128687 128726	AW271273 Al311238	Hs.23767 Hs.104476	ESTs ESTs			-	U1.00				4.02
	128773	NM_004131		granzyme B (granzyme 2; cytotoxic T-lymp					9.00			
	128833	W26667	Hs.184581	ESTs								3.76
٥٨	128870	H39537	Hs.75309	eukaryotic translation elongation factor			2.66			2 40		
80	128878	R25513	Hs.10683	ESTs					11.00	3.10		
	128885 128998	AF134803 W04245	Hs.180141 Hs.107761	cofilin 2 (muscle) ESTs; Weakly similar to PUTATIVE RHO/RAC					. 10		3.21	
	129000	AA744902	Hs.107767	ESTs; Moderately similar to CaM-KII inhi								3.68
05	129038	AW156903	Hs.108124	ribosomal protein L41	04.05					3.17		
85	129098	AW580945	Hs.330466	ESTs	34.60		•					

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	129210		Hs.202949	KIAA1102 protein			2.29					4.09
	129240 129262		Hs.237868 Hs.109843	interleukin 7 receptor ESTs			2.23			3.30		
5	129301	AF182277	Hs.330780	Human cytochrome P450-IIB (hIIB3) mRNA;								4.05 4.09
5	129331 129381		Hs.279772 Hs.110903	ESTs; Highly similar to CGI-38 protein [claudin 5 (transmembrane protein deleted			2.93					4.00
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1				160.80	10.00			
	129595 129613	U09550 AW978517	Hs.1154 Hs.172847	oviductal glycoprotein 1; 120kD ESTs; Weakly similar to collagen alpha 1					10.00	3.40		
10	129782	AW016932	Hs.104105	EST		9.00		07.00				
	129950 129958	F07783 R27496	Hs.1369 Hs.1378	decay accelerating factor for complement annexin A3				87.80 44.60				
	129959	AL036554	Hs.274463	defensin; alpha 1; myeloid-related seque			2.72					
15	130160	AA305688 NM_000328	Hs.267695	UDP-Gal:betaGlcNAc beta 1;3-gatactosyltr retinitis pigmentosa GTPase regulator			2.54	42.20				
13	130259 130273		Hs.153863	MAD (mothers against decapentaplegic; Dr			2.01	51.60				
	130312	AF056195	Hs.15430	DKFZP586G1219 protein						3.16		4.11
	130436 130523	NM_001928 AA999702	Hs. 135597 Hs. 214507	D component of complement (adipsin) ESTs						4.77		
20	130799	AB028945	Hs.12696	ESTs		6.00				3.54		
	130885 131002	NM_005883 AL050295	Hs.22039	adenomatous polyposis coli like KIAA0758 protein						J.54		3.50
	131012	AL039940	Hs.202949	KIAA1102 protein	44.00	20.00						
25	131031 131061	NM_001650 N64328	Hs.288650 Hs.268744	aquaporin 4 ESTs; Moderately similar to KIAA0273 [H.	41.20			31.40				
	131066	AW169287	Hs.22588	ESTS				29.60	0.00			
	131082 131087	AI091121 AF147709	Hs.246218 Hs.22824	ESTs; Weakly similar to zinc finger prot ESTs; Weakly similar to p160 myb-binding					9.00			3.86
••	131161	AF033382	Hs.23735	potassium voltage-gated channel; subfami						3.14		
30	131179 131182	AA171388 Al824144	Hs.184482 Hs.23912	DKFZP586D0624 protein ESTs						3.80		3.67
	131205	NM_003102		superoxide dismutase 3; extracellular			2.98					
	131277	AA131466	Hs.23767 Hs.25227	ESTs ESTs			3.15	32.20				
35	131281 131282	AA251716 X03350	Hs.4	alcohol dehydrogenase 3 (class I); gamma				OL.LU				3.44
	131285	AI567943	Hs.25274 Hs.25956	ESTs; Moderately similar to putative sev DKFZP564D206 protein		8.00				6.40		•
	131355 131391	R52804 AW085781	Hs.26270	ESTs		10.00						
40	131461	AA992841	Hs.27263	butyrate response factor 2 (EGF-response	28.80						4.03	
40	131487 131517	F13036 AB037789	Hs.27373 Hs.263395	Homo saptens mRNA; cDNA DKFZp56401763 (f ESTs; Highly similar to semaphorin VIa [39.00							
	131545	AL137432	Hs.28564	ESTs					11.00 10.00			
	131583 131647	AK000383 AA359615	Hs.323092 Hs.30089	ESTs; Weakly similar to dual specificity ESTs		-	2.47		10.00			
45	131675	H15205	Hs.30509	ESTs	45.80					3.06		
	131676 131708	Al126821 S60415	Hs.30514 Hs.30941	ESTs calcium channel; voltage-dependent; beta	45.00		2.28					
	131717	X94630	Hs.3107	CD97 antigen				40.60				3.78
50	131756 131762	AA443966 AA744902	Hs.31595 Hs.107767	ESTs ESTs; Moderately similar to CaM-KII inhi				40.00				3.67
••	131821	AA017247	Hs.164577	ESTs			2.87				3.48	
	131839 131861	AB014533 AL096858	Hs.33010 Hs.184245	KIAA0633 protein KIAA0929 protein Msx2 interacting nuclea	54.00						5.40	
ے ہے	132015	Al418006	Hs.3731	ESTs				49.20 34.80				
55	132070 132242	BE622641 AA332697	Hs.38489 Hs.42721	ESTs ESTs			2.68	34.00				
	132334	AW080704	Hs.45033	lacrimal proline rich prolein	04.00		4.66					
	132476 132490	AL119844 NM_001290	Hs.49476 Hs.4980	Homo saplens clone TUA8 Cri-du-chat regil UM binding domain 2	34.20		2.66					
60	132533	A1922988	Hs.172510	ESTs		13.00		20.60				
	132598 132619	X80031 H28855	Hs.530 Hs.53447	collagen; type fV; alpha 3 (Goodpasture ESTs; Moderately similar to kinesin ligh				30.60		4.02		
	132652	N41739	Hs.61260	ESTs					44.40	3.18		
65	132726	N52298	Hs.55608 Hs.300842	ESTs; Wealdy similar to cDNA EST yk484g1 ESTs			2.37		11.43			
05	133028 133071	R51604 BE384932	Hs.64313	ESTs			2.27					
	133120	NM_003278		tetranectin (plasminogen-binding protein			2.63					5.49
	133129 133147	AA428580 AA026533	Hs.65551 Hs.66	ESTs Interleukin 1 receptor-like 1			6.20					
70	133151	NM_014051		ESTs		*		31.40		3.69		
	· 133213 133276	AA903424 AW978439	Hs.6786 Hs.69504	ESTs ESTs				31.40	9.00			
	133377	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	41.20 50.20	•						
75	133407 133535	AF017987 AL134030	Hs.7306 Hs.284180	secreted frizzied-related protein 1 protocadherin 2 (cadherin-like 2)	9 0.2 U					3.72		
	133537	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr			2.65					3.35
	133656 133689	BE149455 NM_001872	Hs.75415 Hs.75572	Accession not listed in Genbank carboxypeptidase B2 (plasma)			2.00	90.80				
0.0	133779	T58486	Hs.222566	ESTs			2.00			3.05		
80	133978 133985	AF035718 L34657	Hs.78061 Hs.78146	transcription factor 21 platelet/endothellal cell adhesion molec			2.92	•				3.45
	134000	AW175787	Hs.334841	selenium binding protein 1								4.05
	134111	Al372588 AA285136	Hs.8022 Hs.301914	TU3A protein Homo sapiens mRNA; cDNA DKFZp586K1220 (f			4.49				3.27	
85	134185 134204	AA285136 Al873257	Hs.7994	ESTs; Weakly similar to CGI-69 protein (40.80				

	W	O 02/086	443		PCT/US02/12476					802/12476
	134641	Al092634	Hs.156114	protein tyrosine phosphatase; non-recept				22.22	3.76	
	134677	AA251363	Hs.177711	ESTs		45.00		32.20		
	134745	NM_000685	Hs.89472	angiotensin receptor 1B		15.00				
_	134749	T28499	Hs.89485	carbonic anhydrase IV			3.05			
5	134786	T29618	Hs.89640	anglopoietin 1 receptor; TEK tyrosine ki				57.80		
	134825	U33749	Hs.197764	thyroid transcription factor 1						3.73
	134978	AI829008	Hs.333383	ficolin (collagen/fibrinogen domain-cont			2.52			
	135010	N50465	Hs.92927	ESTs				31.60		
10	135053	AW796190	Hs.93678	ESTs					3.21	
10	135081	AF069517	Hs.173993	RNA binding motif protein 6	28.80					
	135091	AA493650	Hs.94367	ESTs						4.24
	135135	AA775910	Hs.95011	syntrophin; beta 1 (dystrophin-associate		8.00				
	135203	C15737	Hs.269386	ESTs					4.31	
	135236	A1636208	Hs.96901	ESTs	43.00					
15	135266	R41179	Hs.97393	Human mRNA for KIAA0328 gene; partial co					6	5.42
	135346	NM_000928	Hs.992	phospholipase A2; group IB (pancreas)			3.82			
	135378	AW961818	Hs.24379	potassium voltage-gated channel; shaker-			4.15			
	135387	NM_001972	Hs.99863	elastase 2; neutrophil	37.20					
	135388	W27965	Hs.99865	EST	38.80					
20	135402	L12398	Hs.99922	dopamine receptor D4					4.21	
				•						

TABLE 2B shows the accession numbers for those primekeys lacking unigenalD's for Table 2A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

	Pkey:	Unique Eos probeset iden	itifier number
• •	CAT num	ber: Gene cluster number	
30	Accession	n: Genbank accession numb	ers
	Pkey	CAT number Accession	ns
25	108447	434527 AA07912	
35	108550		7 AA084996
	108655		0 AA113013
	102397	443711 U41898	· · · · · · · · · · · · · · · · · · ·
	126303	1525933_1 D78841 D	
40	125810	1554054_1 H00083 F	
40	103627	2615_2 Z48513 Z	
	121366		AA405617 AW276706
	114609 115272		5 AA079537 17 AA211890 AA279425
	108338		7 AA21 1090 AA279425 3 AA070774
45	108434		9 AA078782 AA075788
73	123802	genbank_AA620448	AA620448
	102310	NOT_FOUND_entrez_U33	
	102636	entrez U67092 U67092	
	104776	genbank_AA026349	AA026349
50	120504	genbank AA256837	AA256837
	113502	genbank T89130T89130	
	108499	genbank_AA083103	AA083103
	101308	entrez_L41390 L41390	
	108629	genbank_AA102425	AA102425
55	103098		26593 X02850 D13070 AE000659 M17649 M87869 M87871 X61077 M16286 AF018169 X61079 S59351 X60142 AF043169
	103241	entrez_X76223 X76223	
	103508	entrez_Y10141 Y10141	
	103575	entrez_Z26256 Z26256	
60	119514	NOT_FOUND_entrez_W37	
UU	121082	genbank_AA398722	AA398722
	128634 105817	AA464918_at AA464918	
	121518	genbank_AA397825 genbank_AA412155	AA397825 AA412155
	114449	genbank_AA020736	AA020736
65	114648	genbank AA101056	AA101056
00	121950	genbank_AA429515	AA429515
	107723	genbank_AA015967	AA015967
	101123	BAINDIN LAW 19501	1 m i o o o i

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Table 3A shows 452 genes up-regulated in chronically diseased lung relative to normal tung. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Pkey: ExAccn: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number

UnigeneID: Unigene Title:

R1: R2:

Unigene number
Unigene gene title
80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of AI for normal lung samples.
80th percentile of AI for chronically diseased lung samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and 10

adenocarcinomas

70th percentile of AI for chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by the 90th percentile of normal lung samples, squamous cell carcinomas and adenocarcinomas minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples R3:

15		enronic	any diseased i	ung anu tumor samples			
	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2	R3
20	135423 135378	U50531 AW961818	Hs.138751 Hs.24379	Human BRCA2 region, mRNA sequence CG030 MUM2 protein	12.40		2.13
	135346	NM_000928	Hs.992	phospholipase A2, group IB (pancreas) ESTs	12.40		
	135235 135057	AW298244 U90268	Hs.293507 Hs.93810	cerebral cavernous malformations 1	11.67		
	134951	BE305081	Hs.169358	hypothetical protein	11.07	8.00	
25	134799	M36821	Hs.89690	GRO3 oncogene		8.20	
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous			
	134772	NM_000829	Hs.163697	glutamate receptor, ionotrophic, AMPA 4	29.80		4.00
	134752	BE246762	Hs.89499	arachidonate 5-lipoxygenase			1.93
30	134749	T28499	Hs.89485 Hs.8861	carbonic anhydrase IV ESTs			2.07
30	134696 134636	BE326276 NM 005582	Hs.87205	lymphocyte antigen 64 (mouse) homolog, r	13.60		
	134627	AI018768	Hs.12482	glyceronephosphate O-acyltransferase			1.92
	134622	AW975159	Hs.293097	ESTs, Weakly similar to A55380 faciogeni			1.92
25	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	13.20		4 70
35	134561	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h		6.20	1.78
	134468	NM_001772	Hs.83731 Hs.82921	CD33 antigen (gp67) solute carrier family 35 (CMP-sialic aci		0.20	
	134417 134343	NM_006416 D50683	Hs.82028	transforming growth factor, beta recepto			
	134323	BE170651	Hs.8700	deleted in liver cancer 1			
40	134300	NM_001430	Hs.8136	endothelial PAS domain protein 1			
	134299	AW580939	Hs.97199	complement component C1q receptor	00.00		
	134253	X52075	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	20.60 12.20		
	134182 133985	D52059 L34657	Hs.7972 Hs.78146	KIAA0871 protein platelet/endothelial cell adhesion molec	12.20		
45	133978	AF035718	Hs.78061	transcription factor 21			
	133835	A1677897	Hs.76640	RGC32 protein			•
•	133651	Al301740	Hs.173381	dihydropyrimidinase-like 2			
	133633	D21262	Hs.75337	nucleolar and coiled-body phosphprotein	15.20		
50	133565	AW955776	Hs.313500	ESTs, Moderately similar to ALU7_HUMAN A DNA segment, single copy probe LNS-CAI/L			1.77
50	133548 133488	AW946384 AA335295	Hs.178112 Hs.74120	adipose specific 2			****
	133478	X83703	Hs.31432	cardiac ankyrin repeat protein			2.08
	133337	AF085983	Hs.293676	ESTs		9.60	
<i>F F</i>	133200	AB037715	Hs.183639	hypothetical protein FLJ10210	20.00		1.77
55	133153	AF070592	Hs.66170	HSKM-B protein	30.60 22.60		
	133130 133120	AI128606 NM_003278	Hs.6557 Hs.65424	zinc finger protein 161 tetranectin (plasminogen-binding protein	22,00		
	132928	AW168082	Hs.169449	protein kinase C, alpha	13.80		
	132836	AB023177	Hs.29900	KIAA0960 protein			
60	132799	W73311	Hs.169407	SAC2 (suppressor of actin mutations 2,	41.60		
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	40.40	7 20	
	132548	X12830	Hs.193400 Hs.49476	interleukin 6 receptor Homo sapiens clone TUA8 Crt-du-chat regi		7.20 4.76	
	132476 132439	AL119844 AK001942	Hs.4863	hypothetical protein DKFZp566A1524			1.88
65	132240	AB018324	Hs.42676	KIAA0781 protein	21.20		
	132210	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2			1.99
	132199	AL041299	Hs.165084	ESTs	15.20		1.76
	131751	T96555	Hs.31562 Hs.31447	ESTs ESTs, Moderately similar to A46010 X-li	27.80		1.70
70	131745 131694	A1828559 NM_000246	Hs.3076	MHC class II transactivator	21.00	4.00	
70	131686	NM_012296	Hs.30687	GRB2-associated binding protein 2		•	
	131676	Al126821	Hs.30514	ESTs		6.20	
	131629	Z45794	Hs.238809	ESTs	21.40		
75	131589	C18825	Hs.29191	epithelial membrane protein 2		0.40	
75	131536	AA019201 AB037789	Hs.269210 Hs.263395	ESTs		9.40 3.59	
	131517 131355	R52804	Hs.25956	sema domain, transmembrane domain (TM), DKFZP564D206 protein		4.48	
	131253	R71802	Hs.24853	ESTs	15.00		
	131207	AF104266	Hs.24212	latrophilln			1.75
80	131156	A1472209	Hs.323117	ESTS		0.51	1.84
	131066	AW169287	Hs.22588	ESTs		3.54	
	131061	N64328	Hs.268744	KIAA1796 protein guanine nucleotide binding protein (G pr			1,93
	131053 130895	AA348541 AA641767	Hs.296261 Hs.21015	hypothetical protein DKFZp564L0864 simil	16.60		.,00
85	130762	D84371	Hs.1898	paraoxonase 1	12.00		
				-			

	W	O 02/086	443				
	130657	AW337575	Hs.201591	ESTs			
	130655	AI831962	Hs.17409	cysteine-rich protein 1 (intestinal)			0.00
	130589	AL110226	Hs.16441	DKFZP434H204 protein			2.08
5	130562	D50402	Hs.182611	solute carrier family 11 (proton-coupled		9.60	1.91
5	130555 130365	R69743 W56119	Hs.116774 Hs.155103	integrin, alpha 1 eukaryotic translation Initiation factor	11.60	9.00	
	130273	AW972422	Hs.153863	MAD (mothers against decapentaplegic, Dr	11.00	6.60	
	130259	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator		0.00	1.91
	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	21.20		
10	129958	R27496	Hs.1378	annexin A3		5.05	
	129898	Al672731	Hs.13256	ESTs			
	129875	AA181018	Hs.13056	hypothetical protein FLJ13920	18.60		
	129699	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas			
15	129626	F13272	Hs.111334	ferritin, light polypeptide	22.63		
13	129598 129593	N30436 A1338247	Hs.11556 Hs.98314	Homo sapiens cDNA FLJ12566 fis, clone NT Homo sapiens mRNA; cDNA DKFZp586L0120 (f	22.03		
	129565	X77777	Hs.198726	vasoactive intestinal peptide receptor 1			2.53
	129527	AA769221	Hs.270847	delta-tubulin	39.20		
	129402	W72062	Hs.11112	ESTs			2.11
20	129385	AA172106	Hs.110950	Rag C protein	15.20		
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	12.40		
	129312	T97579	Hs.110334	ESTs, Weakly similar to 178885 serine/th	20.83		
	129240	AA361258	Hs.237868	interleukin 7 receptor			1.95
25	129210	AL039940	Hs.202949	KIAA1102 protein		4.20	
25	129122	AW958473	Hs.301957	nudix (nucleoside diphosphate linked moi		4.20	
	129057 128946	N90866 Y13153	Hs.276770 Hs.107318	CDW52 antigen (CAMPATH-1 antigen) kynurenine 3-monooxygenase (kynurenine 3		5.20	
	128798	AF015525	Hs.302043	chemokine (C-C motif) receptor-like 2		0.20	
	128789	AW368576	Hs.139851	caveolin 2			2.24
30	128778	AA504776	Hs.186709	ESTs, Weakly similar to 138022 hypothet	12.20		
	128766	AW160432	Hs.296460	craniofacial development protein 1	26.40		
	128631	R44238	Hs.155546	KIAA1080 protein; Golgi-associated, gamm			1.78
	128624	BE154765	Hs.102647	ESTs, Weakly similar to TRHY_HUMAN TRICH			2.51
35	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	16.00		
35	128603	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	12.80	4.00	
	128598	AA305407	Hs.102308	potassium inwardly-rectifying channel, s ESTs		4.00	
	128458 128061	H55864 AF150882	Hs.56340 Hs.186877	sodium channel, voltage-gated, type XII,	17.20		
	127968	AA830201	Hs.124347	ESTs	21.30		
40	127959	AJ302471	Hs.124292	Homo saplens cDNA: FLJ23123 fis, clone L			
	127944	AI557081	Hs.262476	S-adenosylmethionine decarboxylase 1	10.60		
	127925	AA805151	Hs.3628	mitogen-activated protein kinase kinase	13.40		
	127896	A1669586	Hs.222194	ESTs	44.00	7.00	
45	127859	AA761802	Hs.291559	ESTs	14.00		
43	127817	AA836641	Hs.163085	ESTs	14.00 11.00		
	127742 127628	AW293496 AI240102	Hs.180138 Hs.322430	ESTs NDRG family, member 4	11.10		
	127609	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture			
	127582	AA908954	Hs.130844	ESTs	19.60		
50	127543	AK000787	Hs.157392	Homo saplens cONA FLJ20780 fis, clone CO	15.40		
	127535	AA558424	Hs.164450	ESTs	17.50		
	127404	Al379920	Hs.270224	ESTs	14.60		
	127396	L31968	Hs.187991	DKFZP564A122 protein	15.40		
55	127374	AA442797	Hs.312110	ESTs, Weakly similar to 138022 hypothet	14.60		
55	127346 127340	AA203616	Hs.44896	DnaJ (Hsp40) homolog, subfamily B, membe ESTs, Wealdy similar to ZN91_HUMAN ZINC	21.00 15.80		
	127340	BE047653 AW962712	Hs.119183 Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	13.50		
	127242	AW390395	Hs.181301	cathepsin S	22.60		
	127167	AA625690	Hs.190272	ESTs	21.40		
60	127046	AA321948	Hs.293968	ESTs	41.20		
	126928	AA480902	Hs.137401	ESTs	11.00		
	126900	AF137386	Hs.12701	plasmolipin		c co	1.78
	126852	AA399961		gb:zu68c01.r1 Soares_testis_NHT Homo sap	40.00	5.60	
65	126816	AA248234	Un 470000	gb:csg2228.seq.F Human fetal heart, Lamb	12.20 17.19		
03	126812	AB037860 AA648886	Hs.173933	nuclear factor I/A	13.57		
	126666 126845	AA316181	Hs.151999 Hs.61635	ESTs six transmembrane epithelial antigen of	15.40		
	126592	Al611153	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K	10.40	4.67	
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	18.00		
70	126433	AA325606		gb:EST28707 Cerebellum II Homo saplens c	16.77		
	126299	AW979155	Hs.298275	amino acid transporter 2	14.60		
	126218	AL049801	Hs.13649	Novel human gene mapping to chomosome 13		3.50	
	126182	AA721331	Hs.293771	ESTs	13.40		
75	126177	AW752782	Hs.129750	hypothetical protein FLJ10546	18.20		
75	126142	H86261	Hs.40568	ESTs	14.00		
	126077	M78772	Hs.210836	ESTs	16.59 17.40		
	125994 125934	Al990529 AA193325	Hs.270799	ESTs hypothelical protein FLJ21901	13.00		
	125934 125847	AM193325 AW161885	Hs.32646 Hs.249034	ESTs	49.57		
80	125831	H04043		gb:yj45c03.r1 Soares placenta Nb2HP Homo			
	125731	R61771	Hs.26912	ESTs	13.20		
	125676	BE612918	Hs.151973	hypothetical protein FLJ23511	11.20		
	125561	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S			
05	125552	H09701	Hs.278366	ESTs, Weakly similar to 138022 hypotheti	12.60		
85	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	33.40		

	W	O 02/086	143					PCT/US02/12476
		AA903229	Hs.153717	ESTs	20.00		1.80	
	125331	Al422996	Hs.161378	ESTs hypothetical protein FLJ13456	38.00 18.20			
	125309 125167	T12411 AL137540	Hs.183745 Hs.102541	netrin 4	10.20		1.95	
5	125139	AW194933	Hs.9788	hypothetical protein MGC10924 similar to			1.84	
	125042	T78906	Hs.269432	ESTs, Moderately similar to ALU1_HUMAN	21.80	40.00		
	124711	NM_004657	Hs.26530 Hs.270594	serum deprivation response (phosphatidyl FLVCR protein	23.20	10.60		
	124631 124578	NM_014053 N68321	Hs.231500	EST EST	21.43			
10	124574	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2			1.77	
	124472	N52517	Hs.102670	EST	37.20			
	124438 124357	BE178536 N22401	Hs.11090	membrane-spanning 4-domains, subfamily A gb:yw37g07.s1 Morton Fetal Cochlea Homo	14.64			
	124306	AW973078	Hs.293039	ESTs		4.00		
15	124214	H58608	Hs.151323	ESTs				
	124097	AW298235	Hs.101689	ESTs		27.20	2.03	
	123978 123972	T89832 T46848	Hs.170278 Hs.70337	ESTs Immunoglobulin superfamily, member 4		6.00	2.00	
	123961	AL050184	Hs.21610	DKFZP434B203 protein			1.79	
20	123936	NM_004673	Hs.241519	angiopoletin-like 1		15.80		
	123802 123734	AA620448 AA609861	Hs.312447	gb:ae58c09.s1 Stratagene lung carcinoma ESTs		4.23 4,20		
	123619	AA602964	16.012441	gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens	33.60			
0.5	123596	AA421130	Hs.112640	EST	10.93		0.40	•
25	123476	AA384564	Hs.108829	ESTs peptidylprolyl isomerase A (cyclophilin	11.20		2.18	
	123340 123190	AA504264 AA489212	Hs.182937 Hs.105228	EST	14.20			
	123136	AW451999	Hs.194024	ESTs		7.00		
20	123073	AA485061	Hs.105652	ESTs	31.20	4.80		
30	123055 122699	AA482005 AA456130	Hs.105102 Hs.301721	ESTs, Weakly similar to reverse transcri KIAA1255 protein		5.00		
	122679	AAB11286	Hs.192837	ESTs, Wealty similar to ALU5_HUMAN ALU S	14.40			
	122633	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg	40.00			
35	122553 122544	AA451884 AW973253	Hs.190121 Hs.292689	ESTs ESTs	15.40			
33	122485	AA524547	Hs.160318	FXYD domain-containing Ion transport reg			1.81	<i>:</i>
	122211	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H		12.10	4.05	
	122127	AW207175	Hs.106771	ESTs gb:zw78a10.s1 Soares_testis_NHT Homo sap			1.95 1.89	
40	122011 121992	AA431082 Al860775	Hs.98506	ESTs		3.60		
	121989	W56487	Hs.193784	Homo sapiens mRNA; cDNA DKFZp586K1922 (f			2.01	
	121835	AB033030	Hs.300670	KIAA1204 protein	12.43		1.85	
	121726 121690	AF241254 AV660305	Hs.178098 Hs.110286	angiotensin I converting enzyme (peptidy ESTs	12.43		1.82	•
45	121643	AA640987	Hs.193767	ESTs				
	121633	AA417011	Hs.98175	EST	14.00	16.40		
	121622 121497	AA416931 AA412031	Hs.126065 Hs.97901	ESTs EST	11.20	10.40		
	121351	AW206227	Hs.287727	hypothetical protein FLJ23132	12.20		4.00	
50	121314	W07343	Hs.182538	phospholipid scramblase 4	22.40		1.83	
	121242 121059	AA400857 AA393283	Hs.97509	ESTs qb:zt74e03.r1 Soares_testis_NHT Homo sap	14.80			
	120934	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	21.20			
55	120755	AA312934	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone	20.00		1.79	
55	120637 120484	AA811804 AA253170	Hs.96473	gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens EST	40.20			
	120336	N85785	Hs.181165	eukaryotic translation elongation factor		6.60		
	120266	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	16.80	4 70		
60	120132 120041	W57554 AA830882	Hs.125019 Hs.59368	ESTs ESTs		4.73	1.75	
00	119996	W88996	Hs.59134	EST		7.20		
	119970	AA767718	Hs.93581	hypothetical protein FLJ10512	11.20	2.70		
	119861 119824	W78816 W74536	Hs.49943 Hs.184	ESTs, Weakly similar to S65657 alpha-1C- advanced plycosylation and product-speci		3.78		
65	119740	AW021407	Hs.21068	hypothetical protein	20.20			
	119271	AI061118	Hs.65328	Fanconi anemia, complementation group F	15.20			
	119221	C14322 R45175	Hs.250700 Hs.117183	typtase beta 1 ESTs	12.60			
	119126 119073	BE245360	Hs.279477	ESTS	.2.00			
70	118928	AA312799	Hs.283689	activator of CREM in testis		10.00		
	118901	AW292577	Hs.94445	ESTs protein klnase NYD-SP15		3.96 9.60		
	118661 118607	AL137554 Al377444	Hs.49927 Hs.54245	ESTs, Weakly similar to \$65824 reverse t	10.40	0.00		
	118449	AI813865	Hs.164478	hypothetical protein FLJ21939 similar to			1.90	
75	118416	N66028	Hs.49105	FKBP-associated protein	16.20	4.00		
	118379 118329	N64491 N63520	Hs.48990	ESTs gb:yy62f01.s1 Soares_multiple_sclerosis_		6.60		
	118320	N63451	Hs.141600	ESTs, Weakly similar to alternatively s	47.65	3.80		
80	118253	AA497044	Hs.20887	hypothetical protein FLJ10392 chromosome 21 open reading frame 37	17.60 14.00			
30	118124 118056	N56968 AB037746	Hs.46707 Hs.42768	hypothetical protein DKFZp76100113			1.86	
	118032	N52802	Hs.47544	- EST		5.00		
	117840 117404	T26379 N39725	Hs.48802 Hs.15220	Homo saplens clone 23632 mRNA sequence zinc finger protein 106		4.00	1.90	
85	117314	N32498	Hs.42829	ESTs	14.20			

	VV	O 02/086	443				
	117209	W03011	Hs.306881	MSTP043 protein			
	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f			2.31
	116814	H50834		gb:yp66a10.s1 Soares fetal liver spleen	20.20		
_	116784	AB007979	Hs.301281	Homo sapiens mRNA, chromosome 1 specific		3.51	
5	116766	Al608657	Hs.95097	ESTs	16.20		
	116712	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp761I071 (fr		6.80	
	116707	H10344	Hs.49050	ESTs, Wealdy similar to A Chain A, Human	18.60		
	116351	AL133623	Hs.82501	similar to mouse Xm1 / Dhm2 protein	19.40		
10	116279	AW971248	Hs.291289	ESTs, Weakly similar to ALU1_HUMAN ALU S			0.42
10	116166	AL039940	Hs.202949	KIAA1102 protein			2.13
	116152	AL040521	Hs.15220	zinc finger protein 106	13.20		1.75
	116117	BE613410	Hs.31575	SEC63, endoplasmic reticulum translocon	30.11		
	116107	AL133916 AA001732	Hs.172572	hypothelical protein FLJ20093	30.11		2.36
15	115965		Hs.173233 Hs.44198	hypothetical protein FLJ10970 intracellular membrane-associated calciu	18.20		2.50
15	115955	AF263613	Hs.332938	hypothetical protein MGC5370	18.57		
	115844 115683	Al373062 AF255910	Hs.54650	junctional adhesion molecule 2	10.31	23.00	
•	115673	AA406341	Hs.269908	Homo saplens cDNA FLJ11991 fis, clone HE	11.82	20.00	
	115672	Al889110	Hs.73251	ESTs	10.60		
20	115566	Al142336	Hs.43977	Human DNA sequence from clone RP11-196N1	10.00		1.76
20	115313	AA808001	Hs.184411	albumin	25.20		1.70
	115279	AW964897	Hs.290825	ESTs	25.25	8.00	
	115230	AA278300	Hs.124292	Homo saplens cDNA: FLJ23123 fis, done L		0.00	1.80
	115110	AK001671	Hs.11387	KIAA1453 protein	14.20		1.00
25	114999	BE246481	Hs.87856	ESTs	19.20		
23	114930	AA237022	Hs.188717	ESTs	10.20	5.60	
	114922	AA235672	Hs.87491	ESTs		3.60	
	114837	BE244930	Hs.166895	ESTs	43.70	0.00	
	114769	AA149060	Hs.296100	ESTs	11.00		
30	114761	AA143781	Hs.126280	hypothetical protein FLJ23393	14.00		
-	114736	Al610347	Hs.103812	ESTs. Moderately similar to ALU1_HUMAN A		4.20	
	114596	AA310162	Hs.169248	cytochrome c	10.71		
	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	20.40		
	114455	H37908	Hs.271616	ESTs, Wealdy similar to ALUS_HUMAN ALU S	20.40		
35	114452	Al369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE		17.20	
	114359	NM_016929	Hs.283021	chloride intracellular channel 5			2.09
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	12.40		
	114251	H15261	Hs.21948	ESTs			2.00
	114138	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr		11.40	
40	114124	W57554	Hs.125019	ESTs		6.04	
	113946	AW083883	Hs.37896	Homo sapiens cDNA FLJ13510 fis, clone PL			1.82
	113695	T96965	Hs.17948	ESTs, Weakly similar to ALUB_HUMAN IIII			
	113606	NM_013343	Hs.278951	NAG-7 protein			2.15
4 -	113590	R49642	Hs.142447	ESTs, Weakly similar to ALU1_HUMAN ALU S		3.60	
45							
10	113560	T91015	Hs.268626	ESTs	32.00		
1.5	113552	Al654223	Hs.16026	hypothetical protein FLJ23191	32.00		
1.5	113552 113540	Al654223 AW152618		hypothetical protein FLJ23191 ESTs	32.00		
13	113552 113540 113502	Al654223 AW152618 T89130	Hs.16026 Hs.16757	hypothetical protein FLJ23191 ESTs gb:ye12d01.s1 Stratagene lung (937210) H		8.35	
	113552 113540 113502 113288	Al654223 AW152618 T89130 Al076838	Hs.16026 Hs.16757 Hs.12967	hypothetical protein FLJ23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs	32.00 12.40		
50	113552 113540 113502 113288 113252	Al654223 AW152618 T89130 Al076838 NM_004469	Hs.16026 Hs.16757 Hs.12967 Hs.11392	hypothetical protein FLJ23191 ESTs gb:ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en		8.35 4.27	
	113552 113540 113502 113288 113252 113238	AI654223 AW152618 T89130 AI076838 NM_004469 R45467	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813	hypothetical protein FLJ23191 ESTs gb:ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs	12.40		
	113552 113540 113502 113288 113252 113238 113203	Al654223 AW152618 T89130 Al076838 NM_004469 R45467 AA743563	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305	hypothetical protein FLJ23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs			4.00
	113552 113540 113502 113288 113252 113238 113203 113195	Al654223 AW152618 T89130 Al076838 NM_004469 R45467 AA743563 H83265	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881	hypothetical protein FLJ23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom	12.40 21.20		1.92
50	113552 113540 113502 113288 113252 113238 113203 113195 113089	AI654223 AW152618 T89130 AI076838 NM_004469 R45467 AA743563 H83265 T40707	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862	hypothetical protein FLJ23191 ESTs gb:ye12401.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs	12.40	4.27	1.92
	113552 113540 113602 113288 113252 113238 113203 113195 113089 113076	AI654223 AW152618 T89130 AI076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198	hypothetical protein FLJ23191 ESTs gb:ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs zinc finger protein 204	12.40 21.20	4.27 6.00	1.92
50	113552 113540 113602 113288 113252 113238 113203 113195 113089 113076 113009	Al654223 AW152618 T89130 Al076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246	hypothetical protein FLJ23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs	12.40 21.20	4.27 6.00 9.40	1.92
50	113552 113540 113502 113288 113252 113203 113195 113069 113076 113009 112937	Al654223 AW152618 T89130 Al076838 NM_004469 R45467 AA743563 H63265 T40707 AF033199 T23699 Al694320	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295	hypothetical protein FLJ23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs zinc finger protein 204 ESTs ESTs, Weakly similar to T17248 hypotheti	12.40 21.20 14.33	4.27 6.00	1.92
50	113552 113540 113602 113288 113252 113238 113203 113195 113009 113009 112937 112891	Al654223 AN152618 T89130 Al076838 NM_004469 R45467 AA743563 H63265 T40707 AF033199 T23699 Al694320 T03927	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246	hypothetical protein FLJ23191 ESTs gb:ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs zinc finger protein 204 ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Mederately similar to A46010 X-li	12.40 21.20 14.33	4.27 6.00 9.40	1.92
50 55	113552 113540 113602 113288 113252 113238 113203 113195 113076 113079 112037 112891 112794	Al654223 AV152618 T89130 Al076838 NM_004469 R45469 R454363 H83265 T40707 AF033199 T23699 Al694320 T03927 R97018	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147	hypothetical protein FLJ23191 ESTs gb.ye12001.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T46010 X-li gb.yq74b08.s1 Soares fetal liver spleen	12.40 21.20 14.33 10.57 26.60	4.27 6.00 9.40	1.92
50	113552 113540 113562 113288 113252 113238 113203 113195 113089 113076 113009 112937 112891 112794 112691	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 Al694320 T03927 T03927	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147	hypothetical protein FLI23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs	12.40 21.20 14.33 10.57 26.60 15.33	4.27 6.00 9.40	1.92
50 55	113552 113540 113502 113288 113252 113238 113203 11395 113076 113009 112937 112891 112799 112799 112799 112799	Al654223 AN7152618 T89130 Al076838 NM_004469 R45467 AA743563 HB3265 T40707 AF033199 T23699 Al694320 T03927 R97018 R88708 AW004045	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.220647 Hs.203365	hypothetical protein FLI23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs zinc finger protein 204 ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs ESTs	12.40 21.20 14.33 10.57 26.60 15.33 15.60	4.27 6.00 9.40	1.92
50 55	113552 113540 113528 113288 113252 113238 113039 113076 113099 112937 112891 112794 112602 112366	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 A454563 H83265 T40707 AF033199 T23699 Al694320 T03927 R97018 R88708 AW004045 AF035318	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.220647 Hs.203365 Hs.12533	hypothetical protein FLI23191 ESTs byse1201.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs zinc finger protein 204 ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb;yq74b08.s1 Soares fetal liver spleen ESTs ESTs Homo saptens clone 23705 mRNA sequence	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40	4.27 6.00 9.40	1.92
50 55	113552 113502 113502 113288 113252 113238 113095 113099 113076 113009 112937 112691 112691 112691 112602 112210	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 Al694320 T03927 T037018 R88708 AV004045 AF035318 R49645	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.189813 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.220647 Hs.2203465 Hs.12533 Hs.12533	hypothetical protein FLI23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs ESTs Homo saplens clone 23705 mRNA sequence ESTs	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00	4.27 6.00 9.40	1.92
50 55 60	113552 113540 113502 113288 113252 113238 113093 113099 112937 112891 112691 112602 112366 112210	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 Al694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.203365 Hs.12533 Hs.7004 Hs.22689	hypothetical protein FLI23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 (f	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00	4.27 6.00 9.40	1.92
50 55	113552 113502 113502 113288 113252 113293 113195 113099 113076 113009 11297 112691 112691 11266 112210 112264 112210 112210 112988	AI654223 AVN152618 T89130 AI076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 AI694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390 R42379	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.220647 Hs.203365 Hs.12533 Hs.7004 Hs.22689 Hs.138283	hypothetical protein FLI23191 ESTs byse12001.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs Zinc finger protein 204 ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb;yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 (f	12.40 21.20 14.33 10.57 26.60 15.33 15.40 14.00 13.00 11.00	4.27 6.00 9.40	1.92
50 55 60	113552 113502 113502 113288 113252 113283 113293 113195 113079 112937 112891 112794 112691 112664 1112964 111987	Al654223 AV152618 T89130 Al076838 NM_004469 R45469 R45463 H83265 T40707 AF033199 T23699 Al694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390 R42379 NM_015310	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.220647 Hs.220647 Hs.220644 Hs.22689 Hs.138283 Hs.6763	hypothetical protein FLJ23191 ESTs Gbye 12001.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs, ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gbyq74b08.s1 Soares fetal liver spleen ESTs ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp586O1318 (f ESTs KIAA0942 protein	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00	4.27 6.00 9.40	
50 55 60	113552 113540 113540 113581 113288 113252 113233 113195 113089 113099 112937 112891 112691 112691 112604 111987 111987 111987	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 Al694320 T03927 R97018 R88708 AV004045 AF035318 R49645 AL049390 R42379 NM_015310 AA593731	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.203365 Hs.12533 Hs.12533 Hs.12533 Hs.12533 Hs.12533 Hs.12689 Hs.138283 Hs.138283	hypothetical protein FLI23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 [f ESTs, Moderately similar to ALU5_HUMAN A	12.40 21.20 14.33 10.57 26.60 15.33 15.40 14.00 13.00 11.00	4.27 6.00 9.40	1.77
50 55 60	113552 113540 113540 113552 113238 113252 113238 113195 113076 113076 113079 112794 112691 112691 112691 112691 112691 112981 112981 112981 112981 112981 112981 112981 112981 112981 112981 112981 112981 112981 111987 111987 111987 111987	AI654223 AVN152618 T89130 AI076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 AI694320 T03927 R97018 R88708 AV004045 AF035318 R49645 AL049390 R42379 NM_015310 H04607	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.220647 Hs.233365 Hs.12533 Hs.7004 Hs.22689 Hs.138283 Hs.6763 Hs.325823	hypothetical protein FLJ23191 ESTs Gyp.41201.s1 Stratagene lung (937210) H ESTs C-fos induced growth factor (vascular en ESTs ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs zinc finger protein 204 ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 [f ESTs KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A ESTs	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40	4.27 6.00 9.40	
50556065	113552 113502 113502 113288 113252 113203 113195 113099 112937 112691 112691 112691 112694 111987 111803 1111987 111803	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 R45463 H83265 T40707 AF033199 T23699 Al694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390 R42379 NM_015310 AA593731 H04607 T91061	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.220647 Hs.220647 Hs.220647 Hs.220345 Hs.12533 Hs.7004 Hs.22689 Hs.138283 Hs.6763 Hs.325823 Hs.9218 Hs.194178	hypothetical protein FLJ23191 ESTs Gyp.412001.s1 Stratagene lung (937210) H ESTs C-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb;yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens chone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp586O1318 (f ESTs KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A ESTs ESTs, Moderately similar to PC4259 ferri	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40	4.27 6.00 9.40	1.77
50 55 60	113552 113502 113288 113252 113288 113252 113203 113195 113009 112937 112891 112794 112691 11264 111987 111803 111737 111803 111737 111803 111737 111803	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 A4743563 H83265 T40707 AF033199 T23699 Al694320 T03927 R97018 R88708 AV004045 AF035318 R49645 AL049390 R42379 NM_015310 AA593731 H04607 T91061 R07856	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.189813 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.220647 Hs.22089 Hs.13253 Hs.7004 Hs.22689 Hs.138283 Hs.6763 Hs.325823 Hs.9218 Hs.194178 Hs.16355	hypothetical protein FLI23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 (f ESTs, Moderately similar to ALU5_HUMAN A ESTs ESTs, Moderately similar to PC4259 ferri ESTs, Moderately similar to PC4259 ferri	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40	4.27 6.00 9.40	1.77 1.86
50556065	113552 113540 113502 113288 113252 113238 113059 113009 113009 112937 112891 112691 112691 112602 112360 11291 112064 111998 111998 111998 111998 111998 111998 111998 1119064 1119064 111918	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 Al694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390 R42379 N40607 T91061 R07856 AL157484	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.8198 Hs.1283 Hs.220647 Hs.220647 Hs.220365 Hs.12533 Hs.7004 Hs.22689 Hs.138283 Hs.6763 Hs.1325823 Hs.94178 Hs.194178 Hs.16355 Hs.122483	hypothetical protein FLI23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 (f ESTs KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A ESTs ESTs, Moderately similar to PC4259 ferri ESTs Homo sapiens mRNA; cDNA DKFZp762M127 (fr	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40 23.00 11.02	4.27 6.00 9.40	1.77
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5055606570	113552 113540 113540 113288 113252 113283 113293 113995 113076 113009 112937 112691 112691 112691 112691 11298 111998	Al654223 AV152618 T89130 Al076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 Al694320 T037018 R88708 AV004045 AF035318 R49645 AL049390 R42379 NM_015310 AA593731 H04607 T91061 R07856 AL157484 AA373527 AVV058350 Al247763	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.19305 Hs.8881 Hs.270862 Hs.8198 Hs.7246 Hs.6295 Hs.293147 Hs.220647 Hs.20365 Hs.12533 Hs.7004 Hs.22689 Hs.325823 Hs.6763 Hs.325823 Hs.6763 Hs.194178 Hs.16355 Hs.16355 Hs.16355 Hs.16355 Hs.16355 Hs.16625 Hs.19385 Hs.16762 Hs.19385 Hs.16762 Hs.16628 Hs.16628 Hs.16628	hypothetical protein FLI23191 ESTs Cytos Induced growth factor (vascular en ESTs Cytos Induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to A46010 X-li gb;yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 (f ESTs KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A ESTs ESTs, Moderately similar to PC4259 ferri ESTs Homo saplens mRNA; cDNA DKFZp762M127 (fr CGI-58 protein Homo saplens mRNA; cDNA DKFZp564B2062 (f ESTs ESTs	12.40 21.20 14.33 10.57 26.60 15.33 15.60 14.00 13.00 11.00 22.40 23.00 11.02 18.40 27.60	4.27 6.00 9.40	1.77 1.86
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505560657075	113552 113502 113502 113288 113252 113283 113203 113195 113079 112937 112937 112691 112694 111987 111803 111737 111605 111510 111347 111247 11247 11247 11247 11247 11247 11247 11247 11247 11247 1124	AI654223 AV152618 T89130 AI076838 NM_004469 R45467 R45467 T40707 AF033199 T23699 AI694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390 R42379 NM_015310 AA593731 H04607 T91061 R07856 AL157484 AA373527 AW058350 AL147763 R63503 AW058463 H03109 AJ767183 AB032417	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.6295 Hs.293147 Hs.220647 Hs.220647 Hs.2203365 Hs.12533 Hs.7004 Hs.22689 Hs.138283 Hs.6763 Hs.325823 Hs.9218 Hs.194178 Hs.16355 Hs.194178 Hs.16355 Hs.1940 Hs.16929 Hs.16929 Hs.108920 Hs.108920 Hs.108920 Hs.108920 Hs.108920 Hs.108920 Hs.108920 Hs.108920 Hs.26942 Hs.19545	hypothetical protein FLJ23191 ESTs Usys 12001.s1 Stratagene lung (937210) H ESTs C-fos induced growth factor (vascular en ESTs ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens chone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp586O1318 (f ESTs KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A ESTs ESTs, Moderately similar to PC4259 ferri ESTs Homo saplens mRNA; cDNA DKFZp762M127 (fr CGI-58 protein Homo saplens mRNA; cDNA DKFZp564B2062 (f ESTs ESTs ESTs zinc-fingers and homeoboxes 1 HT018 protein ESTs ESTs ESTs ESTs	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40 23.00 11.02 18.40 27.60 14.80 24.71 12.20	4.27 6.00 9.40	1.77 1.86 1.88
505560657075	113552 113502 113502 113288 113252 113288 113203 113195 113089 113079 112937 112891 112794 112691 11264 111987 111803 111737 111803 111737 111605 111510 111341 111247 111247 111242 110824 110837 110824 110876	AI654223 AV152618 T89130 AI076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 AI694320 T03927 T03927 R97018 R88708 AV0004045 AF036318 R49645 AL049390 R42379 NM_015310 AA593731 H04607 T91061 R07856 AL157484 AA373527 AVV058350 AI247763 R63503 R63503 R63503 H03109 AI767183 AB032417 H60869	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.270862 Hs.8881 Hs.270866 Hs.6295 Hs.293147 Hs.220647 Hs.22089 Hs.138283 Hs.7004 Hs.22689 Hs.138283 Hs.7004 Hs.22689 Hs.138283 Hs.7054 Hs.16355 Hs.325823 Hs.16355 Hs.16355 Hs.16628 Hs.16928 Hs.16928 Hs.16928 Hs.16928 Hs.16928 Hs.16928 Hs.108920 Hs.108920 Hs.108920 Hs.129440 Hs.108920 Hs.19845 Hs.26942 Hs.19895	hypothetical protein FLI23191 ESTs gb.ye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gb.yq74b08.s1 Soares fetal liver spleen ESTs ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp586O1318 (f ESTs, Moderately similar to ALU5_HUMAN A ESTs Moderately similar to PC4259 ferri ESTs Homo saplens mRNA; cDNA DKFZp564B2062 (f ESTS ESTS chorderately similar to PC4259 ferri ESTS Homo saplens mRNA; cDNA DKFZp564B2062 (f ESTS ESTS ESTS ESTS ESTS ESTS ESTS EST	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40 23.00 11.02 18.40 27.60 14.80 24.71 12.20	6.00 9.40 12.20	1.77 1.86 1.88
505560657075	113552 113502 113502 113288 113252 113293 113195 113099 113076 113009 11297 112691 112691 112691 112691 112691 112794 111898 111987 111805 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11151 111605 11176 111605 11176 11176 11176 111776 1110776	AI654223 AW152618 T89130 AI076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 AI694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390 R42379 NM_015310 AA593731 H04607 T91061 R07856 AL157484 AA373627 AW058350 AV058453 R49645 AL157484 AA593731 H04607 T91061 R07856 AL157484 AA373627 AW058350 AV058463 R49645 AL157484 AA373627 AW058350 AK167763 R63503 AW058463 AW058463 R6350 AW058663 AW	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.27246 Hs.293147 Hs.220647 Hs.2203465 Hs.233145 Hs.220647 Hs.203365 Hs.12533 Hs.7004 Hs.12533 Hs.7004 Hs.18283 Hs.6763 Hs.194178 Hs.194178 Hs.16355 Hs.16355 Hs.16355 Hs.16555 Hs.16762 Hs.19385 Hs.16928 Hs.12940 Hs.12940 Hs.12940 Hs.12940 Hs.12940 Hs.12940 Hs.12940 Hs.12940 Hs.12940 Hs.12942 Hs.19545 Hs.107872	hypothetical protein FLJ23191 ESTs ESTs c-fos induced growth factor (vascular en ESTs C-fos induced growth factor (vascular en ESTs ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs Zinc finger protein 204 ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to A46010 X-li gb;yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 (f ESTs KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A ESTs ESTs, Moderately similar to PC4259 ferri ESTs Homo saplens mRNA; cDNA DKFZp762M127 (fr CGI-58 protein Homo saplens mRNA; cDNA DKFZp564B2062 (f ESTs ESTs Zinc-fingers and homeoboxes 1 HTT018 protein ESTs frizzled (Drosophila) homolog 4 ESTs hypothetical protein FLJ20761	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40 23.00 11.02 18.40 27.60 14.80 24.71 12.20 13.00	6.00 9.40 12.20	1.77 1.86 1.88 2.18 1.75
50 55 60 65 70 75 80	113552 113502 113502 113288 113252 113203 113195 113076 113009 112937 112691 112691 112691 112691 112691 112691 112794 112806 11298 111987 111803 111987 111803 111510 111341 111280 111247 111280 11280 1	AI654223 AVN152618 T89130 AI076838 NM_004469 R45467 AA743563 H83265 T40707 AF033199 T23699 AI694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390 R42379 NM_015310 AA593731 H04607 T91061 R07856 AL157484 AA373527 AW058350 AI247763 R63503 AW058463 H03109 AT767183 AB032417 H60869 AK000768 R44557	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.10305 Hs.8881 Hs.270862 Hs.6295 Hs.6295 Hs.223147 Hs.220647 Hs.220647 Hs.220647 Hs.22689 Hs.133283 Hs.6763 Hs.19385 Hs.19385 Hs.16355 Hs.16762 Hs.19385 Hs.16762 Hs.19385 Hs.16762 Hs.16928 Hs.19385 Hs.16762 Hs.16928 Hs.16928 Hs.16928 Hs.16928 Hs.172940 Hs.172940 Hs.172940 Hs.172940 Hs.172940 Hs.172945 Hs.1737889 Hs.177872 Hs.177872 Hs.177872 Hs.177872 Hs.177872 Hs.177872 Hs.177872	hypothetical protein FLI23191 ESTs Gyp. 12001.s1 Stratagene lung (937210) H ESTs Gyp. 12001.s1 Stratagene lung (937210) H ESTs Gyp. 12001.s1 Stratagene lung (937210) H ESTs Cyp. 12001.s1 Stratagene lung (937210) H ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Weakly similar to T46010 X-li gb;yq74b08.s1 Soares fetal liver spleen ESTs Homo saplens clone 23705 mRNA sequence ESTs Homo saplens mRNA; cDNA DKFZp58601318 (f ESTs KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A ESTs ESTs, Moderately similar to PC4259 ferri ESTs ESTs, Moderately similar to PC4259 ferri ESTs Homo saplens mRNA; cDNA DKFZp762M127 (fr CGI-58 protein Homo saplens mRNA; cDNA DKFZp564B2062 (f ESTs ESTs zinc-fingers and homeoboxes 1 HT018 protein ESTs fritzzled (Drosophila) homolog 4 ESTs	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40 23.00 11.02 18.40 27.60 14.80 24.71 12.20	6.00 9.40 12.20	1.77 1.86 1.88 2.18 1.75
505560657075	113552 113540 113540 113540 113552 113288 113253 113076 113009 112937 112891 112794 112691 112664 111987 111803 111737 111803 111737 111605 111510 111247 111247 111247 111247 111247 110924 110824 110924 110837 110826 110676 110676 110699 1106998	AI654223 AV152618 T89130 AI076838 NM_004469 R45467 A4743563 H83265 T40707 AF033199 T23699 AI694320 T03927 R97018 R88708 AW004045 AF035318 R49645 AL049390 R42379 NM_015310 AA593731 H04607 T91061 R07856 AL157484 AA373527 AW058350 AL247763 R63503 AW058463 H03109 AI767183 AB032417 H60869 AK000768 R44557 AI796320	Hs.16026 Hs.16757 Hs.12967 Hs.11392 Hs.189813 Hs.270862 Hs.8881 Hs.270862 Hs.6295 Hs.293147 Hs.203365 Hs.220647 Hs.22689 Hs.138283 Hs.7004 Hs.22689 Hs.138283 Hs.194178 Hs.16355 Hs.22483 Hs.194178 Hs.16355 Hs.2483 Hs.194178 Hs.16625 Hs.16928 Hs.16928 Hs.16928 Hs.108920 Hs.108920 Hs.108920 Hs.107872 Hs.107872 Hs.107872 Hs.107872 Hs.107872 Hs.107872 Hs.107872 Hs.107872 Hs.107872 Hs.107872 Hs.107872	hypothetical protein FLJ23191 ESTs ESTs gbye12d01.s1 Stratagene lung (937210) H ESTs c-fos induced growth factor (vascular en ESTs ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to S41044 chromosom ESTs ESTs, Weakly similar to T17248 hypotheti ESTs, Moderately similar to A46010 X-li gby.q74b08.s1 Soares fetal liver spleen ESTs Homo sapiens chone 23705 mRNA sequence ESTs Homo sapiens mRNA; cDNA DKFZp586O1318 (f ESTs KIAA0942 protein ESTs, Moderately similar to ALU5_HUMAN A ESTs ESTs, Moderately similar to PC4259 ferri ESTs Homo sapiens mRNA; cDNA DKFZp762M127 (fr CGL-58 protein Homo sapiens mRNA; cDNA DKFZp564B2062 (f ESTs ESTs ESTs Zino-fingers and homeoboxes 1 HT018 protein ESTs hypothetical protein FLJ20761 ESTs hypothetical protein FLJ20761 ESTS Homo sapiens cDNA FLJ13545 fis, clone PL	12.40 21.20 14.33 10.57 26.60 15.33 15.60 15.40 14.00 13.00 11.00 22.40 23.00 11.02 18.40 27.60 14.80 24.71 12.20 13.00	6.00 9.40 12.20	1.77 1.86 1.88 2.18 1.75

	W	O 02/086	443				
	109842	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	23.83		0.04
	109837	H00656	Hs.29792 Hs.12024	ESTs, Weakly similar to 138022 hypotheti		17.20	3.91
	109796 109688	Al800515 R41900	Hs.22245	ESTs ESTs		9.60	
5	109648	H17800	Hs.7154	ESTs	22.80		
	109613	H47315	Hs.27519 Hs.26981	ESTs ESTs			
	109550 109523	AW021488 AW193342	Hs.24144	ESTs			1.89
••	109472	AK001989	Hs.91165	hypothetical protein		6.00	
10	109355	AA524525	Hs.48297	DKFZP586C1620 protein	15.00 25.60		
	109260 108781	AW978515 AA128654	Hs.131915	KIAA0863 protein gb:zn98g07.s1 Stratagene fetal retina 93	14.20		
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheli	11.00		
15	108573	AA086005	11- 00055	gb:zl84c04.s1 Stratagene colon (937204)	26.00		
15	108480 108382	AL133092 NM_006770	Hs.68055 Hs.67726	hypothetical protein DKFZp434f0428 macrophage receptor with collagenous str			1.83
	108174	AA055632	Hs.303070	ESTs	15.20		
	108138	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	45.44	3.60	
20	108087 108048	AA045708 AI797341	Hs.40545 Hs.165195	ESTs Homo sapiens cDNA FLJ14237 fis, clone NT	15.44	11.40	
20	108041	AW204712	Hs.61957	ESTs			
	107997	AL049176	Hs.82223	chordin-like		4.76	
	107994	AA036811	Hs.48469 Hs.61460	LIM domains containing 1 lg superfamily receptor LNIR	14,20		
25	107922 107681	BE153855 BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	51.80		
	107666	AA010611	Hs.60418	EST	29.20		
	107332 107292	T87750 BE166479	Hs.183297 Hs.4789	DKFZP566F2124 protein Homo sapiens serologically defined breas	10.73 32.00		
	107232	AI034467	Hs.34650	ESTs	17.40		
30	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	10.43		
	107160	AA314490 Al076459	Hs.27669 Hs.15978	KIAA1563 protein KIAA1272 protein	11.40		
	107054 107029	AF264750	Hs.288971	myeloid/lymphoid or mixed-lineage leukem	21.40		
25	106999	H93281	Hs.10710	hypothetical protein FLJ20417	35.80		4 70
35	106954	AF128847	Hs.204038	indolethylamine N-methyltransferase serum deprivation response (phosphatidyl			1.76
	106870 106865	Al983730 AW192535	Hs.26530 Hs.19479	ESTs	13.40		
	106844	AA485055	Hs.158213	sperm associated antigen 6		7.13	
40	106820	NM_016831		period (Drosophila) homolog 3	13.00	7.00	
40	106818 106797	AK002135 AI768801	Hs.3542 Hs.169943	hypothetical protein FLJ11273 Homo sapiens cDNA FLJ13569 fis, clone PL	13.00		2.05
	106773	AA478109	Hs.188833	ESTs			
	106747	NM_007118	Hs.171957	triple functional domain (PTPRF interact	12.60 10.60		
45	106743 106667	8E613328 AW360847	Hs.21938 Hs.16578	hypothetical protein FLJ12492 ESTs	10.00		
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr			2.40
	106567	AW450408	Hs.86412	chromosome 9 open reading frame 5			1.78 1.76
	106562 106536	AL031846 AA329648	Hs.152151 Hs.23804	plakophilin 4 ESTs, Weakly similar to PN0099 son3 prot			2.19
50	106533	AL134708	Hs.145998	ESTs	23.20		
	106507	AA259068	Hs.267819 Hs.115537	protein phosphatase 1, regulatory (Inhib putative dipeptidase	15.20		
	106490 106474	AA404265 BE383668	Hs.42484	hypothetical protein FLJ10618	10.44		
~ ~	106211	AA428240	Hs.126083	ESTs		29.80	
55	105986	AB037722	Hs.8707 Hs.25691	KIAA1301 protein receptor (calcitonin) activity modifying		3.70	1.94
	105894 105847	A1904740 AW964490	Hs.32241	ESTs, Weakly similar to \$65657 alpha-1C-			1.75
	105803	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	40.74		2.47
60	105731 105729	AA834664 H46612	Hs.29131 Hs.293815	nuclear receptor coactivator 2 Homo sapiens HSPC285 mRNA, partial cds	10.71		
OU	105688	Al299139	Hs.17517	ESTs	23.40		
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	37.20	0.20	
•	105101 104989	H63202 R65998	Hs.38163 Hs.285243	ESTs hypothetical protein FLJ22029		8.30 8.09	
65	104986	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1			1.92
	104969	A1670947	Hs.78406	phosphatidylinositol-4-phosphate 5-kinas		5.40	
	104903 104896	AI436323 AW015318	Hs.31141 Hs.23165	Homo saplens mRNA for KIAA1568 protein, ESTs	13.80	7.60	
	104865	T79340	Hs.22575	Homo saplens cDNA: FLJ21042 fis, clone C			
70	104825	AA035613	Hs.141883	ESTs			1.87
	104781 104776	AA099904 AA026349	Hs.21610	DKFZP434B203 protein gb:zj99f01.s1 Soares_pregnant_uterus_NbH		10.20	1.93
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor		5.69	
75	104667	AI239923	Hs.30098	ESTs		3.82	
75	104404	H58762	He 27////	gb:EST00057 HE6W Homo sapiens cDNA clone Homo sapiens cDNA FLJ10229 fis, clone HE	27.20	4.20	
	104392 104212	AA076049 AB002298	Hs.274415 Hs.173035	KIAA0300 protein	F1 12/J		1.91
	104074	AL162039	Hs.31422	Homo saplens mRNA; cDNA DKFZp434M229 (fr	11.20		
80	103749	AL135301	Hs.8768	hypothetical protein FLJ10849 succinate-CoA ligase, GDP-forming, alpha	10.86 12.00		
50	103645 103554	AW246253 AI878826	Hs.7043 Hs.323469	caveolin 1, caveolae protein, 22kD	12.00		. 1.80
	103541	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i			
	103496	Y09267 BE383507	Hs.132821 Hs.78921	flavin containing monooxygenase 2 A kinase (PRKA) anchor protein 1	11.20		
85	103428 103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa	19.80		

	W	O 02/0864	143					PCT/US02/12476
	103295	X81479	Hs.2375	egf-like module containing, mucin-like,		3.60		
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula				
	103100	NM 005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)			1.76	
	103025	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t			2.15	
5	102698	M18667	Hs.1867	progastricsin (pepsinogen C)				
•	102659	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	11.00			
	102580	U60808	Hs.152981	CDP-diacylglycerol synthase (phosphatida	25.40			
	102417	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	14.00			
	102363	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc				
10		AA306342	Hs.69171	protein kinase C-like 2	10.86			
	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11				
	102188	U20350	Hs.78913	chemokine (C-X3-C) receptor 1		7.40		
	102151	T27013	Hs.3132	steroidogenic acute regulatory protein	16.40			
		L28824	Hs.74101	spleen tyrosine kinase	15.40			
15	101842	M93221	Hs.75182	mannose receptor, C type 1				
	101771	NM 002432	Hs.153837	myeloid cell nuclear differentiation ant				
	101764	Al198550	Hs.81256	S100 calcium-binding protein A4 (calcium			1.78	
	101716	AF050658	Hs.2563	tachykinin, precursor 1 (substance K, su	18.80			
	101678	M62505	Hs.2161	complement component 5 receptor 1 (C5a1			2.22	
20	101447	M21305		ob:Human alpha satellite and satellite 3	504.80			
	101383	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co		31.00		
	101346	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N			1.75	
	101345	NM_005795	Hs.152175	calcitonin receptor-like				
	101336	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h			2.24	
25	101330	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do				
	101277	BE297626	Hs.296049	microfibrillar-associated protein 4				
	101262	L35854		gb:Human dystrophin (dp140) mRNA, 5' end	19.00			
	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5			2.01	
•	101102	NM_003243	Hs.79059	transforming growth factor, beta recepto				
30	101088	X70697	Hs.553	solute carrier family 6 (neurotransmitte	40.00	7.52		
	101066	AW970254	Hs.889	Charot-Leyden crystal protein	19.38		4.04	
	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	45.40		1.91	
	100893	BE245294	Hs.180789	S164 protein	15.40			•
25	100770	W25797.comp		amyloid beta (A4) precursor protein (pro	11.20			
35	100716	X89887	Hs.172350	HIR (histone cell cycle regulation defec	14.80 33.00			•
	100555	M69181		gb:Human nonmuscle myosin heavy chain-B	16.20			
	100425	NM_014747	Hs.78748	KIAA0237 gene product	10.20	4.00		
	100408	D86640	Hs.56045	src homology three (SH3) and cysteine ri		4.24		
40	100382	D83407	Hs.156007	Down syndrome critical region gene 1-lik		6.20		
40	100351	D64158	11- 2474	growth differentiation factor 10		21.20		
	100299	D49493	Hs.2171			21.20		
	100134	AA305746	Hs.49	macrophage scavenger receptor 1 hyaluronoglucosaminidase 2	•		1.79	
	100108 100095	U09577 Z97171	Hs.76873 Hs.78454	myocilin, trabecular meshwork inducible		5.40		
45	100095	231111	115.70404	thilornith nancedia incamous monornic	11.29	J. 70		
47	100000			•	11160			

TABLE 3B shows the accession numbers for those primakeys tacking unigenelD's for Table 3A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

55 Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

85

~	Pkey	CAT number	Accessions	
60				
	123619	371681_1	AA602964 A	
	126433	127143_1	AA325606 A	A099517 N89423
	125831	1522905_1	H04043 D609	988 D60337
	126816	122973_1	AA248234 A	A090985
65	126852	136135_1	AA399961 A	A128347
- '	121059	273450_1	AA393283 A	A398628
	120637			4809404 AA286907 AW977624
	122011	76172	AA431082	
	120934			A226513 AA383773
70	123802			AA620448
	116814			H50834
	118329			N63520
	104404			
	104776			AA026349
75	113502			
,,,	101262			
	108573			AA086005
	101447			7.1.1.1.1.1.1
	124357			N22401
80	108781			AA128654
80	112794			R97018
	100351			101010
				105 1551030
	100555	vgr_m 2245	MOS 101 MO	109 03 1039

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Table 4A shows 202 genes up-regulated in samples from patients treated with chemotherapy or radiotherapy. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average Intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: average of Al for samples from patients treated with chemotherapy or radiotherapy divided by the average of Al for normal lung samples. 5

10	R1:	average of	Al tor samples	trom patients treated with chemotherapy or radiother	ару оклоес
10	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	1 1.00		2	g	
	100113	NM_001269	Hs.84746	chromosome condensation 1	27.20
15	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3 KIAA0042 gene product	20.60 20.40
13	100210 100225	D26361 D28539	Hs.3104 Hs.167185	glutamate receptor, metabotropic 5	20.60
	100269	NM_001949	Hs.1189	E2F transcription factor 3	29.40
	100438	AA013051	Hs.91417	topolsomerase (DNA) Il binding protein	23.50
20	100877	X80821	Hs.27973	KIAA0874 protein	35.56
20	100893	BE245294	Hs.180789	S164 protein	43.40 21.80
	101273 101447	Z11933 M21305	Hs.162505	POU domain, class 3, transcription facto gb:Human alpha satellite and satellite 3	193.60
	101649	AW959908	Hs.1690	heparin-binding growth factor binding pr	38.40
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	198.80
25	101748	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	78.60
	101809	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	162.20 50.00
	101879 101915	AA176374 AF207881	Hs.243886 Hs.155185	nuclear autoantigenic sperm protein (his cytosolic ovarian carcinoma antigen 1	26.00
	101973	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	37.20
30	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	
	102031	U04898	Hs.2156	RAR-related orphan receptor A	32.00
	102052	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	51.20 13.90
	102391 102420	AA296874 U44060	Hs.77494 Hs.14427	deoxyguanosine kinase Homo sapiens cDNA: FLJ21800 fis, clone H	28.80
35	102610	U65011	Hs.30743	preferentially expressed antigen in mela	110.60
	102829	NM_006183	Hs.80962	neurotensin	116.80
	103000	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	2.30
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (Interstitia) serum/glucocorticoid regulated kinase	181.40 49.20
40	103507 103587	AJ000512 BE270266	Hs.296323 Hs.82128	5T4 oncofetal trophoblast glycoprotein	86.60
40	104660	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	42.60
	104896	AW015318	Hs.23165	ESTs	29.40
	105038	AW503733	Hs.9414	KIAA1488 protein	21.50 32.80
45	105298 105510	BE387790 Z42047	Hs.26369 Hs.283978	hypothetical protein FLJ20287 Homo saplens PRO2751 mRNA, complete cds	20.20
73	105667	AA767526	Hs.220370	paired box gene 5 (B-cell lineage specif	28.40
	106073	AL157441	Hs.17834	downstream neighbor of SON	25.40
	106205	AW965058	Hs.111583	ESTs, Weakly similar to 138022 hypotheti	32.00
50	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (ESTs	40.60 59.80
30	106533 106575	AL134708 AW970602	Hs.145998 Hs.105421	ESTs	43.40
	106654	AW075485	Hs.286049	phosphoserine aminotransferase	50.80
	106851	Al458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	53.40
55	106995	AB023139	Hs.37892	KIAA0922 protein	20.88 23.60
22	107332 107532	T87750 AA443473	Hs.183297 Hs.173684	DKFZP566F2124 protein Homo sapiens mRNA; cDNA DKFZp762G207 (fr	57.20
	107922	BE153855	Hs.61460	lg superfamily receptor LNIR	49.00
	108609	BE409857	Hs.69499	hypothetical protein	19.67
60	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	48.17 59.20
60	109166 109260	AA219691 AW978515	Hs.73625 Hs.131915	RAB6 interacting, kinestn-like (rabkines KIAA0863 protein	28.60
	109280	AK001355	Hs.279610	hypothetical protein FLJ10493	22.80
	109292	AW975746	Hs.188662	KIAA1702 protein	-4
6	109384	AA219172	Hs.86849	ESTs	21.00
65	109415	U80736	Hs.110826	trinucleotide repeat containing 9	31.60 24.20
	109445 109502	AA232103 AW967069	Hs.189915 Hs.211556	ESTs hypothetical protein MGC5487	21.40
	109633	AW003785	Hs.170267	ESTs	20.40
	109786	Al989482	Hs.146286	kinesin family member 13A	19.60
70 ·	109958	AA001266	Hs.133521	ESTS	24.00 28.40
	110920	N47224 AW058463	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi zinc-fingers and homeoboxes 1	36.00
	110924 111084	H44186 ·	Hs.12940 Hs.15456	PDZ domain containing 1	61.20
	111132	AB037807	Hs.83293	hypothetical protein	24.60
75	111229	AW389845	Hs.110855	ESTs	27.20
	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	48.00 37.80
	111987	NM_015310	Hs.6763	KIAA0942 protein CDC14 (cell division cycle 14, S. cerevi	26.80
	112046 112268	AA383343 W39609	Hs.22116 Hs.22003	solute carrier family 6 (neurotransmitte	63.80
80	112685	R87650	Hs.33439	ESTs, Weakly similar to ALU1_HUMAN ALU	26.40
-	112871	AL110216	Hs.12285	ESTs, Weakly similar to 155214 salivary	47.64
	112897	AW206453	Hs.3782	ESTs	22.00 65.00
	112973	AB033023 AL157425	Hs.318127 Hs.133315	hypothetical protein FLJ10201 Homo saplens mRNA; cDNA DKFZp761J1324 (f	42.00
85	112992 113073	N39342	Hs.103042	microtubule-associated protein 18	55.40
				• *	

WO 02/086443 113494 T91451 Hs.86538 22.80 113560 T91015 Hs.268626 **ESTs** 22.80 51.80 113849 AA457211 Hs.8858 bromodomain adiacent to zinc finger doma AI267652 Homo sapiens mRNA; cDNA DKFZp434E082 (fr 28.20 113950 Hs.30504 5 114339 AA782845 Hs.22790 20.20 114365 H42169 Hs.18653 hypothetical protein FLJ14627 21.00 ESTs, Weakly similar to ALU8_HUMAN ALU S suppressor of var1 (S.cerevisiae) 3-like Hs.271616 Hs.106469 114455 H37908 25.80 114518 23.60 AW163267 zinc finger protein 83 (HPF1) 114824 AA960961 Hs.305953 10 114837 BE244930 Hs.166895 **ESTs** 30.20 nucleosome assembly protein 1-like 1 114974 AW966931 Hs.179662 20.80 30.60 Hs.88045 AA814043 115075 **ESTs** hypothetical protein FLJ10618 BE383668 Hs.42484 28.86 115084 hypothetical protein FLJ10461 115291 BE545072 Hs.122579 38.00 15 115313 AA808001 Hs.184411 albumin 22.60 transmembrane protease, serine 4 Hs.63325 173.60 115697 D31382 115909 AW872527 Hs.59761 ESTs, Wealdy similar to DAP1_HUMAN DEATH 116090 Al591147 Hs.61232 20 80 hypothetical protein FLJ20093 116107 AL133916 Hs.172572 Hs.110637 164.20 20 38.00 116399 AA889120 homeo box A10 gb:yv16a11.s1 Soares fetal liver spleen H93699 21.60 117099 butyrate-induced transcript 1 ESTs, Weakly similar to KCC1_HUMAN CALCI Homo saplens mRNA for KIAA1771 protein, 117881 AF161470 Hs.260622 49.40 Hs.47883 Hs.93560 22.40 118091 AW005054 22.00 AA374756 118138 25 gb:za49d07.s1 Soares fetal liver spleen 20.00 118720 N73515 118873 AI824009 Hs.44577 ESTs 19.40 Hs.117183 111.20 119126 R45175 **FSTs** AA918317 B-cell CLL/lymphoma 118 (zinc finger pro 33.00 119717 Hs.57987 Hs.272531 DKFZP586B0319 protein 31.00 119940 AL050097 30 120266 AI807264 Hs.205442 ESTs, Weakly similar to T34036 hypotheti 20.20 gb:zr59c10.s1 Soares_NhHMPu_S1 Homo sapi achaete-scute complex (Drosophila) homo! 120515 120859 25.00 AA258356 AA826434 Hs.1619 95.40 120983 AA398209 Hs.97587 105.20 121054 AW976570 Hs.97387 **ESTs** 38.80 35 121369 AW450737 Hs.128791 Hs.241551 CGI-09 protein 41.60 122335 AA443258 chloride channel, calcium activated, fam 30.80 AA974832 19.60 122612 Hs.128708 AA487200 A1733692 gb:ab19f02.s1 Stratagene lung (937210) H ESTs 123130 33.20 23.17 Hs.112488 123440 123596 40 AA421130 Hs.112640 EST gb:no97c02.s1 NCI_CGAP_Pr2 Homo sapiens 28.80 123619 AA602964 Hs.270016 Hs.271630 124006 124169 Al147155 ESTs 77.60 22.20 RF079334 **ESTs** Al333756 Hs.111801 arsenate resistance protein ARS2 42.20 124281 45 124472 N52517 Hs.102670 **EST** 32.60 124617 AW62R16R Hs.152684 **FSTs** 21.80 124631 FLVCR protein NM 014053 Hs.270594 124839 Hs.140942 21.20 **ESTs** 125186 AA610620 Hs.181244 major histocompatibility complex, class 42.80 50 27.00 125321 TB6652 Hs.178294 **ESTs** 125535 NM_013243 Hs.22215 23.80 secretogranin III 125646 AA628962 Hs.75209 protein kinase (cAMP-dependent, catalyti 23,20 Homo saplens cDNA: FLJ21663 fis, clone C 21.20 Hs.158849 Hs.295978 125684 AWSR9427 Homo sapiens mRNA full length insert cDN AL360190 125724 55 Hs.249034 31.00 125847 AW161885 hypothetical protein FLJ21901 125934 AA193325 Hs.32646 21.20 49.80 126077 M78772 Hs.210836 **ESTs** AW979155 amino acid transporter 2 126299 Hs.298275 hypothetical protein FLJ12929 gb:EST28707 Cerebellum II Homo saplens c ESTs 71.00 126395 A1468004 Hs.278956 60 126433 AA325606 23.20 23.80 Hs.23850 126509 R47400 coronin, actin-binding protein, 1C 126538 AB030656 Hs.17377 126666 Hs.151999 36.00 AA648886 126812 AB037860 Hs.173933 nuclear factor I/A 20.80 gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su 65 AW450979 46.29 126872 AA321948 Hs.293968 127046 **ESTs** 127431 AW771958 Hs.175437 ESTs, Moderately similar to PC4259 ferri 30.00 127489 AA650250 Hs.272076 **ESTs** 20.80 AW297206 25.20 127521 Hs.164018 **ESTs** 70 127742 AW293496 Hs.180138 ESTs 28.00 AA805151 Hs.3628 mitogen-activated protein kinase kinase 21.20 127925 127930 AA809672 Hs.123304 ESTs ESTs 20.54 AA830201 28.20 Hs.124347 127968 AI022103 19.60 127987 Hs.124511 **ESTs** Homo sapiens, clone IMAGE:3867243, mRNA survival of motor neuron protein interac 75 Hs.286014 Hs.102456 128116 H07103 20.40 34.40 NM 003616 128609 AI878918 Hs.10526 cysteine and glycine-rich protein 2 53.80 128777 128949 AA009647 Hs.8850 a disintegrin and metalloproteinase doma 23.00 Al132988 Hs.109052 chromosome 14 open reading frame 2 37.60 129168 80 129404 129527 Hs.317584 Hs.270847 28.60 Al267700 **ESTs** delta-tubulin AA769221 40.80 UMP-CMP kinase 31.20 AA026815 Hs.11463 129574 Homo sapiens cDNA FLJ12566 fis, clone NT 129598 N30436 Hs.11556 29.60 72.20 129785 H19006 Hs.184780 **ESTs** 85 chromosome 12 open reading frame 4 22.20 AV655806 Hs.296198 129970

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	**	0 02,000			
	130149	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase	29.60
	130199	Z48579	Hs.172028	a disintegrin and metalloproteinase doma	27.60
	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	28.36
_	130466	W19744	Hs.180059	Homo sapiens cDNA FLJ20653 fis, clone KA	20.20
5	130482	AW409701	Hs.1578	bacutovirat IAP repeat-containing 5 (sur	22.40
	130617	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	19.60
	130703	R77776	Hs.18103	ESTs ·	19.40
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)	21.40
4.0	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype	110.00
10	131028	Al879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	25.20
	131086	AL035461	Hs.2281	chromogranin B (secretogranin 1)	40.60
	131284	NM_001429	Hs.25272	E1A binding protein p300	24.60
	131775	AB014548	Hs.31921	KiAA0648 protein	21.00
	131860	BE383676	Hs.334	Rho guanine nucleotide exchange factor (33.40
15	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	60.80
	132040	NM_001196	Hs.315689		. 20.40
	132084	NM_002267	Hs.3886	karyopherin alpha 3 (Importin alpha 4)	29.40
	132389	AA310393	Hs.190044	ESTs	32.40
	132437	AA152106	Hs.4859	cyclin L ania-6a	27.40
20	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	75.60
	132617	AF037335	Hs.5338	carbonic anhydrase XII	31.36
	132632	AU076916	Hs.5398	guanine monphosphate synthetase	32.40
	132672	W27721	Hs.54697	Cdc42 guanine exchange factor (GEF) 9	23.40
~ =	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	61.20
25	132771	Y10275	Hs.56407	phosphoserine phosphatase	22.33
	133070	U92649	Hs.64311	a disintegrin and metalloproteinase doma	23.50
	133153	AF070592	Hs.66170	HSKM-B protein	30.00
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	23.80
20	133282	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	51.60
30	133350	Al499220	Hs.71573	hypothetical protein FLJ10074	33.00
	133592	AV652066	Hs.75113	general transcription factor IIIA	82.00
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	***
	133865	AB011155	Hs.170290	discs, large (Drosophila) homolog 5	69.33
25	134032	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	33.20
35	134125	NM_014781	Hs.50421	KIAA0203 gene product	31.60
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	30.60
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-lin	23.40
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	49.20 20.20
40	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	20.20
40	134753	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	20.60 37.60
	135002	AA448542	Hs.251677	G antigen 78	
	135029	H58818	Hs.187579	hydroxysteroid (17-beta) dehydrogenase	53.40 31.60
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	28.80
15	135345	X53655	Hs.99171	neurotrophin 3	20.00
45					

TABLE 4B shows the accession numbers for those primekeys tacking unigenetio's for Table 4A. For each probeset we have listed the gene cluster number from which the digonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

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	Pkey	CAT number	Accessions
60	123619	371681_1	AA602964 AA609200
	126433	127143_1	AA325606 AA099517 N89423
	126872	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359
	106851	322947_1	BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
	118720	genbank_N7351:	AI458623 AA639708 AA485409 R22065 AA485570
65	120515 117099 101447 123130	genbank_AA258 321871_1 entrez_M21305 genbank_AA487	356 AA258356 H93699 H97976 H80036 M21305

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Table 5A shows 680 genes up-regulated in squamous cell carcinoma or adenocarcinoma lung tumors relative to normal lung and chronically diseased lung. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

	Э .	Pkey:	Unique Eos probeset identifier number
		ExAcon:	Exemplar Accession number, Genbank accession number
	•	UnigenelD:	Unigene number
		Unigene Title:	Unigene gene title
_	•	R1:	70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically
1	0		diseased lung samples.
		D3.	sort comparties of All adoptically diseased lung tumor samples divided by the 90th percentile of All for normal and chronically diseased lung samples.

R2: R3: R4:

useased rung samples.

80th percentile of AI denocarcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.

80th percentile of AI squamous cell carcinoma lung tumor samples divided by the 90th percentile of AI for normal and chronically diseased lung samples.

80th percentile of AI adenocarcinoma lung tumor samples divided by the 80th percentile of AI for squamous cell carcinoma lung tumor samples.

70th percentile of AI for squamous cell carcinoma and adenocarcinoma lung tumor samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples divided by 90th percentile of AI for normal and chronically diseased lung samples minus the 15th percentile of AI for all normal lung, chronically diseased lung and tumor samples R5: 15

			•	•					•
20	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2	R3	R4	R5
20	100035			AFFX control: GAPDH					6.76
	100036		•	AFFX control: GAPDH					5.77
	100037	•		AFFX control: GAPDH		0.00			5.75
25	100071	A28102	11- 00000	Human GABAa receptor alpha-3 subunit		8.00			5.71
25	100114 100154	X02308 H60720	Hs.82962 Hs.81892	thymidylate synthetase KIAA0101 gene product	3.84				•
	100187	D17793	Hs.78183	aldo-keto reductase family 1, member C3	3.33				
	100188	AW247090	Hs.57101	minichromosome maintenance deficient (S.					4.52
••	100202	BE294407	Hs.99910	phosphofructokinase, platelet					5.49
30	100216	AA489908	Hs.1390	proteasome (prosome, macropain) subunit,	2.55				5.67
	100269	NM_001949	Hs.1189 Hs.1600	E2F transcription factor 3 chaperonin containing TCP1, subunit 5 (e	2.00				5.66
	100287 100297	AU076657 AU077258	Hs.182429	protein disulfide isomerase-related prot					3.81
	100330	AW410976	Hs.77152	minichromosome maintenance deficient (S.					4.50
35	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.07				4.00
	100360	W70171	Hs.75939	uridine monophosphate kinase					4.82 3.79
	100372	NM_014791	Hs.184339	KIAA0175 gene product			•	15.65	3.73
	100474 100486	NM_000699 T19006	Hs.300280 Hs.10842	amylase, alpha 2A; pancrealic RAN, member RAS oncogene family				10.00	5.49
40	100400	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)					4.17
••	100516	D90278	Hs.11	carcinoembryonic antigen-related cell ad		7.20			
	100522	X51501	Hs.99949	prolactin-induced protein	0.40			14.20	
	100559	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	3.10			9.30	
45	100576	X00356 AA015693	Hs.37058 Hs.21291	calcitonin/calcitonin-related polypeptid mitogen-activated protein kinase kinase				20.60	
43	100629 100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.85				
	100677	AA353686	Hs.57813	zinc ribbon domain containing, 1		8.60			
	100696	D14887	Hs.121686	general transcription factor IIA, 1 (37k			04.00	10.00	
50	100709	N26539	Hs.100469	myeloid/lymphoid or mixed-lineage leukem		7.60	24.80		
50	100761 100830	BE208491 AC004770	Hs.295112 Hs.4756	KIAA0618 gene product flap structure-specific endonuclease 1		1.00			7.99
	100867	U14622	F15.4730	gb:Human transketolase-like protein gene		10.20			
	100902	M16029	Hs.287270	ret proto-oncogene (multiple endocrine n		8.00			
~ ~	100906	AU076916	Hs.5398	guanine monphosphate synthetase	0.57				5.16
55	100960	J00124	Hs.117729	keratin 14 (epidermolysis bullosa simple	2.57				4.69
	101045	J05614 NM_000175	Hs.180532	gb:Human proliferating cell nuclear anti glucose phosphate Isomerase					4.19
	101061 101071		Hs.84244	potassium voltage-gated channel, Shab-re		12.91			
	101124	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.12				
60	101175	U82671	Hs.36980	melanoma antigen, family A, 2	3.50				5.69
	101181	BE262621	Hs.73798	macrophage migration inhibitory factor (4.08				3.03
	101204 101210	L24203 L29301	Hs.82237 Hs.2353	ataxta-telangiactasia group D-associated optold receptor, mu 1	4.00		6.40		
	101216	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.53		4		
65	101228	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (7.90
	101233	AL135173	Hs.878	sorbital dehydrogenase					4.45
	101273	Z11933	Hs.182505	POU domain, class 3, transcription facto	8.50				4.17
	101342	U52112	Hs.182018 Hs.77348	interleukin-1 receptor-associated kinase hydroxyprostaglandin dehydrogenase 15-(N				21.89	7.11
70	101346 101369	AI738616 NM_000892	Hs.1901	kallikrein B, plasma (Fletcher factor) 1				12.80	
, 0	101396	BE267931	Hs.78996	proliferating cell nuclear antigen	3.24				
	101431	BE185289	Hs.1076	small proline-rich protein 1B (comitin)					7.90
	101448	NM_000424	Hs.195850	keratin 5 (epidermolysis bullosa simplex	8.31			38.80	
75	101462	AL035668	Hs.73853	bone morphogenetic protein 2 glutamic-oxaloacetic transaminase 2, mit				30.00	4.01
13	101466 101484	BE262660 AA053486	Hs.170197 Hs.20315	interferon-induced protein with tetratri				12.00	
	101502	M26958	110.20010	gb:Human parathyrold hormone-related pro	10.50				
	101505	AA307680	Hs.75692	asparagine synthetase					4.46
00	101526	NM_002197	Hs.154721	aconitase 1, soluble	4.02				4.65
80	101535	X57152	Hs.99853	fibrillarin				9.09	7.00
	101577 101649	M34353 AW959908	Hs.1041 Hs.1690	v-ros avian UR2 sarcoma virus oncogene h heparin-binding growth factor binding pr	54.00			0.00	
	101663	NM_003528	Hs.2178	H2B histone family, member Q	5.59				
	101664	AA436989	Hs.121017	H2A histone family, member A	7.00				
85	101669	L24498	Hs.80409	growth arrest and DNA-damage-inducible,		7.60			

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	101695	M69136	Hs.135626	chymase 1, mast cell	4.79				
	101724	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	15.21				
	101748 101759	NM_001944 M80244	Hs.1925 Hs.184601	desmogleln 3 (pemphigus vulgaris anligen solute carrier family 7 (cationic amino	55.50				4.10
5	101771	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant				18.57	
	101804	M86699	Hs.169840	TTK protein kinase	4.50				
	101809 101833	M86849 AU076442	Hs.323733 Hs.117938	gap junction protein, beta 2, 26kD (conn collagen, type XVII, alpha 1	140.00 2.56				
10	101842	M93221	Hs.75182	mannose receptor, C type 1				12.80	
10	101851	BE260964	Hs.82045	midkine (neurite growth-promoting factor		7.80			5.88
	102002 102039	NM_002484 AL134223	Hs.81469 Hs.306098	nucleotide binding protein 1 (E.coli Min aldo-keto reductase family 1, member C1		7.00			4.35
	102072	U09410	Hs.78743	zinc finger protein 131 (clone pHZ-10)			7.40		
15	102083	T35901	Hs.75117	interleukin enhancer binding factor 2, 4 sulfotransferase family, cytosolic, 2A,				12.00	5.12
13	102111 102123	L36196 NM_001809	Hs.81884 Hs.1594	centromere protein A (17kD)	6.20			12.00	
	102154	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.62		•		
	102193 102217	AL036335 AA829978	Hs.313 Hs.301613	secreted phosphoprotein 1 (osteopontin, JTV1 gene	5.85				6.18
20	102224	NM_002810	Hs.148495	proteasome (prosome, macropain) 26S subu					4.49
	102234	AW163390	Hs.278554	heterochromatin-like protein 1					5.80
	102251 102305	NM_004398 AL043202	Hs.41706 Hs.90073	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep chromosome segregation 1 (yeast homolog)	4.50				5.15
	102330	BE298063	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta					4.17
25	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	0.07			9.33	
	102348 102368	U37519 U39817	Hs.87539 Hs.36820	aldehyde dehydrogenase 3 family, member Bloom syndrome	8.87 15.91				
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	10.01		19.20		
20	102404	NM_005429	Hs.79141	vascular endothelial growth factor C				14.00	
30	102537 102581	U57094 AU077228	Hs.50477 Hs.77256	RAB27A, member RAS oncogene family enhancer of zeste (Drosophila) homolog 2				12.00	4.57
	102605	Al435128	Hs.181369	ubiquitin fusion degradation 1-like					3.98
	102610	U65011	Hs.30743	preferentially expressed antigen in mela melanoma antigen, family A. 9	77.50 12,50				
35	102623 102642	AW249285 AA205847	Hs.37110 Hs.23016	G protein-coupled receptor	12,30		22.00		
	102654	AV649989	Hs.24385	Human hbc647 mRNA sequence		12.00			
	102659 102669	BE245169 U71207	Hs.211610 Hs.29279	CUG triplet repeat, RNA-binding protein eyes absent (Drosophila) homolog 2	6.50			12.80	
	102672	U72066	Hs.29287	retinoblastoma-binding protein 8	8.50				
40	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C					9.24
	102696 102768	BE540274 U82321	Hs.239	forkhead box M1 gb:Homo saplens clone 14.98 mRNA sequenc		6.60			5.54
	102781	BE258778	Hs.108809	chaperonin containing TCP1, subunit 7 (e		0.00			3.78
45	102784	U85658	Hs.61796	transcription factor AP-2 gamma (activat			44.40		4.26
45	102824 102829	U90916 NM_006183	Hs.82845 Hs.80962	Homo sapiens cDNA: FLJ21930 fis, clone H neurotensin	8.00		14.40		
	102888	Al346201	Hs.76118	ubiquilin carboxyl-terminal esterase L1	0.00				5.50
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	4.64		6.70		
50	102913 102935	NM_002275 BE561850	Hs.80342 Hs.80506	keratin 15 small nuclear ribonucleoprotein polypept	2.93				
	102951	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol				11.40	
	102983 103023	BE387202 AW500470	Hs.118638 Hs.117950	non-metastatic cells 1, protein (NM23A) multifunctional polypeptide similar to S	3.01				7.26
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	27.90				
55	103038	AA926960	Hs.334883	CDC28 protein kinase 1					8.79
	103060 103099	NM_005940 Al693251	Hs.155324 Hs.8248	matrix metalloproteinase 11 (stromelysin NADH dehydrogenase (ubiquinone) Fe-S pro		9.80			4.27
	103119	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.05				
60	103168	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	3.07				5.62
00	103185 103192	NM_006825 M22440	Hs.74368 Hs.170009	transmembrane protein (63kD), endoplasmi transforming growth factor, alpha		7.40	•		3.02
	103223	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (g			400.00		4.70
	103242 103316	X76342 X83301	Hs.389 Hs.324728	alcohol dehydrogenase 7 (class IV), mu o SMA5			100.00	9.80	
65	103375	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	9.71			0.00	
	103376	AL036166	Hs.323378	coated vesicle membrane protein similar to rat HREV107	14.00			11.00	•
	103385 103391	NM_007069 X94453	Hs.37189 Hs.114366	pyrroline-5-carboxylate synthetase (glut	2.93			11.00	
70	103404	BE394784	Hs.78596	proteasome (prosome, macropain) subunit,					5.15
70	103430 103446	BE564090 X98834	Hs.20716 Hs.79971	translocase of inner mitochondrial membr sal (Drosophila)-like 2				21.40	3.98
	103476	Y07701	Hs.293007	aminopepiidase puromycin sensitive		13.00		21110	
	103477	AJ011812	Hs.119018	transcription factor NRF	E 00		6.40		
75	103478 103515	BE514982 Y10275	Hs.38991 Hs.56407	S100 calcium-binding protein A2 phosphoserine phosphalase	5.02 10.50				
	103558	BE616547	Hs.2785	keratin 17	6.41				
	103580	AA328046	Hs.46405	polymerase (RNA) II (DNA directed) polyp	70 50				3.84
	103587 103594	BE270266 Al368680	Hs.82128 Hs.816	5T4 oncofetal trophoblast glycoprotein SRY (sex determining region Y)-box 2	78.50 6.51				•
80	103636	NM_006235	Hs.2407	POU domain, class 2, associating factor	3.50				
	103768	AF086009	11- 20470	gb:Homo saplens full length insert cDNA		8.00			4.48
	103841 103847	AA314821 AF219946	Hs.38178 Hs.102237	hypothetical protein FLJ23468 tubby super-family protein		10.40			
O.F	103913	AW967500	Hs.133543	ESTs				15.60	
85	104094	AA418187	Hs.330515	ESTs			6.60		

	33 /	O 02/086	113						PCT/IIS	02/12476
	104150	AL122044	Hs.331633	hypothetical protein OKFZp566N034				26.00	1 0 1703	92/124/0
	104257	BE560621	Hs.9222	estrogen receptor binding site associate		6.80				
	104261 104331	AW248364 AB040450	Hs.5409 Hs.279862	RNA polymerase I subunit cdk inhibitor p21 binding protein		6.80			3.98	
5	104415	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha		10.29				
_	104558	R56678	Hs.88959	hypothetical protein MGC4816	4.21					
	104590	AW373062	Hs.83623	nuclear receptor subfamily 1, group I, m				15.79		
	104658 104660	AA360954 BE298665	Hs.27268 Hs.14846	Homo sapiens cDNA: FLJ21933 fis, clone H Homo sapiens mRNA; cDNA DKFZp564D016 (fr	6.40			17.40		
10	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	0.70				6.55	
	104754	AI206234	Hs.155924	cAMP responsive element modulator				10.00		
	104758	BE560269	Hs.7010	NPD002 protein	0.07				4.47	
	104971 105011	BE311926 BE091926	Hs.15830 Hs.16244	hypothetical protein FLJ12691 mitotic spindle coiled-coil related prot	2.87 3.83					
15	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.86					
	105026	AA809485	Hs.124219	hypothetical protein FLJ12934		11.00				
	105076 105132	A1598252 AA148164	Hs.37810 Hs.247280	hypothetical protein MGC14833 HBV associated factor					5.01 3.99	
	105132	A1368836	Hs.24808	ESTs, Weakly similar to 138022 hypotheti			11.00		3.33	
20	105158	AW976357	Hs.234545	hypothetical protein NUF2R		16.00				
	105175	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	4.32					
	105200 105264	AA328102 AA227934	Hs.24641	cytoskeleton associated protein 2 gb:zr57e08.s1 Soares_NhHMPu_S1 Homo sapi	3.00			10.00		
	105298	BE387790	Hs.26369	hypothelical protein FLJ20287	3.69			10.00		
25	105409	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8				9.20		
	105460	AW296078	Hs.271721	Homo sapiens, clone IMAGE:4179986, mRNA,	4.12		7.80			
	105667 105743	AA767526 BE246502	Hs.22030 Hs.9598	paired box gene 5 (B-cell lineage specif sema domain, immunoglobulin domain (lg),	3.82					
20	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro			27.00			
30	105848	AW954064	Hs.24951	ESTs			7.60			
	105891 106019	U55984 AF221993	Hs.289088 Hs.46743	heat shock 90kD protein 1, alpha McKusick-Kaufman syndrome			16.80		4.14	•
	106069	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip			23.40	•		
25	106073	AL157441	Hs.17834	downstream neighbor of SON	9.50					
35	106126 106159	AA576953 AK001301	Hs.22972 Hs.3487	hypothetical protein FLJ13352 hypothetical protein FLJ10439	6.00				3.95	*
	106220	D61329	Hs.32196	mitochondrial ribosomal protein L36					6.04	
	106260	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU S			13.20			
40	106300 106307	Y10043 AA436174	Hs.19114 Hs.37751	high-mobility group (nonhistone chromoso ESTs, Weakly similar to putative p150 (6.60			5.02	
-10	106318	AA025610	Hs.9605	cleavage and polyadenylation specific fa		0.00			5.04	
	106341	AF191020	Hs.5243	hypothetical protein, estradiol-induced					7.25	
	106440 106481	AA449563 D61594	Hs.151393 Hs.17279	glulamate-cysteine ligase, catalytic sub tyrosylprotein sulfotransferase 1	4.75		13.80			
45	106586	AA243837	Hs.57787	ÉSTs	7.70			10.84		
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	an an			45.60		
	106654 106785	AW075485 Y15227	Hs.286049 Hs.20149	phosphoserine aminotransferase deleted in lymphocytic leukemia, 1	28.00 3.00					
5 0	106813	C05766	Hs.181022	CGI-07 protein			11.40			
50	106895	AK001826	Hs.25245	hypothetical protein FLJ11269		0.50	6.00			
	106913 106919	AI219346 AW043637	Hs.86178 Hs.21766	M-phase phosphoprotein 9 ESTs, Weakly similar to ALU5_HUMAN ALU S		6.56			4.27	·
	107054	A1076459	Hs.15978	KIAA1272 protein				34.80		
55	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	4.71			24.00		
<i>JJ</i>	107098 107104	AI823593 AU076640	Hs.27688 Hs.15243	ESTs nucleolar protein 1 (120kD)				24.80	7.05	
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.60		•			
	107198	AV657225	Hs.9846	KIAA1040 protein		19.20				
60	107203 107217	D20426 Al.080235	Hs.41639 Hs.35861	programmed cell death 2 DKFZP586E1621 protein	9.50	7.60				
	107284	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	2.71					
	107318	T74445	Hs.5957	Homo sapiens clone 24416 mRNA sequence			8.71		4 22	•
	107516 107529	X57152 BE515065	Hs.99853 Hs.296585	fibrillarin nucleolar protein (KKE/D repeat)					4.33 4.00	
65	107728	AA019551	Hs.294151	Homo sapiens, cione IMAGE:3603836, mRNA,		10.80				
	107851	AA022953	Hs.61172	EST	0.40		8.00			•
	107901 107922	L42612 BE153855	Hs.335952 Hs.61460	keratin 6B Ig superfamily receptor LNIR	3.40 2.88			•		
	107932	AW392555	Hs.18878	hypothetical protein FLJ21620	7.50					
70	108015	AW298357	Hs.49927	protein kinase NYD-SP15				23,40		
	108056 -108075	AA043675 Al867370	Hs.62633 Hs.139709	ESTs hypothetical protein FLJ12572		•		12.80 12.80		
	108187	BE245374	Hs.27842	hypothetical protein FLJ11210		7.00		. 4.00		
75	108296	N31256	Hs.161623	ESTs		6.60		44.00		
75	108305 108393	AA071391 AA075211		gb:zm61e06.r1 Stratagene fibroblast (937 gb:zm86a08.r1 Stratagene ovarian cancer				11.80 11.80		
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434l0428				20.80		
	108554	AA084948		gb:zn13b09.s1 Stratagene hNT neuron (937		6.40		25 40		
80	108573 108584	AA086005 AA088326	Hs.120905	gb:zi84c04.s1 Stratagene colon (937204) Homo saplens cDNA FLJ11448 fis, clone HE		9.60		25.40		
-•	108597	AK000292	Hs.278732	hypothetical protein FLJ20285	_			14.60		
	108695	AB029000	Hs.70823	KIAA1077 protein ESTs	3.00			10.00		
•-	108699 108700	AA121514 AA121518	Hs.70832 Hs.193540	ESTs, Moderately similar to 2109260A B c			11.00	10.00		
85	108780	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.21					

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	108810	AW295647	Hs.71331	hypothetical protein MGC5350	8.50				
	108816	AA130884	Hs.270501	ESTs, Moderately similar to ALU2_HUMAN	4.00	7.40			
	108857 108860	AK001468 AA133334	Hs.62180 Hs.129911	anillin (Drosophila Scraps homolog), act ESTs	4.00 6.09				
5	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	3.00				
_	109010	NM_007240	Hs.44229	dual specificity phosphatase 12	2.69				
	109121	BE389387	Hs.49767	NADH dehydrogenase (ubiquinone) Fe-S pro					4.53
	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	10.58	0.00			
10	109227 109415	AA766998 U80736	Hs.85874 Hs.110826	Human DNA sequence from clone RP11-16L21 trinucleotide repeat containing 9		9.00 51.40			
10	109418	AI866946	Hs.161707	ESTs		01.40		11.00	
	109454	AA232255	Hs.295232	ESTs, Moderately similar to A46010 X-li			17.60		
	109502	AW967069	Hs.211556	hypothetical protein MGC5487			9.49		
15	109543	AA564994	Hs.222851	ESTs .		12.67		10.40	
13	109648 109680	H17800 AB037734	Hs.7154 Hs.4993	ESTs KIAA1313 protein			33.20	10.40	
	109700	F09609		gb:HSC33H092 normalized infant brain cDN				16.00	
	109704	AJ743880	Hs.12876	ESTs			11.00		
20	109792	R49625	N- 00000	gb:yg61f03.s1 Soares infant brain 1NIB H	4.00			12.60	
20	109981	BE546208 AL042201	Hs.26090 Hs.21273	hypothetical protein FLJ20272 transcription factor NYD-sp10	4.00	7.80			
	109998 110039	H11938	Hs.21907	histone acelyltransferase		7.00			
	110156	AA581322	Hs.4213	hypothetical protein MGC16207					4.24
0.5	110500	AA907723	Hs.36962	ESTs	4.50				
25	110551	AW450381	Hs.14529	ESTs		8.60			
	110561 110854	AA379597 BE612992	Hs.5199 Hs.27931	HSPC150 protein similar to ubiquitin-con hypothetical protein FLJ10607 similar to	3.06	6.80			
	110886	AW274992	Hs.72249	three-PDZ containing protein similar to		0.00	8.80		
	110916	BE178102	Hs.24349	ESTs		6.80			
30	111003	N52980	Hs.83765	dihydrofolate reductase				16.80	
	111337	AA837396	Hs.263925	LIS1-interacting protein NUDE1, rat homo	2.54			0.00	
	111434 111439	R01608 Al476429	Hs.142736 Hs.19238	ESTs ESTs		•		9.80 10.40	
	111540	U82670	Hs.9786	zinc finger protein 275			15.40	10.40	
35	111597	R11499	Hs.189716	ESTs				9.20	
	111895	T80581	Hs.12723	Homo sapiens clone 25153 mRNA sequence		6.80			•
	111929	AF027208	Hs.112360	prominin (mouse)-like 1		10.80		14.67	
	112054 112210	R43590 R49645	Hs.7004	gb:yc85g02.s1 Soares Infant brain 1NIB H ESTs		10.00		10.20	
40	112244	AB029000	Hs.70823	KIAA1077 protein	2.99			10.20	
	112382	R59904		gb:yh07g12.s1 Soares infant brain 1NIB H		6.60			
	112392	R60763	Hs.193274	ESTs, Moderately similar to I57588 HSrel	0.00		7.10		
	112442	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	3.00			37.20	
45	112539 112772	R70318 AI992283	Hs.339730 Hs.35437	ESTs ESTs, Moderately similar to 138026 MLN 6				14.60	
10	112869	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin				******	4.83
	112935	R71449	Hs.268760	ESTs	2.73				
	112970	AA694010	Hs.6932	Homo sapiens clone 23809 mRNA sequence	44 50			12.00	
50	112973 112992	AB033023 AL157425	Hs.318127 Hs.133315	hypothetical protein FLJ10201 Homo sapiens mRNA; cDNA DKFZp761J1324 (f	11.50		10.89		
50	113063	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	15.00		10.03		
	113073	N39342	Hs.103042	microtubule-associated protein 18			15.31		
	113078	T40444	Hs.118354	CAT56 protein		7.00			•
55	113238	R45467	Hs.189813	ESTs				41.20	
22	113591 113702	T91881 T97307	Hs.200597	KIAA0563 gene product gb:ye53h05.s1 Soares fetal liver spleen	25.00			9.40	
	113844	Al369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	20.00			13.91	
	113984	R96696	Hs.35598	ESTs		7.80			
C O	114073	R44953	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f		7.20			
60	114162	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	3.42		6 74		
	114208 114251	AL049466 H15261	Hs.7859 Hs.21948	ESTs ESTs			6.74	33.20	
	114285	R44338	Hs.22974	ESTs				13.20	
	114313	H18456	Hs.27946	ESTs				10.00	•
65	114339	AA782845	Hs.22790	ESTs		7.80			444
	114407	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f				9.80	4.14
	114560 114699	AI452469 AA127386	Hs.165221	ESTs gb:zn90d09.r1 Stratagene lung carcinoma		7.60		3.00	
	114767	A1859865	Hs.154443	minichromosome maintenance deficient (S	3.21				
70	114793	AA158245		gb:zo76c03.s1 Stratagene pancreas (93720			6.00		
	114833	Al417215	Hs.87159	hypothetical protein FLJ12577				11.40	4.04
	115047		Hs.82916 Hs.198249	chaperonin containing TCP1, subunit 6A (gap junction protein, beta 5 (connexin 3					4.31 4.03
	115060 115097	AF052693 AA256213	Hs.72010	ESTs				35.40	7.00
75	115113		12010	gb:zr81a04.s1 Soares_NhHMPu_S1 Homo sapl				15.20	
•	115123	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m					4.19
	115134		Hs.194331	ESTs, Highly similar to A55713 inositol	05.00			12.40	
	115291	BE545072 AA356792	Hs.122579 Hs.334824	hypothetical protein FLJ10461 hypothetical protein FLJ14825	25.00	7,00			
80	115347 115414		Hs.283099	AF15q14 protein	3.25				
	115522		Hs.333893	c-Myc target JPO1	3.68				
	115536	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	10.50				
	115566		Hs.43977	Human DNA sequence from clone RP11-196N1	A 47			24.40	
85	115645 115648	Al207410 AW016811	Hs.69280 Hs.234478	Homo sapiens, clone IMAGE:3636299, mRNA, Homo sapiens cDNA: FLJ22648 fis, clone H	4.17		6.00		
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	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	3.81	•			
	115697	D31382	Hs.63325	transmembrane protease, serine 4	62.14			44.00	
	115793	AA424883	Hs.70333	hypothetical protein MGC10753				11.80 9.71	
5	115816 115892	BE042915 AA291377	Hs.287588 Hs.50831	Homo sapiens cDNA FLJ13675 fis, clone PL ESTs			27.40	3 .71	
3	115906	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.53				
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	11.82			04.00	
	115965	AA001732	Hs.173233	hypothetical protein FLJ10970				34.29	8.23
10	115978 115985	AL035864 AA447709	Hs.69517 Hs.268115	cDNA for differentially expressed CO16 g ESTs, Wealdy similar to T08599 probable	3.00				u.25
10	116090	AI591147	Hs.61232	ESTs	5.17				
	116096	AA682382	Hs.59982	ESTs			8.20		
	116127	AF126743	Hs.279884	DNAJ domain-containing		10.60			E 02
15	116157	BE439838	Hs.44298	mitochondrial ribosomal protein S17 ESTs, Weakly similar to T22341 hypotheti					5.82 4.08
13	116190 116278	A1949095 NM_003686	Hs.67776 Hs.47504	exonuclease 1	9.50				4.55
	116335	AK001100	Hs.41690	desmocollin 3	3.67				
	116496	AW450694	Hs.21433	hypothetical protein DKFZp547J036		7.00		40.00	
20	116503	AI925316	Hs.212617	ESTs			32.00	12.60	
20	116674 116929	AI768015 AA586922	Hs.92127 Hs.80475	ESTs polymerase (RNA) II (DNA directed) polyp		7.60	02.00		
	116973	AI702054	Hs.166982	phosphatidylinositol glycan, class F		9.80			
	116993	AJ417023	Hs.40478	ESTS				10.20	
25	117079	H92325	Un 42222	gb:ys85f05.s1 Soares retina N2b4HR Homo ESTs				15.20 13.40	
23	117317 117326	AI263517 N23629	Hs.43322 Hs.241420	Homo sapiens mRNA for KIAA1756 protein,				20.60	
	117396	W20128	Hs.296039	ESTs				10.60	
	117412	N32536	Hs.42645	ESTs				16.00	
30	117519	N32528	Hs.146286	kinesin family member 13A mitochondrial ribosomal protein L42				9.11	4.01
30	117693 117721	AW179019 N46100	Hs.112110 Hs.93939	EST				19.80	4.01
	117881	AF161470	Hs.260622	butyrate-induced transcript 1	2.71				
	117903	AA768283	Hs.47111	ESTs				17.80	144
25	117992	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586l2022 (f				10.60	4.17
35	118013 118017	AI674126 AI813444	Hs.94031 Hs.42197	ESTs ESTs			8.82	10.00	,
	118186	N22886	Hs.42380	ESTs		7.00			
	118325	A1868065	Hs.166184	intersectin 2			• • •	13.80	
40	118367	N64269	Hs.48946	EST	3.14		6.14		
40	118368 118472	N64339 AL157545	Hs.48956 Hs.42179	gap junction protein, beta 6 (connexin 3 bromodomain and PHD finger containing, 3	3.14		12.40		
	118709	AA232970	Hs.293774	ESTs				12.20	_
	119025	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	4.50				
15	119027	AF086161	Hs.114611	hypothetical protein FLJ11808	3.22	9.60			
45	119052 119164	R10889 AF221993	Hs.46743	gb:yf38d02.s1 Soares fetal liver spleen McKusick-Kaufman syndrome		5.00	6.60		
	119186	AI979147	Hs.101265	hypothetical protein FLJ22593				10.80	
	119243	T12603		gb:CHR90123 Chromosome 9 exon Il Homo sa				9.44	
50	119490	AA195276	Hs.263858 Hs.55080	ESTs, Moderately similar to B34087 hypot ESTs			14.80	11.80	
30	119499 119599	Al918906 W45552	กร.จอบอบ	gb:zc26d03.s1 Soares_senescent_fibroblas		12.60	14.00		
	119780	NM_016625	Hs.191381	hypothetical protein	17.00				
	119845	W79123	Hs.58561	G protein-coupled receptor 87	13.50	8.00			
55	119941 119994	AA699485 AA642402	Hs.58896 Hs.59142	ESTs ESTs	7.73	0.00			
33	120102	W67353	Hs.170218	KIAA0251 protein			39.60		
	120104	AK000123	Hs.180479	hypothetical protein FLJ20116	2.91		0.00		•
	120294	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	8.73		8.20		
60	120486 120599	AW368377 AA804448	Hs.137569 Hs.104463	tumor protein 63 kDa with strong homolog ESTs	0.73	7.00			
00	120699	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos				10.00	
	120715	AA292700		gb:zs59a06.s1 NCI_CGAP_GCB1 Homo saplens		9.40		40.00	
	120821	Y19062	Hs.96870	staufen (Orosophila, RNA-binding protein		9.00		13.80	
65	120859 120880	AA826434 AA360240	Hs.1619 Hs.97019	achaete-scute complex (Drosophila) homol EST		15.60			
05	120983	AA398209	Hs.97587	EST			27.66		•
	121034	AL389951	Hs.271623	nucleoportn 50kD			20.80		
	121121	AA399371	Hs.189095	similar to SALL1 (sal (Orosophila)-like		22,80		10.00	
70	121313 121369	AA402713 AW450737	Hs.97872 Hs.128791	ESTs CGI-09 protein	25.71			10.00	
70	121376	AA448103	Hs.187958	solute carrier family 6 (neurotransmitte					5.42
	· 121476	AA412311	Hs.97903	ESTs		8.30			
	121509	AA868939	Hs.97888	ESTs	18.50	8.59			
75	121553 121753	AA412488 AK000552	Hs.48820 Hs.323518	TATA box binding protein (TBP)-associat WD repeat domain 5	7.00				
, 5	121838	AA425680	Hs.98441	ESTs				10.40	
	121857	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.00			40.00	
	121991	AA430058	Hs.98649	EST			8.60	12.20	
80	122089 122105	AW016543 AW241685	Hs.98682 Hs.98699	hypothetical protein FKSG32 ESTs			6.14		
50	122163	AA435702	Hs.98829	EST				10.40	
	122318	AA429743		gb:zv60b05.r1 Soares_testis_NHT Homo sap	40.50			18.20	
	122335	AA443258	Hs.241551	chloride channel, calcium activated, fam ESTs	13.50 4.80				
85	122338 122414	AA443311 AI313473	Hs.98998 Hs.99087	ESTs, Weakly similar to S47073 finger pr		8.00			
				•					

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		AF053305 AA449352	Hs.98658 Hs.99217	budding uninhibited by benzimidazoles 1 ESTs			8.80	9.40	
	122702	A1220089	Hs.99439	ESTs		9.20			
5	122852 122925	A1580056	Hs.98992	ESTs		6.80		10.40	
,	123005	AW268962 AW369771	Hs.111335 Hs.52620	ESTs integrin, beta 8		0.00	12.60		
	123044	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro					5.35
	123160 123315	AA488687 AA496369	Hs.284235	ESTs, Weakly similar to 138022 hypotheti gb:zv37d10.s1 Soares ovary tumor NbHOT H			6.06 12.40		
10	123329	Z47542	Hs.179312	small nuclear RNA activating complex, po			11.80		
	123497	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein		12.00	40.00		
	123518 123519	AL035414 AW015887	Hs.21068 Hs.112574	hypothetical protein ESTs		12.20	13.00		
	123614	AK000492	Hs.98806	hypothetical protein			7.80		
15	123616	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	23.00			10.60	
	123673 123727	BE550112 AI083986	Hs.158549 Hs.282977	ESTs, Weakly similar to T2D3_HUMAN TRANS hypothetical protein FLJ13490	23.00	7.00			
	123731	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma			9.80		
20	123752 123900	AA227714 AA621223	Hs.179703 Hs.112953	KIAA0129 gene product - EST	3.50			12.80	
20	124006	Al147155	Hs.270016	ESTs	97.00			12.00	
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	3.02		07.00		
	124069 124191	AF134160 T96509	Hs.7327 Hs.248549	claudin 1 ESTs, Moderately similar to S65657 alpha			27.80	35.80	
25	124273	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma		7.20			
	124297	AL080215 AW963221	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f gb:EST375294 MAGE resequences, MAGH Homo				11.00 16.00	
	124305 124676	AVV903221 Al360119.com	npHs.181013	phosphoglycerate mutase 1 (brain)				10.00	6.08
20	124874	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog		0.40		21.00	
30	124904 124969	AK000483 Al650360	Hs.93872 Hs.100256	KIAA1682 protein ESTs		9.40		10:80	
	125000	T58615	Hs.110640	ESTs				9.80	
	125201	AA693960	Hs.103158	ESTs, Weakly similar to T33296 hypotheti ESTs, Highly similar to LCT2_HUMAN LEUKO		7.60 6.59			
35	1252 66 125299	W90022 T32982	Hs.186809 Hs.102720	ESTs		0.55		9.57	
	125356	Al057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC				14.00	<i>:</i>
	125370 125418	AA256743 AA777690	Hs.134158 Hs.188501	Homo saplens, Similar to KIAA0092 gene p ESTs			8.20	13.20	•
40	125433	AL162066	Hs.54320	hypothetical protein DKFZp762D096		21.40			
40	125437	A1609449	Hs.140197	ESTs		6.98 8.80			
	125446 125711	BE219987 AA305800	Hs.166982 Hs.5672	phosphatidylinositol glycan, class F hypothetical protein AF140225		0.00		11.20	
	125756	BE174587	Hs.289721	growth arrest specific transcript 5				45.00	4.31
45	125757 125769	AJ274908 BE270266	Hs.166835 Hs.82128	ESTs, Highly similar to 1814460A p53-ass 5T4 oncofetal trophoblast glycoprotein	3.20			15.60	
7.5	125839	AW836261	Hs.337717	ESTs		8.20			
	125850 125875	W85858 H14480	Hs.99804	ESTs gb:ym18b09.r1 Soares infant brain 1NIB H	2.65	7.40			•
	125924	BE272506	Hs.82109	syndecan 1		1.40			4.23
50	125972	Al927475	Hs.35406	ESTs, Highly similar to unnamed protein				40.00	3.98
	126034 126327	H60340 AA432266	Hs.44648	gb:yr39b04.r1 Soares fetal liver spleen ESTs		11.60		10.60	
	126345	N49713		gb:yv23f06.s1 Soares fetal liver spleen		6.67		40.00	
55	126435 126487	AW614529 AA283809	Hs.285847 Hs.184601	CGI-19 protein solute carrier family 7 (cationic amino				10.60	4.38
55	126521	AI475110	Hs.203933	ESTs		6.60			4.05
	126522	W31912		gb:zc76d03.s1 Pancreatic Islet Homo sapl				14.80	- 4.01
	126543 126567	AL035864 AA058394	Hs.69517 Hs.57887	cDNA for differentially expressed CO16 g ESTs, Wealdy similar to KIAA0758 protein			7.80		4.01
60	126605	AA676910		gb:zj65h07.s1 Soares_fetal_fiver_spleen_				11.60	
	126627 126628	AA497044 N49776	Hs.20887 Hs.170994	hypothetical protein FLJ10392 hypothetical protein MGC10946	8.00			14.60	
	126737	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.92				
65	126795	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	7.50	11.60			
03	126802 126892	AW805510 AF121856	Hs.97056 Hs.284291	hypothetical protein FLJ21634 sorting nexin 6	3.50	11.00			
	126928	AA480902	Hs.137401	ESTs				22.83	
	126979 126986	AA210954 Al279892	Hs.46801	gb:zq89h10.r1 Stratagene hNT neuron (937 sorting nextn 14				11.80 11.60	
70	126992	Al809521		gb:wf30e03.x1 Soares_NFL_T_GBC_S1 Homo s				20.80	
	127066	R25066		gb:yg42c07.r1 Soares Infant brain 1NIB H gb:EST54026 Fetal heart II Homo sapiens				27.60 21.60	
	127099 127139	AA347668 AA830233	Hs.293585	ESTs				11.20	
75	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil	3.10				
75	127221 127225	BE062109 AA315933	Hs.241551 Hs.120879	chloride channel, calcium activated, fam ESTs	2.76			16.80	
	127313	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	14.00				•
	127444	AW978474 AW971353	Hs.7560 Hs.162115	Homo sapiens mRNA for KIAA1729 protein, ESTs		11.20		13.60	
80	127500 127524	AV97 1333 AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin			7.80		
	127540	N45572	Hs.105362	Homo saplens, clone MGC:18257, mRNA, com	3.53			13.80	
	127599 127609	AA613204 X80031	Hs.150399 Hs.530	ESTs collagen, type IV, atpha 3 (Goodpasture				28.00	
05	127662	W80755	Hs.8294	KIAA0196 gene product				19.80	
85	127668	Al343257	Hs.139993	ESTs				11.20	

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		Al239495	Hs.120189	ESTs				14.18	
	127812		Hs.291434	ESTs	4.50			04.00	
	127817		Hs.163085	ESTs Homo sapiens cDNA: FLJ23123 fis, clone L				24.60 9.20	
5	127959 127960	Al302471 Al613226	Hs.124292 Hs.41569	phosphatidic acid phosphatase type 2A				16.83	
	127969	F06498	Hs.93748	Home sapiens cDNA FLJ14676 fis, clone NT		13.60			
	128015	Z21169	Hs.334659 Hs.164153	hypothetical protein MGC14139 ESTs		7.00		37.40	
	128027 128077	Al433721 Al310330	Hs.128720	ESTs				9.60	
10	128166	NM_006147	Hs.11801	interferon regulatory factor 6				9.24	
	128226	A1284940	Hs.289082	GM2 ganglioside activator protein	19.00			10.40	
	128305 128341	A1954968 AA191420	Hs.279009 Hs.185030	matrix Gla protein ESTs		9.00		10.70	•
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul					4.30
15	128539	R46163	Hs.258618	ESTs		12.60			4.56
	128568 128572	H12912 AA933022	Hs.274691 Hs.256583	adenylate kinase 3 interleukin enhancer binding factor 3, 9				10.00	4.50
	128777	AI878918	Hs.10526	cystelne and glycine-rich protein 2			16.80		
20	128781	N71826	Hs.105465	small nuclear ribonucleoprotein polypept		8.12			4.48
20	128796 128920	AJ000152 AA622037	Hs.105924 Hs.166468	defensin, beta 2 programmed cell death 5		0.12			4.62
	128924	BE279383	Hs.26557	plakophilin 3					4.04
	128971	H05132	Hs.107510	ESTs		12.60 8.80			
25	129008 129041	AL079648 BE382756	Hs.301088 Hs.169902	ESTs solute carrier family 2 (facilitated glu		0.00			6.05
23	129075	BE250162	Hs.83765	dihydrofolate reductase	2.59				
	129105	Al769160	Hs.108681	Homo saplens brain tumor associated prot	•	8.00	6.67		
	129189 129229	AB023179 AF013758	Hs.9059 Hs.109643	KIAA0962 protein polyadenylate binding protein-interactin	4.00	0.00			
30	129241	AI878857	Hs.109706	hematological and neurological expressed					4.06
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	2.55				
	129404 129457	Al267700 X61959	Hs.317584 Hs.207776	ESTs aspartylglucosaminidase	18.00 6.50				
	129466	L42583	Hs.334309	keratin 6A	12.94				
35	129494	Al148976	Hs.112062	ESTs				11.00	4.46
	129605 129641	AF061812 Al911527	Hs.115947 Hs.11805	keratin 16 (focal non-epidermolytic palm ESTs				12.00	4.40
	129665	AW163331	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic					4.70
40	129703	BE388665	Hs.179999	Homo saplens, clone IMAGE:3457003, mRNA					4.02 5.71
40	129720 129748	AA156214 M16707	Hs.12152 Hs.123053	APMCF1 protein H4 histone, family 2	3.50				5.71
	129890	A1868872	Hs.282804	hypothetical protein FLJ22704					4.21
	129896	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	2.56				4.03
45	129945 130010	BE514376 AA301116	Hs.165998 Hs.142838	PAI-1 mRNA-binding protein nucleolar phosphoprotein Nopp34			7.00		4.03
75	130026	T40480	Hs.332112	EST		6.40			
	130080	X14850	Hs.147097	H2A histone family, member X	2.74				4.65
	130149 130285	AW067805 AA063546	Hs.172665 Hs.75981	methylenetetrahydrofolate dehydrogenase ubiquitin specific protease 14 (tRNA-gua	2.74		7.40		
50	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic					3.91
	130482	AW409701	Hs.1578	bacutoviral IAP repeat-containing 5 (sur	4.87			9.60	
	130500 130524	AB007913 U89995	Hs.158291 Hs.159234	KIAA0444 protein forkhead box E1 (thyroid transcription f			13.40	3.00	
	130541	X05608	Hs.211584	neurofilament, light polypeptide (68kD)			8.20		2.02
55	130553	AF062649	Hs.252587	pituitary tumor-transforming 1			7.00		6.06
	130567 130577	AA383092 M69241	Hs.1608 Hs.162	replication protein A3 (14kD) insulin-like growth factor binding prote	3.04		7.00		
	130627	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	3.87				
60	130648	AI458165	Hs.17296	hypothetical protein MGC2376				16.20 17.80	
OU	130697 130744	1.29472 H59696	Hs.1802 Hs.18747	major histocompatibility complex, class POP7 (processing of precursor, S. cerevi				11.00	5.23
	130800	Al187292	Hs.19574	hypothetical protein MGC5469	40.04				4.43
	130867	NM_001072	Hs.284239	UDP glycosyltransferase 1 family, polype uridine monophosphate synthetase (orotat	16.84				4.92
65	130869 130925	J03626 AF093419	Hs.2057 - Hs.169378	multiple PDZ domain protein				9.60	
00	130994	W17044	Hs.327337	ESTs	40.04	12.40			
	131028	A1879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP), aquaporin 4	10.21			9.80	
	131031 131041	NM_001650 T15767	Hs.288650 Hs.22452	Homo saplens mRNA for KIAA1737 protein,				9.60	
70	131058	W28545	Hs.101514	hypothetical protein FLJ10342	0.74			17.00	
	131090	AI143139	Hs.2288 Hs.168950	visinin-like 1 Homo saplens mRNA; cDNA DKFZp566A1046 (f	2.74		8.80		
	131112 131148		Hs.303125	p53-induced protein PIGPC1	3.12				
7.	131185	BE280074	Hs.23960	cyclin B1	3.07				
75	131200		Hs.293732	hypothetical protein MGC3195 small inducible cytokine subfamily B (Cy	3.07 2.87				
	131219 131257	W25005 AW339037	Hs.24395 Hs.24908	ESTs	2.01			14.67	
	131375	AW293165	Hs.143134	ESTs			19.20		
9Λ	131460	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.50 15.00				
80	131476 131510		Hs.334644 Hs.27842	hypothetical protein FLJ14668 hypothetical protein FLJ11210	10.00		7.80		
	131646		Hs.30057	MRS2 (S. cerevislae)-like, magnesium hom			7.00		
	131786	BE000971	Hs.306083	Novel human gene mapping to chomosome 22	2.65			35.20	
85	131839 131843		Hs.33010 Hs.184062	KIAA0633 protein putative Rab5-interacting protein				30.20	4.11
5 5	,51040			F					

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	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	19.00					
	131885 131921	BE502341 AA456093	Hs.3402 Hs.34720	ESTs ESTs	6.48		8.40			
_	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	56.00		5.1.5			•
5	131958	NM_014062	Hs.3566	ART-4 protein	2.02				3.82	
	131965 132000	W79283 AW247017	Hs.35962 Hs.36978	ESTs melanoma antigen, family A, 3	3.03	9.80				
	132040	NM_001196	Hs.315689	Homo sapiens cDNA: FLJ22373 fis, clone H	3.30	0.00				
10	132109	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	21.00	8.40				
10	132114 132162	NM_006152 AA315805	Hs.40202 Hs.94560	lymphold-restricted membrane protein desmoglein 2		0,40			12.25	
	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio	2.70					
	132180	NM_004460	Hs.418	fibroblast activation protein, alpha	2.71					
15	132181 132182	AW961231 NM_014210	Hs.16773 Hs.70499	Homo saplens clone TCCCIA00427 mRNA seque ecotropic viral integration site 2A	3.83			13.20		
	132231	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	9.50					
	132277	AK001745	Hs.184628 Hs.44896	hypothetical protein FLJ10883 DnaJ (Hsp40) homolog, subfamily B, membe	4.50			9.20		
	132328 132394	NM_014787 AK001680	Hs.30488	DKFZP434F091 protein				19.80		
20	132424	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A			8.60			•
	132528 132543	T78736 BE568452	Hs.50758 Hs.5101	SMC4 (structural maintenance of chromoso protein regulator of cytokinesis 1	4.38		27.40			
	132544	L19778	Hs.51011	H2A histone family, member P		7.00				
25	132550	AW969253	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.64			15.83		
23	132552 132581	BE621985 AK000631	Hs.296922 Hs.52256	thiopurine S-methyltransferase hypothetical protein FLJ20624			6.60	10.00		
	132617	AF037335	Hs.5338	carbonic anhydrase XII	4.95					
	132638	AI796870	Hs.54277 Hs.54451	DNA segment on chromosome X (unique) 992 laminin, gamma 2 (nicein (100kD), kalini	4.38	8.20				
30	132653 132669	Z15008 W38586	Hs.293981	guanine nucleotide binding protein (G pr	4.50				4.36	
	132710	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	4.60					•
	132771 132799	Y10275 W73311	Hs.56407 Hs.169407	phosphoserine phosphatase SAC2 (suppressor of actin mutations 2,	3.71			9.48		
	132833	U78525	Hs.57783	eukaryotic translation initiation factor					5.83	
35	132892	AW834050	Hs.9973	tensin	0.00			12.00		
	132906 132959	BE613337 AW014195	Hs.234896 Hs.61472	geminin ESTs, Weakly similar to YAE6_YEAST HYPOT	3.09				3.87	ě
	132962	AA576635	Hs.6153	CGI-48 protein	3.50					
40	132990	X77343	Hs.334334	transcription factor AP-2 alpha (activat	6.18 3.19					
40	132994 133000	AA112748 AL042444	Hs.279905 Hs.62402	clone HQ0310 PRO0310p1 p21/Cdc42/Rac1-activated kinase 1 (yeast	2.96					
	133050	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	2.55				4.00	
	133083 133086	BE244588 L17131	Hs.6456 Hs.139800	chaperonin containing TCP1, subunit 2 (b high-mobility group (nonhistone chromoso					4.00 8.96	
45	133134	AF198620	Hs.65648	RNA binding motif protein 8A					4.28	
	133155	M58583	Hs.662	cerebellin 1 precursor	2 00			10.80		
	133181 133204	X91662 BE267696	Hs.66744 Hs.254105	twist (Drosophila) homolog (acrocephalos enolase 1, (alpha)	3.00				4.63	
50	133412	U41493	Hs.73112	guanine nucleotide binding protein (G pr		12.50				
50	133421	AF134160	Hs.7327	claudin 1 ubiquinol-cytochrome c reductase hinge p	2.85				4.66	
	133451 1 33 453	AW970026 Al659306	Hs.73818 Hs.73826	protein tyrosine phosphatase, non-recept		6.80			4.00	
	133504	NM_004415	Hs.74316	desmoplakin (DPI, DPII)	6.14				A EE	
55	133506 133615	BE562958 M62843	Hs.74346 Hs.75236	hypothetical protein MGC14353 ELAV (embryonic lethal, abnormal vision,				17.80	4.55	
55	133627	NM_002047	Hs.75280	glycyl-tRNA synthetase					4.85	
	133649	U25849	Hs.75393	acid phosphatase 1, soluble				14.00	6.34	
	133669 133749	NM_006925 L20852	Hs.166975 Hs.10018	splicing factor, arginine/serine-rich 5 solute carrier family 20 (phosphate tran			6.11	14.00		
60	133776	BE268649	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-					4.91	
	133865 133946	AB011155 AJ001258	Hs.170290 Hs.173878	discs, large (Drosophila) homolog 5 NIPSNAP, C. elegans, homolog 1	3.07				4.60	
	133973	N55540	Hs.78026	ESTs, Weakly similar to similar to ankyr				13.00		
CE	134047	BE262529	Hs.78771	phosphoglycerate kinase 1	0.50				3.85	
65	134098 134107	BE513171 NM_005629	Hs.79086 Hs.187958	mitochondrial riposomal protein 1.3 solute carrier family 6 (neurotransmitte	2.56		8.20			,·*
	134112	AW449809	Hs.79150	chaperonin containing TCP1, subunit 4 (d			5.55		4.08	
	134158	U15174	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro fibrillin 2 (congenital contractural ara	31.00		24.60			
70	134160 134168	T98152 AA398908	Hs.79432 Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L			24.00		6.71	
	134185	AA285136	Hs.301914	neuronal specific transcription factor D				14.74		ē
	134201 134272	L35035 X76040	Hs.79886 Hs.278614	ribose 5-phosphate isomerase A (ribose 5 protease, serine, 15	4.50	8.40				
	134276	BE083936	Hs.80976	antigen identified by monoclonal antibod	1.00	9.00				
75	134353	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	0.00			16.40		
	134367 134380	AA339449 AU077143	Hs.82285 Hs.179565	phosphoribosylglycinamide formyltransfer minichromosome maintenance deficient (S.	2.80 4.68					
	134423	H53497	Hs.83006	CGI-139 protein					3.84	
80	134469	AA279661	Hs.83753	small nuclear ribonucleoprolein polypept CDC28 protein kinase 2					5.81 4.21	
30	134470 134498	X54942 AW246273	Hs.83758 Hs.84131	threonyl-IRNA synthetase					7.30	
	134502	BE148534	Hs.84168	UV-B repressed sequence, HUR 7		13.60		0 30		
	134510 134548	NM_002757 N95406	Hs.250870 Hs.333495	mitogen-activated protein kinase kinase Deleted in split-hand/split-foot 1 regio				9.70	4.63	
85	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	6.00					

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	134724	AF045239	Hs.321576	ring finger protein 22				12.00	
	134743	AA044163	Hs.89463	potassium large conductance calcium-acti	4.00				
	134781	AA374372	Hs.89626	parathyroid hormone-like hormone			25.20		
_	134806	AD001528	Hs.89718	spermine synthase					4.58
5	134853	BE268326	Hs.90280	5-aminoimidazole-4-carboxamide ribonucle					4.79
	134859	D26488	Hs.90315	KIAA0007 protein			6.20		
	134891	R51083	Hs.90787	ESTs			7.40		
	134960	BE246400	Hs.285176	acetyl-Coenzyme A transporter	4.00				
	134993	BE409809	Hs.301005	purine-rich element binding protein B					4.48
10	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	9.50				
	135080	A1761180	Hs.94211	rcd1 (required for cell differentiation,	5.00				
	135103	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)		11.00			
	135145	AW014729	Hs.95262	nuclear factor related to kappa 8 bindin					4.01
4 ~	135184	U13222	Hs.96028	forkhead box D1			7.00		
15	135242	A1583187	Hs.9700	cyclin E1	13.50				
	135286	AW023482	Hs.97849	ESTs	6.46				
	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to		8.80			
	135355	AK001652	Hs.99423	ATP-dependent RNA helicase	10.00				
00	135371	NM_006025	Hs.997	protease, serine, 22	8.00				
20	135393	L11244	Hs.99886	complement component 4-binding protein,				14.60	

TABLE 58 shows the accession numbers for those primekeys lacking unigeneiD's for Table 5A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number 30 Genbank accession numbers Accession: Pkey CAT number Accessions H92325 T97125 AW963221 AA344870 AA344871 H93331 117079 1621717_1 35 124305 242183_1 101502 M26958 18202 -6 R49625 F10674 109792 754958_1 126034 1598157_1 H60340 N91637 102768 44641_1 1653833_1 U82321 H66077 40 N49713 N49819 W03810 126345 1703458_1 R25066 R20144 R20145 Z43845 127066 AA347668 AW956810 Z44271 F07065 F07064 R13506 T12603 T12604 244301_1 1774795 1 127099 119243 1566433_1 H14480 N98295 125875 45 1538292_1 R43590 F10439 112054 126979 171411<u>_</u>Î AA210954 AA211007 Al809521 H12174 Z42556 880655 1 126992 AA429743 AA442754 122318 292419_1 114699 135322_1 AA127386 R15644 AA127404 AA158245 AA158235 50 114793 150742 1 111550_1 AA071391 AA069892 AA069891 108305 108393 113411_ AA075211 AA075245 AA075126 AA074946 100867 tigr_HT4586 U14622 genbank_AA609839 AA609839 123731 55 genbank_F09609 F09609 109700 120715 genbank_AA292700 AA292700 genbank_T97307 T97307 113702 genbank AA256460 115113 AA256460 entrez_J05614 J05614 101045 60 108554 108573 genbank AA084948 AA084948 genbank AA086005 AA086005 149538_1 119052 416020_1 W31912 Al167491 126522 AA676910 AA778853 AA778865 W86800 126605 439280_1 65 W42667 Al580740 Al690440 Al561350 AW467906 AW151450 Al825927 AL041716 Al885600 Al742213 AW248624 Al955498 AA033947 46922 1 103768 AA845593 AI623711 N68583 C00064 AA193567 AW083868 AW163216 AA191595 AA522778 AI628008 AI915518 AA843508 AI926195 AA176265 AW167963 AA992115 W93647 AW103572 AI862994 AI342059 AA911719 AA176155 AA024712 AA069988 AA205591 AI591107 AI199673 AI811766 AI275832 AI422233 AI191852 AI096682 AI580124 AI683612 AA582453 AA927559 AA486415 T32414 AI084978 H44849 H44848 H20477 T91695 W47039 AA070055 AA024795 AA328855 AA379248 AA379330 AA385580 W25920 W03688 AA448359 AA093881 AW362477 AA089997 Al350265 W93479 N99688 AA932257 AW351469 H68590 AA663402 AA069771 AW087986 Al858420 AA600214 70 AJ970774 AI857712 AI683081 AI885584 AW131150 AI567881 AW002714 AW189973 AW075495 AW168303 AA953714 AW516881 AI357375 AI566663 AW512676 AI570580 AI023690 AA448216 AI079853 AI422707 AA779516 AW026972 AW130082 AW162307 AW438646 AA709332 AW192394 AI167350 AI217879 AI129152 AA719509 AI350480 AA663418 AI003634 AW118546 AA180261 AA442833 AI268625 AA888881 AW192394 A1167/300 A1217679 A1129152 AA715959 A1359400 AA603418 AU033554 AW116594 AA7160201 AA442635 A1606665 AA666666 A1606666 A 75 A1884391 A1241580 A1003539 AW176687 AA009650 N34566 A1333493 A1186070 AA070827 AA411683 A1280884 AA872023 AA207255 AA021576 N71953 A1885888 AW076039 T15777 A1537673 AW248048 H09554 W93480 W47001 AW079114 AA063160 AA757453 R60788 A1859431 H20478 AA218882 AA757465 AA100995 A1864135 A1934209 AA070503 H47008 AA219646 W61039 W93907 AW385050 W37967 80 AISS9431 H20478 AA218882 AA737405 AA100995 AISS4135 AISS4205 AA070503 H47006 AA219946 W0 1035 949397 AV35505 W78028 AA1889007 AA479136 R93650 AA442312 T30287 AA847628 AA180262 AA009549 C03892 AW149464 AA310963 AA219693 AA069747 R29207 AA094784 AA293615 AA47848 AIS84167 N90393 C05097 N56499 AW292351 AW149681 AW473258 AA629322 AI004409 AW105577 AI954937 AI811070 AA902422 AW514437 AA535460 AA916877 AW517122 AA974657 AA975649 AW517130 AW517129 F31737 W07688 AA193645 AA378994 AA489273 F32267 W39303 AA021181 N86810 AA406524 AA062553 AA436801 H08985 H15979 N40310 85

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AA436789 AA232172 AW360778 W25862 R60282 AA436530 AA378894 AA187461 AI940535 AA604210 AA089514 AA360421 N88243 N84281

AA209340 N56174 N88374 AA191088 AW247691 AA249013 AA093111 AA972536 AW298594 AA375893 T12139 W28186 AW243849

AI288629 AA843996 W15260 AI188286 AW248079 R15836

genbank_W45552 W45552
genbank_R59904 R59904
genbank_A4227934 AA227934
entrez_A28102 A28102

714071_1 AA496369 AA496646

119599 5 112382 105264 100071

123315

10

Table 6A shows 99 genes up-regulated nonsmokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15 Pkey: ExAcon: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number UnigenelD: Unigene number
Unigene Title: Rt:

ornigene gene due average of AI for samples from non-smokers with adenocarcinoma divided by the 90th percentile of AI for samples from smokers with adenocarcinoma average of AI for samples from non-smokers with squamous cell carcinoma divided by the 90th percentile of AI for samples from smokers with squamous cell 20 R2:

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
25	100971	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte		3.64
	101174	L17330	Hs.280	pre-T/NK cell associated protein	15.00	
	101296	Y12490	Hs.85092	thyroid hormone receptor interactor 11		2.46
	101304	AA001021	Hs.6685	thyroid hormone receptor interactor 8		12.00
	101806	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias		2.68
30	101972	S82472		gb:beta -pol=DNA polymerase beta (exon a		2.11
	102274	U30930	Hs.158540	UDP glycosyltransferase 8 (UDP-galactose	7.50	
	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.50	
	102832	U92015		gb:Human clone 143789 defective mariner	13.50	
25	103010	X52509	Hs.161640	tyrosine aminotransferase	9.50	2.50
35	103439	X98266		gb:H.sapiens mRNA for ligase tike protei	9.00	2.00
	103563	L02911	Hs.150402	activin A receptor, type I	5.00	3.94
	103857	A1076795	Hs.45033	lacrimal proline rich protein	13.50	3.34
	104239	AB002367	Hs.21355	doublecortin and CaM kinase-like 1 nuclear receptor subfamily 1, group I, m	10.50	12.66
40	104590	AW373062 AA055829	Hs.83623 Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU	16.50	,,,,,,
40	104907 106131	BE514788	Hs.296244	SNARE protein	10.00	2.17
	106672	H47233	Hs.30643	ESTs	7.00	
	106872	T56887	Hs.18282	KIAA1134 protein	11.50	
	106960	AA156238	Hs.32501	ESTs		2.38
45	106971	Z43846	Hs.194478	Homo saplens mRNA; cDNA DKFZp434O1572 (f	9.50	
	107982	AA035375	Hs.57887	ESTs, Weakly similar to KIAA0758 protei		2.95
	108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720	16.50	
	108599	AB018549	Hs.69328	MD-2 protein	13.00	
	108663	BE219231	Hs.292653	ESTs, Weakly similar to T26845 hypotheti		2.40
50	109247	AA314907	Hs.85950	ESTs	7.00	F 00
	109630	R44607	Hs.22672	ESTs	40.50	5.00
	110193	A1004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	12.50	
	110234	H24458	Hs.32085	EST CALAMATA	16.50 8.00	
55	110644	R94207	Hs.268989	ESTs, Highly similar to type II CALM/AF1	17.00	
55	110886	AW274992	Hs.72249	three-PDZ containing protein similar to	16,50	
	111057	T79639	Hs.14629 Hs.110457	ESTs Wolf-Hirschhorn syndrome candidate 1	11.00	
	111950 112291	AF071594 R53972	Hs.26026	ESTs	. 1.00	3.00
	112956	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)		2.79
60	113009	T23699	Hs.7246	ESTs		4,50
OO	113060	BE564162	Hs.250820	hypothetical protein FLJ14827	9.79	
	113073	N39342	Hs.103042	microtubule-associated protein 1B	32,50	
	113074	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t		3.82
	113121	T48011	Hs.8764	EST		2.21
65	113125	AA968672	Hs.8929	hypothetical protein FLJ11362	19.50	
	113757	AA703095	Hs.18631	ESTs		2.65
	113848	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	6.00	6.00
	113884	Al333076	Hs.28529	chromosome 12 open reading frame 2		6.00
70	113936	W17056	Hs.83623	nuclear receptor subfamily 1, group 1, m		4.63 7.00
70	114875	AA235609	Hs.236443	Homo saplens mRNA; cDNA DKFZp564N1063 (6.00
	114987	AA251016	Hs.87808	EST		2.27
	115460	AW958439	Hs.38613	ESTs ESTs		9.00
	115722	W91892 AA481788	Hs.59609 Hs.190150	ESTs	9.50	•
75	116261 116830	H61037	Hs.70404	ESTs, Weakly similar to ALU2_HUMAN ALU	8.50	
13	116970	AB023179	Hs.9059	KIAA0962 protein	7.50	
	117178	H98675	Hs.269034	ESTs		2.68
	117757	AF088019	Hs.46732	EST	7.50	
	118283	AA287747	Hs.173012	ESTs, Wealdy similar to A46010 X-linked	16.50	
80	118384	AF217525	Hs.49002	Down syndrome cell adhesion molecule		2.50
	118657	AI822106	Hs.49902	ESTs		2.39
	120328	AA923278	Hs.290905	ESTs, Weakly similar to protease (H.sapi		3.50
	120404	AB023230	Hs.96427	KIAA 1013 protein	7.00	
0.5	120524	AA261852	Hs.192905	ESTs	6.00	
85	120688	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	17.92	

	WC	02/0864	143				PCT/US02/12476
	121558	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sap		2.95	
	121676	H56037	Hs.108146	ESTs	10.00		
	121936	Al024600	Hs.98612	ESTs	15.00		
	121938	AA428659	Hs.98610	ESTs	14.00		
5	122177	AA435789	Hs.98833	EST	8.93		
_	123442	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.04		
	123551	AA608837		ob:af03h12.s1 Soares_testis_NHT Homo sap	11.50		
	123756	AA609971	Hs.112795	EST	11.00		
	123861	AA620840		ob:af89g01.s1 Soares_testis_NHT Homo sap		2.50	
10	124371	N24924	Hs.188601	ESTs	6.50		
	127477	BE328720	Hs.280651	ESTs		4.33	
	127591	Al190540	Hs.131092	ESTs		3.02	
	128252	AA455924	Hs.192228	ESTs	7.00		
	128426	AI265784	Hs.145197	ESTs		2.08	
15	128925	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT		2.11	
	128945	Al990506	Hs.8077	Homo saplens mRNA; cDNA DKFZp547E184 (fr	10.00		
	129105	Al769160	Hs.108681	Homo saplens brain tumor associated prot	15.50		
	129235	AW977238	Hs.126084	KIAA1055 protein		4.25	
	129506	AB020684	Hs.11217	KIAA0877 protein	6.50		
20	129595	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9		10.00	
	130160	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	20.00		
	130340	D82326	Hs.239106	solute carrier family 3 (cystine, dibasi	11.50		
	131220	AB023194	Hs.300855	KIAA0977 protein	17.50		
	131430	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.10		
25	132114	NM_006152	Hs.40202	tymphoid-restricted membrane protein		6.15	
	132458	AA935315	Hs.48965	Homo sapiens cDNA: FLJ21693 ffs, clone C		5.58	
	132647	NM_006927	Hs.54432	sialyltransferase 4B (beta-galactosidase	7.50		
	132655	D49372	Hs.54460	small inducible cytokine subfamily A (Cy		2.53	
••	132682	A1077500	Hs.54900	serologically defined colon cancer antig		2.50	
30	132747	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein		2.83	
	132812		Hs.92186	Leman colled-coll protein		3.82	
	133337	AF085983	Hs.293676	ESTs		5.00	
	133876	AL134906	Hs.771	phosphorylase, glycogen; liver (Hers dis		3.00	
0.5	134119	AW157837	Hs.79226	fasciculation and elongation protein zet		2.06	
35	134464	AA302983	Hs.239720	CCR4-NOT transcription complex, subunit		2.27	
	134542	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi		11.50	• •
	135002	AA448542	Hs.251677	G antigen 78	87.00		
	135305	AA203555	Hs.98288	Homo sapiens cDNA FLJ14903 ffs, clone PL		6.50	

TABLE 6B show the accession numbers for those primekeys lacking unigenelD's for Table 6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

50		
	Pkey	CAT number Accessions
55	108562 103439 123551 123861 102832	36375_1 AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274 35330_1 X98266 N41124 genbank_AA608837 AA608837 genbank_AA620840 AA620840 entrez_U92015 U92015
60	101972 121558	entrez_S82472 S82472 genbank_AA412497 AA412497

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Table 7A shows 98 genes down-regulated in non-smokers with lung cancer relative to smokers with lung cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5

Pkey: Unique Eos probeset identifier number

ExAcon: Unigenetic: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of AI for samples from smokers with adenocarcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma divided by the average of AI for samples from non-smokers with squamous cell carcinoma. 10

carcinoma.

		carcinon	na.			
	Pkey	ExAcen	UnigenelD	Unigene Title	R1	R2
15	100187 100380	D17793 D82343	Hs.78183 Hs.18551	aldo-keto reductase family 1, member C3 neuroblastoma (nerve tissue) protein		164.10 77.40
	100576	X00356	Hs.37058	calcitonin/calcitonin-related polypeptid	102.40	
	100971 101046	BE379727 K01160	Hs.83213	fatty acid binding protein 4, adipocyte (NONE)	463.80 672.00	
20	101066	AW970254	Hs.889	Charol-Leyden crystal protein	66.00	
	101175	U82671	Hs.36980	melanoma antigen, family A, 2		77.20
	101497	W05150	Hs.37034	hameo bax A5	62.80	_
	101663	NM_003528	Hs.2178	H2B histone family, member Q	78.00	-
25	101677	NM_000715	Hs.1012 Hs.150403	complement component 4-binding protein, dopa decarboxylase (aromalic L-amino aci	186.20 80.08	
23	101745 101941	M88700 S77583	ns. 130403	gb:HERVK10/HUMMTV reverse transcriptase	99.20	
	102125	NM_006456	Hs.288215	sialytransferase	00120	103.10
	102242	U27185	Hs.82547	retinoic acid receptor responder (tazaro	67.00	
20	102340	U37055	Hs.278657	macrophage stimulating 1 (hepatocyte gro	71.60	20.70
30	102369	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	153.00	69.70
	102457 102669	NM_001394 U71207	Hs.2359 Hs.29279	dual specificity phosphatase 4 eyes absent (Drosophila) homolog 2	153.00	65.70
	102796	AL079646	Hs.107019	symplekin; Huntingtin interacting protei		58.80
	102829	NM_006183	Hs.80962	neurotensin		268.80
35	103207	X72790		gb:Human endogenous retrovirus mRNA for	70.00	01010
	103242	X76342	Hs.389	atcohol dehydrogenase 7 (class IV), mu o		212.10
	103260 103351	X78416 X89211	Hs.3155	casein, alpha gb:H.sapiens DNA for endogenous retrovir	64.60	130.70
	104212	AB002298	Hs.173035	KIAA0300 protein	66.80	
40	104252	AF002246	Hs.210863	cell adhesion molecule with homology to	63.80	
	104258	AF007216	Hs.5462	solute carrier family 4, sodium blcarbon	94.40	
	105024	AA126311	Hs.9879	ESTS	68.20	74.60
	106260 106440	Al097144 AA449563	Hs.5250 Hs.151393	ESTs, Weakly similar to ALU1_HUMAN ALU S glutamate-cysteine ligase, catalylic sub		71.10
45	106566	BE298210	110.101000	gb:601118016F1 NIH_MGC_17 Homo saplens c	73.20	
	106605	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	83.80	
	106614	AA648459	Hs.335951	hypothetical protein AF301222		62.30
	106654 106999	AW075485 H93281	Hs.286049 Hs.10710	phosphoserine aminotransferase hypothetical protein FLJ20417		202.40 89.60
50	100333	AA121518	Hs.193540	ESTs, Moderately similar to 2109260A B c		66.40
• •	108810	AW295647	Hs.71331	hypothetical protein MGC5350		95.50
	108857	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act		63.40
	109597	AA989362	Hs.293780	ESTS	85.00	E0 70
55	109691 109704	T65568 A1743880	Hs.12860 Hs.12876	ESTs ESTs		58.70 60.60
	110942	R63503	Hs.28419	ESTs	76.40	40.00
	111722	R23924	Hs.23596	EST	74.60	
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-II	64.80	WA 70
60	112992	AL157425	Hs.133315 Hs.103042	Homo sapiens mRNA; cDNA DKFZp761J1324 (f		76.70 120.20
00	113073 114251	N39342 H15261	Hs.21948	microtubule-associated protein 1B ESTs	127.20	120.20
	115230	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	174.00	
	115291	BE545072	Hs.122579	hypothetical protein FLJ10461		91.00
65	115815	AW905328	Hs.180842	ribosomal protein L13	66.40	000.00
65	115909 115965	AW872527 AA001732	Hs.59761 Hs.173233	ESTs, Weakly similar to DAP1_HUMAN DEATH hypothetical protein FLI10970	82.80	226.60
	116107	AL133916	Hs.172572	hypothetical protein FLJ20093	02.00	361.60
	116552	D20508	Hs.164649	hypothetical protein DKFZp434H247	69.00	•••••
70	116571	D45652		gb:HUMGS02848 Human adult lung 3' direct	64.20	
70	118466	N66741	11. 00.170	gb:yz33g08.s1 Morton Fetal Cochlea Homo	94.00	63.50
	120484 120983	AA253170 AA398209	Hs.96473 Hs.97587	EST EST	81.60	81.10
	121034	AL389951	Hs.271623	nucleoporin 50kD		66.20
	121423	AW973352	Hs.290585	ESTs	64.40	
75	122553	AA451884	Hs.190121	ESTs		60.40
	122946	A1718702	Hs.308026	major histocompatibility complex, class	188.60	00.00
	123130	AA487200 N52617	Ue innere	gb:ab19f02.s1 Stratagene lung (937210) H	71.00	80.20
	124472 124526	N52517 N62096	Hs.102670 Hs.293185	EST ESTs, Wealdy similar to JC7328 amino aci	. 1.00	104.90
80	125489	H49193	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A		72.00
	125731	R61771	Hs.26912	ESTs		69.90
	- 125747	NM_002884	Hs.865	RAP1A, member of RAS oncogene family	69.00	co 40
	126020	H79863	Hs.114243	ESTs transmembrane 4 superfamily member 3		62.40 62.80
85	126547 126966	U47732 R38438	Hs.84072 Hs.182575	solute carrier family 15 (H+/peptide tra		60.10
	,	- 100 100	. 10. 102.010	TOTAL SERVICE SERVICE TO SERVICE SERVI		

	W	O 02/086	443				PCT/US02/12476
	127472	AA761378	Hs.192013	ESTs	70.20		
	127610	AA960867	Hs.150271	ESTs, Highly similar to unnamed protein	64.00		
	127742	AW293496	Hs.180138	ESTs	85.20		
	127987	AI022103	Hs.124511	ESTs	96.60		
5	128233	AW889132	Hs.11916	ribokinase		78.90	
_	128420	AA650274	Hs.41296	fibronectin leucine rich transmembrane p		106.90	
	128766	AW160432	Hs.296460	craniofacial development protein 1	66.80		
	129014	AW935187	Hs.170162	KIAA1357 protein		58.53	
	129215	AB040930	Hs.126085	KIAA1497 protein	64.20		
10	130090	H97878	Hs.132390	zinc finger protein 36 (KOX 18)	63.80		
	130385	AW067800	Hs.155223	stanniocalcin 2		139.60	
	130732	AW890487	Hs.63984	cadherin 13, H-cadherin (heart)		64.60	
	131025	AB040900	Hs.6189	KIAA1467 protein	64.40		
	131241	BE501914	Hs.24654	Homo sapiens cDNA FLJ11640 fis, clone HE	76.20		
15	131775	AB014548	Hs.31921	KIAA0648 protein	97.80		
	132240	AB018324	Hs. 42676	KIAA0781 protein		71.00	
	132856	NM_001448	Hs.58367	glypican 4		88.40	
	132977	AA093322	Hs.301404	RNA binding motif protein 3	133.20		
	133749	L20852	Hs.10018	solute carrier family 20 (phosphate tran		59.30	
20	133818	AI110684	Hs.7645	fibrinogen, B beta polypeptide	341.00		
	134264	AF149297	Hs.8087	NAG-5 protein		64.30	
	134265	M83772	Hs.80876	flavin containing monooxygenase 3		232.53	
	134346	X84002	Hs.82037	TATA box binding protein (TBP)-associate	66.00		
	134395	AA456539	Hs.8262	lysosomal-associated membrane protein 2		75.80	
25	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su		108.30	
	135056	N75765	Hs.93765	lipoma HMGIC fusion partner	71.40		
	135309	AI564123	Hs.42500	ADP-ribosylation factor-like 5	70.40		
20						and a subsequent to the first of the subsequent	and the state of t
30	digonuc	leolides were de	signed. Gene	ers for those primekeys lacking unigenelD's for Tal o clusters were compiled using sequences derived out Tools (DoubleTwist Oakland California). The G	from Genbank ES	Ts and mRNAs. These sequ	ences were clustered based on sequer

30	TABLE 7B shows the accession numbers for those primekeys lacking uniqueelD's for Table 7A. For each probeset we have listed the gene cluster number from which the
	dinamiclarities were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence
	similarity using Clustering and Alignment Tools (DoubleTwist, Oaldand California). The Genbank accession numbers for sequences comprising each cluster are listed in the
	"Accession" column.

35		Unique Eos probeset identifier number Gene cluster number
	Accession:	Genbank accession numbers

40	Pkey	CAT number Accessions	
40	103207 106566		BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 Al333584 Al369742 Al039658 B885299 Al985381 AW592624 AW340136 Al266556 AA456390 Al310815 AA484951
45	116571 118466 101046 101941	genbank_045652 D45652 genbank_N66741 N66741 entrez_K01160 K01160 entrez_S77583 S77583	IBBD2233 AISCONGT ATTOSEEVEN AND AND THE AISCONGT AND SOUTH AND
50	103351 123130	entrez_X89211 X89211 genbank_AA487200 AA487200	

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Table 8A shows 1720 genes either up or down-regulated in lung tumors or chronically diseased lung relative to a broad collection of over 40 distinct normal body tissues. Chronically diseased lung samples represent chronic non-malignant lung diseases such as fibrosis, emphysema, and bronchitis. These genes were selected from 39494 probesets on the Eos/Affymetrix Hu02 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Pkey: Unique Eos probe ExAccn: Exemplar Access UnigenelD: Unigene number

5

Ningene Title: Unigene gene little

R1: 70th percentile of AI for lung tumors divided by 90th percentile of AI for normal lung

R2: 70th percentile of AI for chronically diseased lung divided by 90th percentile of AI for normal lung 10

	R2: 70th percentile of All for chronically diseased lung divided by 90th percentile of All for north						
	Pkey	ExAcen	UnigenelD	Unigene Title	R1	R2	
15	300097	Al916973	Hs.213603	ESTs	5.46	4.69	
	300117	AW189787	Hs.147474	ESTs	0.58	0.56	
	300197	Al686661	Hs.218286	ESTs	4.26	5.44	
	300201	AI308300	•	gb:ta90c06.x1 NCt_CGAP_Bm20 Homo sapien	0.62	0.83	
~~	300225	A1989963	Hs.197505	ESTs	1.68	1.75	
20	300247	AW274682	Hs.161394	ESTs	1.08 0.86	2.28 1.00	
	300256	Al469095	Hs.298241	Transmembrane protease, serine 3	5.80	9.09	
	300337 300362	A1707881 Z42308	Hs.202090	ESTs gb:HSC0FB121 normalized infant brain cDN	4.18	12.78	
	300374	Al859947	Hs.314158	ESTs	2.99	4.38	
25	300387	AW270150	Hs.254516	ESTs	1.50	2:53	
	300440	Al421541	Hs.146164	ESTs	3.98	5.25	
	300441	R10367	Hs.307921	EST, Weakly similar to Z232_HUMAN ZINC F	3.18	6.80	
	300449	Al362967	Hs.132221	hypothetical protein FLJ12401	0.43	0.62	
20	300469	AW135830	Hs.233955	hypothetical protein FLJ20401	0.16	0.83	
30	300552	X85711	Hs.21838	hypothetical protein FLJ11191	4.10	9.75	
	300627	W27363	11- 400757	gb:ab37d01.r1 Stratagene HeLa cell s3 93	4.60 2.91	12.60 5.86	
	300630	AW118822	Hs.128757	ESTs	1.00	0.92	
	300716 300738	Al216113 Al623332	Hs.126280 Hs.130541	hypothetical protein FLJ23393 KIAA1542 protein	1.82	1.71	
35	300736	AA235361	Hs.96840	KIAA1527 protein	4.48	8.22	
33	300790	Al492471	Hs.188270	ESTs	1.29	1.18	
	300832	AI688147	Hs.220615	ESTs, Weakly similar to T03829 transcrip	5.51	8.56	
	300836	Z44942	Hs.22958	calcium channel alpha2-delta3 subunit	4.90	6.34	
4.0	300838	AI582897	Hs.192570	hypothetical protein FLJ22028	1.70	2.81	
40	300878	AW449802	Hs.285901	Homo sapiens cONA FLJ20428 fis, clone KA	4.56	7.91	
	300897	A1890356	Hs.127804	ESTs, Weakly similar to T17233 hypotheti	2.23 2.13	1.58 3.50	
	300926	AA504860	Us Acoust	gb:ab03a10.s1 Stratagene felal retina 93	2.13 2.74	3.50 4.46	
	300960	AI041019	Hs.152454 Hs.312716	ESTs ESTs, Wealdy similar to unnamed protein	1.00	1.00	
45	300961 300962	AW204069 AA593373	Hs.293744	ESTs	1.46	1,51	
73	300967	AA565209	Hs.269439	ESTs	0.39	1.30	
	300987	AW450840	Hs.148590	ESTs, Weakly similar to AF208846 1 BM-00	1.49	1.08	
	300988	AI927208	Hs.208952	ESTs	0.16	0.37	
	301050	AW136973	Hs.288516	ESTs, Wealdy similar to S69890 mitogen t	3.23	1.94	
50	301098	AA677570	Hs.185918	ESTs	6.76	14.28	
	301157	AA729905	Hs.231916	ESTs	3.16 1.68	8.85 7.18	
	301162	A1142118	Hs.129004	ESTS	4.40	6.42	
	301170 301192	AA737594 Al808751	Hs.247606 Hs.121188	ESTs ESTs	6.38	11.59	
55	301193	AA758115	Hs.128350	ESTs, Wealty similar to JC5423 2-hydroxy	4.35	7.78	
55	301267	AW297762	Hs.255690	ESTs	1.56	1.61	
	301281	AA843986	Hs.190586	ESTs	2.19	1.78	
	301341	AI819198	Hs.208229	ESTs	0.76	0.76	
	301382	AA912839	Hs.163369	ESTs	1.00	1.81	
60	301407	AW450466	Hs.126830	ESTs	1.48	1.51	
	301452	AA975688	Hs.159955	ESTs	0.51 2.40	1.46 5.02	
	301483	AW272467	Hs.254655	Untitled	2.79	3.41	
	301494	AI678034	Hs.131099 Hs.133011	ESTs zinc finger protein 117 (HPF9)	0.67	0.67	
65	301521 301531	A1733621 A1077462	Hs.134084	ESTs	2.52	3.76	
03	301580	Al878959	Hs.73737	splicing factor, arginine/serine-rich 1	7.41	11.92	
	301676	Z43570	Hs.27453	ESTs, Moderately similar to G01251 Rar p	8.31	10.70	
	301690	F05865	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	2.70	4.22	
=-	301718	F07744	Hs.7987	DKFZP434F162 protein	4.20	8.78	
70	301799	AA384252	Hs.286132	D15F37 (pseudogene)	5.93	7.04	
	301804	AA581004	Hs.62180	anillin (Drosophila Scraps homolog), act	1.70	0.76	
	301822	X17033	Hs.271986	integrin, alpha 2 (CD498, alpha 2 subuni	1.58 1.00	1.36 1.00	
	301846	R20002	Hs.6823	hypothetical protein FLJ10430 ESTs, Weakly similar to pH sensitive max	2.88	5.49	
75	301868	T71508 T78054	Hs.13861	gb:yc97g09.r1 Soares infant brain 1NiB H	2.28	3.80	
13	301882 301905	Al991127	Hs.117202	ESTs	1.00	1.00	
	301948	AA344647	Hs.116724	aldo-keto reductase family 1, member B11	5.28	2.28	
	301960	AW070252	Hs.27973	KIAA0874 protein	5.38	6.48	
	302011	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	3.03	3.42	
80	302016	N40834	Hs.23495	hypothetical protein FLJ11252	1.00	1.25	
	302041	NM_001501		gonadotropin-releasing hormone 2	0.71	0.99	
	302072	AJ238381	Hs.132576	paired box gene 9	1.60	1.71	
	302094	A1286176	Hs.6786	ESTs Homo saplens BAC clone RP11-120J2 from 7	0.52 2.75	1.20 4.93	
85	302095 302148	AW044300 AW269618	Hs.137506 Hs.23244	ESTs	3.04	3.87	
35	302148	A44709010	113-23299	Luis	•.• •		

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	302155	AI088485	Hs.144759	ESTs	0.45	1.15
	302201	AJ006276	Hs.159003	transient receptor potential channel 6	0.33	0.84
	302202	AF097159	Hs.159140	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	0.52	0.94
5	302206	AI937193	Hs.41143	phosphoinosliide-specific phospholipase	2.76 1.00	3.65 1.00
)	302209 302235	AF047445 AL049987	Hs.159297 Hs.166361	killer cell lectin-like receptor subfami Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.68	1.50
	302290	AL117607	Hs.175563	Homo saplens mRNA: cDNA DKFZp564N0763 (f	1.00	2.11
	302328	AA354849	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	9.38	13.08
	302346	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	3.27	7.24
10	302360	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.54	1.88
	302384	Y08982	Hs.202676	synaptonemal complex protein 2	1.00	0.91
	302406	U86751	Hs.211956	CD3-epsilon-associated protein; antisens	2.63	2.67
	302409	AF155156	Hs.218028	adaptor-related protein complex 4, epsil	5.82	9.34
15	302423	AB028977	Hs.225974	KIAA1054 protein	3.66 2.44	3.18 6.77
15	302432	AL080068	Hs.272534	Homo sapiens mRNA; cDNA DKFZp564J062 (fr sine oculis homeobox (Drosophila) homolo	0.44	0.84
	302435 302437	AF092047 AB024730	Hs.227277 Hs.227473	UDP-N-acetylglucosamine:a-1,3-D-mannosid	4.18	5.64
	302455	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	1.85	0.92
	302472	AA317451	Hs.6335 ·	SWI/SNF related, matrix associated, acti	2.04	2.13
20	302476	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	1.44	1.89
	302489	T80660	Hs.230424	Homo sapiens cDNA FLJ 13540 fis, clone PL	0.51	1.10
	302490	AA885502	Hs.187032	ESTs	2.64	4.87
	302562	AJ005585	Hs.48956	gap junction protein, beta 6 (connexin 3	5.34	2.68
25	302566	AA085996	Hs.248572	hypothetical protein FLJ22965	1.00	1.21
25	302630	AB029488	Hs.272100	SMS3 protein	0.52 1,00	1.24 1.00
	302634	AB032953 AA463798	Hs.173560 Hs.102696	odd Oz/ten-m homolog 2 (Drosophila, mous MCT-1 protein	1.58	1.02
	302638 302647	X57723	Hs.198273	NADH dehydrogenase (ubiquinone) 1 beta s	2.72	6.85
	302655	AJ227892	Hs.146274	ESTs	1.00	4.32
30	302656	AW293005	Hs.70704	Homo sapiens, clone IMAGE:2823731, mRNA,	2.97	0.93
	302668	AA580691	Hs.180789	S164 protein	0.80	0.95
	302679	H65022		gb:yu66g11.r1 Weizmann Olfactory Epithel	1.68	5.04
	302680	AW192334	Hs.38218	ESTs	2.70	7.98
25	302697	AJ00140B		gb:Homo saplens mRNA for Immunoglobulin	4.25	8.13
35	302705	U09060		gb:Human immunoglobulin heavy chain, V-r	3.91 2.20	8.68 2.73
	302711	L08442	Hs.288959	gb:Human autonomously replicating sequen hypothetical protein FLJ20920	0.54	1.02
	302719 302742	W69724 L12069	NS.200333	gb:Homo saplens (clone WR4.10VH) anti-th	4.28	11.57
	302755	AW384815	Hs.149208	KIAA1555 protein	1.57	2.38
40	302771	H98476	Hs.42522	ESTs	2.94	4.68
	302789	AJ245067		gb:Homo sapiens mRNA for immunoglobulin	3.49	6.31
	302795	AJ245313	Hs.272838	hypothetical protein FLJ10494	0.80	2.74
	302802			gb:H.sapiens mRNA for variable region of	1,13	0.77
45	302803	AA442824	Hs.293961	ESTs, Moderately similar to putative DNA	3.14	10.68
45	302812	N31301	Hs.152664	hypothetical protein FLJ20051	3.04 1.80	8.24 1.92
	302847	X98940	U= 420407	gb:H.sapiens rearranged Ig heavy chain (1.00	1.00
	302885 302943	AL137763 AI581344	Hs.132127 Hs.127812	hypothetical protein LOC57822 ESTs, Weakly similar to T17330 hypotheti	0.53	0.67
	302977	AW263124	Hs.315111	hypothetical protein FLJ 12894	2.45	2.62
50	303006	AF078950	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	4.88	8.61
-	303011	AF090405		gb:Homo sapiens clone 2A1 scFV anitbody	1.41	1.86
	303013	F07898	Hs.288968	RAB22A, member RAS oncogene family	1.51	1.19
	303061	AF151882	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l	0.72	0.76
	303077	AF163305		gb:H.sapiens T-cell receptor mRNA	1.17	3.90
55	303090	AA443259	Hs.146286	kinesin family member 13A	4.08	6.46 4.37
	303091	AF192913	Hs.130683	zinc finger protein 180 (HHZ168)	2.50 5.38	8.38
	303094 303095	AF195513 AF202051	Hs.278953 Hs.134079	Pur-gamma NM23-H8	3.26	4.08
	303131	AW081061	Hs.103180	DC2 protein	2.02	1.83
60	303195	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	1.32	3.95
	303196	AA082298	Hs.59710	ESTs	0.77	0.53
	303216	AA581439	Hs.152328	ESTs	0.24	0.63
	303222	AA333538	Hs.204501	hypothetical protein FLJ10534	3.56	6.22
c =	303234	AA132255	Hs.143951	ESTs	2.28	3.17
65	303251	AW340037	Hs.115897	protocadherin 12	0.38 2.30	1.02 1.00
	303295	AA205625	Hs.208067	ESTs Homo saplens clone 24468 mRNA sequence	1.86	4.48
	303297	T80072 AF033122	Hs.13423 Hs.14125	p53 regulated PA26 nuclear protein	0.10	0.80
	303316 303467	AA398801	Hs.323397	ESTs	4.54	9.65
70	303506	AA340605	Hs. 105887	ESTs, Weakly similar to Homolog of rat Z	0.09	0.04
. •	303552	AA359799	Hs.224662	ESTs, Weakly similar to unnamed protein	1.00	1.72
	303598	AA382814		gb:EST96097 Testis I Homo sapiens cDNA 5	4.96	9.14
	303637	AF056083	Hs.24879	phosphatidic acid phosphatase type 2C	2.06	2.02
75	303655	AA504702	Hs.258802	ATPase, (Na+)/K+ transporting, beta 4 po	1.00	1.24
75	303756	A1738488	Hs.115838	ESTs	1.08	1.43
	303856	AA968589	Hs.180532	glucose phosphate isomerase	1.76	1.31
	303893	N88597	Hs.113503	karyopherin (importin) beta 3	2.30 3.10	2.57 5.79
	303907	AW467774	Hs.171880	polymerase (RNA) II (DNA directed) polyp Homo saplens cDNA FLJ12363 fis, clone MA	5.06	11.86
80	303946	AW474198	Hs.306637	gb:xo43c12.x1 NCI_CGAP_Ut1 Homo saplens	5.14	7.31
30	303978 303981	AW513315 AW513804	Hs.278834	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.83	4.06
	303990	AW515465	1 10161 0004	gb:xu71a11.x1 NCI_CGAP_Kid8 Homo sapiens	1.15	2.35
	303998	AW516449		ab:xl68f05.x1 NCI_CGAP_Ut2 Homo sapiens	2.20	9.35
	303999	AW516611		gb:xp70b11.x1 NCI_CGAP_Ov39 Homo sapiens	4.85	6.28
85	304006	AW517947		gb:xt66h02.x1 NCI_CGAP_Ut2 Homo saplens	3.21	4.07

	W	O 02/08	6443			
	304008	AW518198	Hs.3297	ribosomal protein S27a	6.50	11.08
	304009	AW518206	Hs.181165	eukaryotic translation elongation factor	1.88	3.27
	304024	T03036		gb:FB21B7 Fetal brain, Stratagene Homo s	2.15	3.55
5	304026	T03160		gb:FB26F2 Fetal brain, Stratagene Homo s	5.88 5.59	11.80
3	304028	T03266 T16855	Hs.244621	gb:FB7C1 Fetal brain, Stratagene Homo sa ribosomal protein S14	5.55 6.55	13.46 14.43
	304036 304046	T54803	115.244021	gb:yb42d06.s1 Stratagene fetal spleen (9	6.18	12.19
	304061	T61521		gb:yb73g01.s1 Stratagene ovary (937217)	2.64	8.23
	304063	T62536		gb:yc04c12.s1 Stratagene lung (937210) H	0.53	1.61
10	304097	R25376	Hs.177592	ribosomal protein, large, P1	6.49	11.67
	304114	R78946		gb:yi87g02.s1 Soares placenta Nb2HP Homo	2.90 1.00	4.18 2.76
	304122 304155	H28966 H68696		gb:ym31a06.s1 Soares infant brain 1NIB H gb:yr78b06.s1 Soares fetal liver spleen	0.79	1.18
	304203	N56929		gb:yy82d08.s1 Soares_multiple_sclerosis_	4.28	11.34
15	304234	W81608		gb:zd88h06.s1 Soares_fetal_heart_NbHH19W	6.47	11.03
	304267	AA064862	Hs.73742	ribosomal protein, large, PO	1.34	1.16
	304270	AA069711	Hs.297753	vimentin	3.40	5.40
	304287	AA079286	Hs.78456	proteasome (prosome, macropain) 26S sub	2.93 3.98	4.42 10.96
20	304348	AA179868	Hs.169476	gb:zp38g12.s1 Stratagene muscle 937209 H glyceraldehyde-3-phosphate dehydrogenase	3.32	5.99
20	304415 304430	AA290747 AA347682	HS. 105410	gb:EST54044 Fetal heart II Homo saplens	1.00	1.00
	304456	AA411240		gb:zv26g05.s1 Soares_NhHMPu_S1 Homo sapi	1.42	3.33
	304521	AA464716		gb:zx82c11.s1 Soares ovary tumor NbHOT H	2.18	1.15
0.5	304526	AA476427		gb:zx02c05.s1 Soares_total_fetus_Nb2HF8_	5.38	14.11
25	304542	AA482602	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.16	8,23
	304546	AA486074	Hs.297681	serine (or cysteine) proteinase inhibito gb:nh85e08.s1 NCI_CGAP_Br1.1 Homo sapien	0.55 1.95	1.20 2.10
	304607 304640	AA513322 AA524440	Hs.111334	ferritin, light polypeptide	2.10	2.83
	304650	AA527489	Hs.3463	ribosomal protein S23	3.33	12.62
30	304735	AA576453		gb:nm75h11.s1 NCI_CGAP_Co9 Homo saplens	1.33	0.88
	304760	AA580401		gb::nn13g09.s1 NCI_CGAP_Co12 Homo saplens	3.68	8.14
	304849	AA588157	Hs.13801	KIAA1685 protein	2.77	3.70
	304917	AA602685	Hs.284136	PRO2047 protein vimentin	7.16 2.47	11.01 4.24
35	304921 304966	AA603092 AA613893	Hs.297753 Hs.282435	ESTs .	6.78	11.66
55	304987	AA618044	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.90	1.23
	305016	AA626876		gb:zu89h06.s1 Soares_testis_NHT Homo sap	6.46	10.17
	305034	AA630128		gb:ab99c04.s1 Stralagene lung (937210) H	1.00	1.00
40	305072	AA641012	11- 202405	gb:nr72a12.s1 NCI_CGAP_Pr24 Homo sapiens	5.68 1.48	11.59 1.37
40	305111 305148	AA644187 AA654070	Hs.303405	ESTs gb:nt01g08.s1 NCI_CGAP_Lym3 Homo sapiens	1.76	4.61
	305159	AA659166	Hs.275668	EST, Weakly similar to EF1D_HUMAN ELONG	1.00	2.15
	305190	AA665955	,,_,_,	gb:ag57d12.s1 Gessler Wilms tumor Homo s	5.31	8.14
45	305232	AA670052	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	0.78	1.18
45	305235	AA670480	11- 04200	gb:ag37e01.s1 Jia bone marrow stroma Hom	3.11 4.38	8.66 7.53
	305245 305312	AA676695 AA700201	Hs.81328	nuclear factor of kappa light polypeptid gb:zj44f07.s1 Soares_fetal_fiver_spleen_	2.13	2.66
	305322	AA701597	Hs.163019	EST	1.20	1.40
	305394	AA720942	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.16	0.68
50	305413	AA724659		gb:ai10f08.s1 Soares_parathyroid_tumor_N	5.86	9.87
	305447	AA737856	U. 007446	gb:nx10c08.s1 NCI_CGAP_GC3 Homo sapiens hypothetical protein FLJ11726	2.21 3.36	2.86 6.54
	305476 305483	AA745664 AA748030	Hs.287445 Hs.303512	EST	1.00	2.02
	305528	AA769156	113.000012	gb:nz12e05.s1 NCI_CGAP_GCB1 Homo sapiens	6.44	9.10
55	305612	AA782347	Hs.272572	hemoglobin, alpha 2	0.19	0.79
	305614	AA782866		gb:aj09h02.s1 Soares_parathyrold_tumor_N	1.00	1.00
	305616	AA782884	Hs.275865	ribosomal protein S18	7.57 4.78	10.20 12.42
	305637	AA806124 AA806138		gb:oe29a12.s1 NCI_CGAP_Pr25 Homo sapiens gb:oe29c12.s1 NCI_CGAP_Pr25 Homo sapiens	0.89	0.70
60	305639 305650	AA807709		gb:nw31e04.s1 NCI_CGAP_GCB0 Homo sapiens4		8.71
-	305690	AA813477		gb:al67a05.s1 Soares_testis_NHT Homo sap	4.91	9.40
	305726	AA828156	Hs.73742	ribosomal protein, large, P0	0.19	0.81
	305728	AA828209		gb:of34a02.s1 NCI_CGAP_Kd6 Homo sapiens	5.12	9.29
65	305759	AA835353		gb:ak72b06.s1 Barstead spleen HPLRB2 Hom gb:ak84a08.s1 Barstead spleen HPLRB2 Hom	1.66 2.34	4.11 4.25
05	305792 305864	AA845256 AA864374	Hs.73742	ribosomal protein, large, PO	0.30	1.40
	305901	AA872968	110.10142	gb:oh63h08.s1 NCI_CGAP_Kid5 Homo sapiens	2.10	5.21
	305910	AA875981		gb:nx21h02.s1 NCI_CGAP_GC3 Homo saplens	0.32	1.01
70	306015	AA897116		gb:am08b07.s1 Soares_NFL_T_GBC_S1 Homo s1		1.12
70	306017	AA897221	Hs.109058	ribosomal protein S6 kinase, 90kD, polyp	5.21 1.96	7.90 6.59
	306020	AA897630	Hs.130027	EST gb:ok03g03.s1 Soares_NFL_T_GBC_S1 Homo s	7.38	20.69
	306063 306065	AA906316 AA906725		ab:ok78a02.s1 NCI_CGAP_GC4 Homo sapiens	7.19	13.48
	306104	AA910956		gb:ok85h11.s1 NCI_CGAP_Kid3 Homo sapiens	6.50	9.13
75	306109	AA911861		gb:og21a07.s1 NCI_CGAP_PNS1 Homo saplens	4.21	5.25
	306148	AA917409	Hs.288036	tRNA isopentenyipyrophosphate transferas	2.20	2.70 5.35
	306242	AA932805		gb:oo60g04.s1 NCI_CGAP_Lu5 Homo saplens gb:oi53h05.s1 NCI_CGAP_HN3 Homo saplens	2.84 1.60	5.35 1.12
	306288 306325	AA936900 AA953072	Hs.210546	interleukin 21 receptor	1.65	2.26
80	306353	AA961382	Hs.275865	ribosomal protein S18	3.78	6.32
	306375	AA968650	Hs.276018	EST, Moderately similar to JC4662 ribos	4.30	5.74
	306396	AA970223		gb:op09d05.s1 NCI_CGAP_Kid6 Homo saplens	0.95	2.45
	306428	AA975110	Hs.191228	hypothetical protein FLJ20284 gb:oq35e09.s1 NCI_CGAP_GC4 Homo sapiens	3.19 4.67	4.10 7.44
85	306442 306446	AA976899 AA977348		gb:oq35au9.51 NCI_CGAP_GCG Homo saplens	3.92	6.27
0,5	CONTROL	10.001.1040		Benedi retreet trailed a Trace trains relient		

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	306458	AA978186		gb:op33c06.s1 Soares_NFL_T_GBC_S1 Homo s	3.35	5.77
	306467	AA983508	Hs.163593	ribosomal protein L18a	3.72	5.37
	306510	AA988546		gb:or84d07.s1 NCI_CGAP_Lu5 Homo sapiens	1.00	1.00
5	306555	AA994304	Hs.276083	EST, Wealdy similar to RL23_HUMAN 60S R	6.61 16.20	10.91 31.83
)	306557 306572	AA994530 AA995686		gb:ou57e08.s1 NCI_CGAP_Br2 Homo sapiens gb:os25c12.s1 NCI_CGAP_Kid5 Homo sapiens	2.51	6.52
	306582	AA996248		gb:os18c10.s1 NCI_CGAP_Kid5 Homo sapiens	1.42	3.13
	306598	Al000320	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.91	8.68
• •	306605	Al000497	Hs.119500	ribosomal protein, large P2	1.96	8.60
10	306656	AI004024		gb:ou11b07.x1 Soares_NFL_T_GBC_S1 Homo s	0.11	0.45
	306676	Al005603	Hs.284136	PRO2047 protein	9.56 1.86	17.28 3.60
	306686 306702	AI015615 AI022565	Hs.307670	gb:ov29f10.x1 Soares_testis_NHT Homo sap EST	1.47	1.19
	306702	Al027359	Hs.272572	hemoglobin, alpha 2	1.28	2.83
15	306751	AI032589	10.2.2012	gb:ow70h12.s1 Soares_fetal_liver_spleen_	3.91	5.21
	306767	AI038963	Hs.249118	ESTs	3.33	6.06
	306892	A1092465		gb:qa75h12x1 Soares_fetal_heart_NbHH19W	3.77	7.46
	306897	A1093967		gb:qa33c06.s1 Soares_NhHMPu_S1 Homo sapi	2.12	2.85 10.52
20	306956	AJ125111		gb:am66f03.s1 Barstead spleen HPLRB2 Hom gb:am55e09.x1 Johnston frontal cortex Ho	6.10 1.72	1.56
20	306958 307035	AI125152 AI142774	Hs.119122	ribosomal protein L13a	2.00	4.70
•	307033	Al144243	113.113122	gb:gb85b12.x1 Soares_fetal_heart_NbHH19W	9.12	12.56
	307091	A1167439		gb:ox70h06.s1 Soares_NhHMPu_S1 Homo sapi	4.88	8.52
~~	307181	Al189251		gb:qc99g06.x1 Soares_pregnant_uterus_NbH	3.55	6.44
25	307297	AI205798	Hs.111334	ferritin, light polypeptide	2.46	4.65
	307317	A1208303	Hs.147333	EST CDCS anti-an	5.64 3.18	10.13 5.15
	307327 307382	Al214142 Al223158	Hs.246381 Hs.147885	CD68 antigen ESTs	2.02	3.73
	307410	AI241715	Hs.77039	ribosomal protein S3A	0.72	0.48
30	307415	Al242118	1101111000	gb:qh92b02.x1 Soares_NFL_T_GBC_S1 Homo s	2.38	3.51
	307423	Al243206	Hs.179573	collagen, type I, alpha 2	2.60	5.44
	307426	A1243364		gb:qh30g11.x1 Soares_NFL_T_GBC_S1 Homo s	3.18	7.67
	307517	A1275055		gb:qi72d03.x1 Soares_NhHMPu_S1 Homo sapi	1.00 3.40	1.00 11.20
35	307551 307561	Al281556 Al282207		gb:qu52f11.x1 NCI_CGAP_Lym6 Homo sapiens gb:qp65a12.x1 Soares_fetal_lung_NbHL19W	4.74	15.51
33	307608	Al290295		ob:om01f02x1 Soares_NhHMPu_S1 Homo sapi	3.50	7.19
	307657	AI306428	Hs.298262	ribosomal protein S19	1.76	2.44
	307691	Al318285		gb:tb17b01.x1 NCI_CGAP_Ov37 Homo sapiens	1.59	1.31
40	307701	Al318583	Hs.276672	EST, Weakly similar to RL6_HUMAN 60S RI	1.90	2.13
40	307718	Al333406	Hs.83753	small nuclear ribonucleoprotein polypept	0.45 1.51	0.99 0.99
	307730 307760	Al336092 Al342387		gb:qt43b07.x1 Soares_fetal_lung_NbHL19W gb:qt27f07.x1 Soares_pregnant_uterus_NbH	1.00	1.00
	307764	Al342731		gb:qo26a07.x1 NCI_CGAP_Lu5 Homo saplens	4.52	12.58
	307783	Al347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	1.42	1.00
45	307796	A1350556		gb:qt18f09.x1 NCI_CGAP_GC4 Homo saplens	6.57	9.61
	307807	Al351799		gb:qt09d02.x1 NCI_CGAP_GC4 Homo saplens	3.38	7.68
	307808	Al351826		gb:qt09g03.x1 NCI_CGAP_GC4 Homo sapiens gb:qt94a11.x1 NCI_CGAP_Co14 Homo sapiens	0.33 7.94	0.86 21.57
	307820 307830	Al355761 Al358722	Hs.276737	EST, Weakly similar to R5HU22 ribosomal	2.05	3.32
50	307852	Al365541	110.2.1 01 01	gb:qz08g05.x1 NCI_CGAP_CLL1 Homo sapiens	3.18	5.21
-	307902	Al380462		gb:tg02h05.x1 NCI_CGAP_CLL1 Homo sapiens	3.13	4.99
	307997	Al434512	Hs.181165	eukaryotic translation elongation factor	1.00	3.01
	308002	Al435240	Hs.283442	ESTS	5.86 3.79	12.64 5.83
55	308011	AI439473	Hs.251577	gb:ti60a08.x1 NCI_CGAP_Lym12 Homo sapien hemoglobin, alpha 1	0.38	0.88
55	308023 308041	A1452732 A1458824	Hs.169476	glyceraldehyde-3-phosphate dehydrogenase	4.36	6.06
	308059	Al468938	Hs.276877	EST, Wealty similar to RL10_HUMAN 60S R	1.80	1.98
	308085	AI474135	Hs.181165	eukaryotic translation elongation factor	3.38	4.14
60	308101	A1475950	Hs.181165	eukaryotic translation elongation factor	1.30	3.87 8.72
60	308106	A1476803	Un 200444	gb:tj77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S2	.30 2.70	3.86
	308122 308154	A1480123 A1500600	Hs.309411	EST gb:tn93d08.x1 NCI_CGAP_Ut2 Homo sæpiens	0.66	1.33
	308171	A1523632	Hs.298766	ESTs, Weakly similar to schlafen4 [M.mu	2.48	4.86
	308211	Al557029	Hs.278572	anaplastic lymphoma kinase (KI-1)	2.43	2.14
65	308213	Al557041		gb:PT2.1_12_E04.r tumor2 Homo saplens cD	3.34	3.79
	308216	AI557135		gb:PT2.1_13_H06.r tumor2 Homo sapiens cD	4.61	4.78
	308219	ALS57246	Un acaaca	gb:PT2.1_15_D07.r tumor2 Homo saplens cD	4.87 2.40	7.94 6.35
	308271 308319	AI567844 AI583983	Hs.252259 Hs.181165	ribosomal protein S3 eukaryotic translation elongation factor	2.45	3.33
70	308362	A1613519	Hs.105749	KIAA0553 protein	1.24	1.41
. •	308413	A1636253	Hs.196511	ESTs	3.16	4.82
	308450	A1660860	Hs.96840	KIAA1527 protein	1.79	2.68
	308464	AI672425	Hs.277117	EST, Moderately similar to 138055 myosi	4.87	8.27 5.64
75	308588	Al718299		gb:as51g12.x1 Barstead aorta HPLRB6 Homo gb:as47d07.x1 Barstead aorta HPLRB6 Homo	3.90 3.32	5.64 5.12
13	308599 308615	AI719893 AI738593	Hs.101774	go:as4/du/xt Bastead aona HPLKbo Hollo hypothetical protein FLJ23045	3.32 3.11	2.36
	308643	A1745040	110.101114	gb:tr19a12x1 NCL_CGAP_Ov23 Homo sapiens	3.98	3.69
	308673	AI760864		gb:wi09c10.x1 NCI_CGAP_CLL1 Homo sapiens	0.82	0.99
	308697	AI767143		gb:wi97a07.x1 NCI_CGAP_Kid12 Homo sapien	2.76	5.59
80	308762	Al807405	Hs.259408	ESTs	3.17	6.30
	308778	AI811109	11.0455	gb:tr04c11.x1 NCI_CGAP_Ov23 Homo saplens	1.00 2.94	1.00 5.15
	308782 308808	AI811767 AI818289	Hs.2186	eukaryotic translation elongation factor gb:wk52c01.x1 NCI_CGAP_Pr22 Homo saplens	4.41	8.34
	308823	Al824118	Hs.217493	annexin A2	1.85	1.92
85	308875	AI832332		gb:at48g03.x1 Barstead colon HPLRB7 Homo	2.52	3.80

	W	O 02/086	443			
	308879	AI832763	Hs.75968	thymosin, beta 4, X chromosome	3.38	7.96 2.55
	308886	AI833240		gb:at76d10.x1 Barstead colon HPLRB7 Homo gb:wl32d10.x1 NCI_CGAP_Ut1 Homo sapiens	3.06 2.45	2.65 3.44
	308898 308934	A1858845 A1865023	Hs.177	phosphatidylinositol glycan, class H	4.14	6.76
5	308966	AI870704		gb:w/47h01_x1 NCI_CGAP_Ut1 Homo sapiens	1.00	1.00
	308979	AI873111		gb:wl52h05.x1 NCI_CGAP_Bm25 Homo sapien	7.15	11.10
	309045	AI910902		gb:tq39f01.x1 NCI_CGAP_Ut1 Homo sapiens gb:wd78d01.x1 NCI_CGAP_Lu24 Homo sapiens	0.61 1.78	0.59 4.42
	309051 309069	A1911975 A1917366	Hs.78202	SWI/SNF related, matrix associated, act	3.27	5.88
10	309083	Al922426	Hs.119598	ribosomal protein L3	2.39	3.34
	309105	Al925503	Hs.265884	ESTs	5.54	17.78
	309122	Al928178	11- 400040	gb:wo95a11.x1 NCI_CGAP_Kid11 Homo sapien	1.00 1.38	2.92 5.55
	309128 309164	Al928816 Al937761	Hs.180842	ribosomal protein L13 gb:wp84b09.x1 NCI_CGAP_Bm25 Homo sapien	2.43	3.11
15	309177	AI951118		gb:wx63g05.x1 NCI_CGAP_Br18 Homo sapiens	0.81	0.97
	309288	Al991525	Hs.299426	ESTs	4.86	7.46
	309299	AW003478		gb:wq66c06.x1 NCI_CGAP_GC6 Homo sapiens	4.36 2.88	9.43 7.54
	309303 309411	AW004823 AW085201	Hs.244144	gb:ws93a08.x1 NCI_CGAP_Co3 Homo sapiens EST	4.30	7.14
20	309437	AW090702	Hs.278242	tubulin, alpha, ubiquitous	2.49	3.11
	309459	AW117645	Hs.65114	keratin 18	2.88	4.55
	309476	AW129368		gb:xe14b05.x1 NCI_CGAP_Ut4 Homo sapiens	2.08	6.60 3.55
	309499 309529	AW136325 AW150807	Hs.279771 Hs.181357	Homo sapiens clone PP1596 unknown mRNA taminin receptor 1 (67kD, ribosomal pro	2.82 4.78	3.95
25	309532	AW151119	115.101557	gb:xg33e10.x1 NCI_CGAP_Ut1 Homo sapiens	1.18	4.40
	309626	AW192004	Hs.297681	serine (or cysteine) proteinase inhibit	4.46	12.06
	309641	AW194230	Hs.253100	EST, Moderately similar to GHHU Ig gamm	1.47	1.39 15.20
	309675	AW205681 AW237221	Hs.253506	EST, Moderately similar to ATPN_HUMAN A laminin receptor 1 (67kD, ribosomal prot	5.68 1.00	1.00
30	309693 309695	AW237221	Hs.181357 Hs.295605	mannosidase, alpha, class 2A, member 2	5.45	9.61
-	309700	AW241170	Hs.179661	tubulin, beta polypeptide	1.41	1.25
	309747	AW264889		gb:xq36h02.x1 NCI_CGAP_Lu28 Homo saplens	5.00	8.35
	309769	AW272346	U- 456140	gbxs13c10x1 NCI_CGAP_Kid11 Homo sapien immunoglobulin kappa constant	5.76 0.42	11.90 0.69
35	309782 309783	AW275156 AW275401	Hs.156110 Hs.254798	EST	1.00	4.11
55	309799	AW276964	110.201700	gb:xp58h01.x1 NCI_CGAP_Ov39 Homo saplens	1.68	1.44
	309866	AW299916		gb:xs44c01.x1 NCI_CGAP_Kid11 Homo sapien	3.02	5.04
	309903	AW339071	Hs.300697	immunoglobulin heavy constant gamma 3 (G qb:hd05q08.x1 Soares_NFL_T_GBC_S1 Homo s	1.05 2.30	1.18 3.67
40	309923 309928	AW340684 AW341418		gb:hd08c03.x1 Soares_NFL_T_GBC_S1 Homo s	7.41	13.71
••	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	1.20	12.70
	309933	AW341936		gb:hb73f10.x1 NCI_CGAP_Ut2 Homo sapiens	4.90	18.29
	309964	AW449111	Hs.257111 Hs.323079	hypothetical protein MGC3265 Homo sapiens mRNA; cDNA DKFZp564P116 (fr	1.99 0.20	3.07 0.47
45	310002 310096	AI439096 AW136822	Hs.172824	ESTs, Weakly similar to B48013 proline-r	1.51	1.22
	310098	AI685841	Hs.161354	ESTs	0.31	0.76
	310109	Al203094	Hs.148633	ESTs	2.06 2.92	5.83 3.55
	310112 310115	AW197233 AI611317	Hs.147253 Hs.223796	ESTs ESTs	1.25	0.84
50	310121	AW195642	Hs.148901	ESTs	1.00	2.71
•	310146	AJ206614	Hs.197422	ESTs	9.50	15.31
	310193	Al627653	Hs.147562	ESTs	2.85 4.26	4.18 10.63
	310255 310261	AW450439 AI240483	Hs.153378 Hs.201217	ESTs ESTs	3.28	4.40
55	310264	AI915771	Hs.74170	metallothionein 1E (functional)	0.26	0.86
	310275	AJ242102	Hs.213636	ESTs	5.43	8.19
	310282	AI243332	Hs.156055	ESTs	3.15 2.19	8.06 3.12
	310290 310333	AW013815 Al253200	Hs.149103 Hs.145402	ESTs ESTs	1.17	1.91
60	310346	AJ261340	Hs.145517	ESTs	4.81	9.95
	310385	AI263392	Hs.156151	ESTs	5.96	7.79
	310443	AW119018	Hs.164231	ESTS	2,90 0,85	4.63 1.01
	310444 310446	AW196632 AI275715	Hs.252956 Hs.145926	ESTs ESTs	2.18	3.85
65	310468	AI984074	Hs.196398	ESTs	3.39	5.19
	310477	AI948801	Hs.171073	ESTs	1.00	1.00
	310512	AW275603	Hs.200712	ESTs	3,87 3,30	8.12 7.33
	310514 310524	AJ681145 AW082270	Hs.160724 Hs.12496	ESTs ESTs, Highly similar to AC004836 1 simil	0.72	1.44
70	310547	Al302654	Hs.208024	ESTs	3.26	3.46
	310584	AI653007	Hs.156304	ESTs	2.39	4.08
	310608	Al962234	Hs.196102	ESTs gb:Human endogenous retrovirus. H proteas	5.60 4.91	6.49 9.09
	310624 310636	AI341594 AI814373	Hs.164175	ESTs	1.85	1.71
75	310648	AI347863	Hs.156672	ESTs	0.17	0.69
•	310694	A1654370	Hs.157752	Homo sapiens mRNA full length insert cDN	5.40	13.22
	310695	A1472124 A1418446	Hs.157757 Hs.157882	ESTs ESTs	4.82 1.76	6.27 3.51
	310714 310722	A)989803	Hs.157002 Hs.157289	ESTS	1.14	6.85
80	310756	AI916560	Hs.158707	ESTs	8.46	13.01
	310764	AJ376769	Hs.167172	ESTs	4.76	7.37
	310848	AI459554 AW201714	Hs.161286	ESTs ESTs	2.84 1.00	1.96 2.32
	310851 310854	AW291714 AJ421677	Hs.221703 Hs.161332	ESTS	6.37	7.94
85	310858	AI871000	Hs.161330	ESTs	6.07	9.84

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	310864	Al924558	Hs.161399	ESTs	0.87	0.78
	310875	T47764	Hs.132917	ESTS	1.00 7.07	3.63 16.68
	310896 310922	AW157731 AW195634	Hs.270982 Hs.170401	ESTs, Moderately similar to ALU7_HUMAN A ESTs	1.00	1.00
5	310955	AI560210	Hs.263912	ESTs	10.08	17.66
	310957	AW190974	Hs.196918	ESTs	2.18 3.06	3.18 6.64
	311000 311012	AI521830 AW298070	Hs.171050 Hs.241097	ESTs ESTs	1.23	3.77
	311034	AI564023	Hs.311389	ESTs, Moderately similar to PT0375 natur	2.44	2.09
10	311074	AW290922	Hs.199848	ESTs	6.04	14.19
	311134	A1990849	Hs.196971	ESTs	3.54 0.65	6.96 0.95
	311174 311187	AW450552 AI638374	Hs.205457 Hs.224189	periaxin ESTs	2.46	2.78
	311220	A1656040	Hs.196532	ESTs	1.10	2.52
15	311230	AI989808	Hs.197663	ESTs	1.41 2.18	1.75 2.11
	311236	AI653378 AW016812	Hs.197674 Hs.200266	ESTs ESTs	0.63	5.11
	311242 311258	AVIO10012 AJ671221	Hs.199887	ESTs	1.00	1.41
	311277	AW072813	Hs.270868	ESTs, Moderately similar to ALU4_HUMAN A	2.56	1.94
20	311294	AA826425	Hs.291829	ESTs	1.04 1.96	2.69 6.70
	311308 311351	F12664 Al682303	Hs.49000 Hs.201274	ESTs ESTs	4.77	9.38
	311390	AW392997	Hs.202280	ESTs	2.80	6.06
0.5	311405	AW290961	Hs.201815	ESTs	3.80	11.66
25	311409	AI698839	Un 200927	gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.84 5.30	6.94 12.56
	311420 311443	Al936291 Al791521	Hs.209867 Hs.192206	ESTs ESTs	4.39	6.09
	311467	A1934909	Hs.175377	ESTs	1.00	1.04
••	311479	AI933672	Hs.211399	ESTs	2.76	5.61
30	311488	R57390	Hs.301064	arfaptin 1	2.50 3.63	5.73 6.09
	311495 311511	AW300077 AW444568	Hs.221358 Hs.210303	ESTs . ESTs	2.00	2.87
	311534	AW130351	Hs.243549	ESTs	0.31	1.33
~~	311537	A)805121	Hs.211828	ESTs	3.69	5.85
35	311543	AI681360	Hs.201259	ESTs POM (POM121 rat homolog) and ZP3 fusion	1.73 3.31	- 1.34 6.12
	311551 311557	AW449774 Al819230	Hs.296380 Hs.211238	Interleukin-1 homolog 1	1.00	1.00
	311558	Z44432	Hs.63128	KIAA1292 protein	2.25	3.41
40	311559	AW008271	Hs.265848	similar to rat myomegalin	2.68	5.90 3.32
40	311563	AI922143	Hs.211334	ESTs ESTs	2.39 2.47	3.85
	311586 311616	AI827834 AW450675	Hs.211227 Hs.212709	ESTs	1.00	1.00
	311621	Al924307	Hs.213464	ESTs	4.16	6.74
4 =	311635	A1928456	Hs.213081	ESTs	2.17 2.60	3.76 3.12
45	311668	AW193674 R11807	Hs.240044 Hs.20914	ESTs hypothetical protein FLJ23056	2.79	5.18
	311672 311683	AW183738	Hs.232644	ESTs	0.19	0.96
	311700	R49601	Hs.171495	retinoic acid receptor, beta	6.28	8.83
50	311714	AW131785	Hs.246831	ESTs, Weakly similar to CIKG_HUMAN VOLTA Homo saplens cDNA FLJ12981 fis, clone NT	5.00 0.96	8.17 0.72
50	311735 311743	AW294416 T99079	Hs.144687 Hs.191194	ESTs	1.00	1.95
	311783	AJ682478	Hs.13528	hypothetical protein FLJ14054	0.16	0.77
	311785	AI056769	Hs.133512	ESTs	1.34	3.97
55	311799	AA780791	Hs.14014	ESTs, Weakly similar to KIAA0973 protein	8.52 3.58	13.32 3.91
33	311819 311823	AW265275 AI089422	Hs.254325 Hs.131297	ESTs ESTs	1.40	1.72
	311877	AA349893	Hs.85339	G protein-coupled receptor 39	0.95	0.91
	311886	AA522738	Hs.132554	ESTS	0.88	0.87 1.13
60	311896	AW206447	Hs.22579	gb:UI-H-BI1-afg-g-02-0-UI.s1 NCI_CGAP_Su Homo sapiens clone CDABP0036 mRNA sequen	1.66 1.66	2.30
UU	311910 311923	N28365 T60843	Hs.189679	ESTs	0.42	2.63
	311933	Al597963	Hs.118726	ESTs	1.88	3.02
	311959	T67262	Hs.124733	ESTs	2.02 3.87	2.33 6.62
65	311960 311967	AW440133 Al382726	Hs.189690 Hs.182434	ESTs ESTs	5.80	8.14
05	311975	AAB04374	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	0.98	3.26
	312005	T78450	Hs.13941	ESTs	0.12	1.39
	312028	T78886	Hs.284450	ESTs	3.78 4.11	4.92 7.32
70	312046	AI580018	Hs.268591	ESTs ESTs	2.36	3.08
70	312058 312064	T83748 AA676713	Hs.268594 Hs.191155	ESTs	3.34	5.28
	312088	AW303760	Hs.13685	ESTs	1.60	1.15
	312093		Hs.121296	ESTS	0.68 3.05	0.85 4.48
75	312094		He 112180	gb:HSZ78390 Human fetal brain S. Meier-E zinc finger protein 148 (pHZ-52)	4.52	9.70
, 5	312097 312118		Hs.112180 Hs.178294	ESTs	2.40	2.60
	312128		Hs.17631	Homo saplens cDNA FLJ20118 fis, clone CO	2.39	3.53
	312147	T89855	Hs.195648	ESTs	0.67 5.85	1.03 10.60
80	312175		Hs.127554 Hs.269864	ESTs ESTs	5.85 2.41	3.32
30	312179 312201		Hs.209804 Hs.91139	solute carrier family 1 (neuronal/epithe	0.24	0.89
	312207		Hs.191330	ESTs	2.20	4.55
	312220	N74613	11. 4 4600-	gb:za55a07.s1 Soares fetal liver spleen	4.28 1.64	11.13 1.57
85	312252 312304		Hs.143655 Hs.269392	ESTs ESTs	0.12	2.47
0,	312309	MM431343	110.203332	2013		

	W	O 02/086	5443			
	312318	AW235092	Hs.143981	EST ₈	3.46	5.69
	312319	AA216698	Hs.180780	TERA protein	5.78	4.46
	312321	R66210	Hs.186937	ESTs 5015	0.44	1.74
_	312331	AA825512	Hs.289101	glucose regulated protein, 58kD	3.73	5.96 0.95
5	312339	AA524394	Hs.165544	ESTs	3.07 10.08	16.73
	312363 312375	A1675558 A1375096	Hs.181867 Hs.172405	ESTs cell division cycle 27	2.78	3.71
	312376	R52089	Hs.172717	ESTs	1.00	1.00
	312389	Al863140		gb:tz43h12.x1 NCI_CGAP_Bm52 Homo sapien	2.37	3.98
10	312437	AA995028		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	4.06	5.41
	312440	AI051133	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00	1.00
	312451	R59989	Hs.176539	ESTs	4.96	10.04
	312458	Al167637	Hs.146924	ESTs	1.11	1.00
1.5	312507	Al168177	Hs.143653	ESTs	5.89	8.24
15	312520	AI742591	Hs.205392	ESTs	3.30 1.38	8.92 1.65
	312548	AI566228	Hs.159426	hypothetical protein PRO2121	0.40	0.77
	312564 312583	H21520 Al193122	Hs.35088 Hs.124141	ESTs ESTs	0.13	0.94
	312599	A1155122 A1865073	Hs.125720	ESTs	3.75	5.29
20	312602	AA046451	Hs.165200	ESTs	6.78	12.93
20	312645	H52121	Hs.193007	ESTs	0.38	1.13
	312666	Al240582	Hs.214678	ESTs	0.98	2.03
	312689	AW450461	Hs.203965	ESTs	0.21	0.61
0.5	312817	H75459	Hs.233425	ESTs	1.51	0.85
25	312846	AW152104	Hs.200879	ESTs	8.93 4.20	13.78 6.23
	312873	AI690071	Hs.283552	ESTs, Weakly similar to unnamed protein	4.20 2.67	3.15
	312893	AI016204	Hs.172922	ESTs ESTs, Wealty similar to T2D3_HUMAN TRANS	1.19	0.71
	312902	AW292797 N90868	Hs.130316 Hs.271695	ESTs	2.50	4.25
30	312925 312936	Al681581	Hs.121525	ESTs	1.00	1.17
30	312975	AI640506	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.30	4.80
	312978	N24887	Hs.292500	ESTs	0.80	1.05
	312980	AA497043	Hs.115685	ESTs	3.12	3.60
~ ~	312984	N25871	Hs.177337	ESTs	2.03	2.13
35	313000	AI147412	Hs.146657	ESTs	5.52	8.42
	313029	AA731520	Hs.170504	ESTs	0.96 6.48	1.39 13.20
	313039	A1419290	Hs.149990	ESTs, Weakly similar to unnamed protein	6.44	10.73
	313049	AW293055 Al651930	Hs.119357 Hs.135684	ESTs ESTs	1.51	2.04
40	313056 313058	D81015	Hs.125382	ESTs	0.25	1.50
70	313070	A1422023	Hs.161338	ESTs	8.56	11.60
	313097	Al676164	Hs.204339	ESTs	3.72	4.56
	313130	AW449171	Hs.168677	ESTs	3.28	5.06
	313136	N59284	Hs.288010	ESTs	0.49	1.36
45	313153	AI240838	Hs.132750	ESTs	5.36	5.52
	313210	N74077	Hs.197043	ESTS	0.30 5.16	0.66 8.76
	313236	AW238169	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	3.87
	313239	W19632 N93466	Hs.124170 Hs.121764	ESTs ESTs, Weakly similar to testicular tekti	0.74	2.06
50	313265 313267	A1770008	Hs.129583	ESTs	0.23	1.30
50	313275	AI027604	Hs.159650	ESTs	6.68	9.57
	313290	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.34	1.07
	313292	Al362991	Hs.202121	ESTs, Weakly similar to env protein [H.s	2.00	4.32
	313325	AJ420611	Hs.127832	ESTs	1.20	2.27
55	313357	AW074848	Hs.201501	ESTs	4.02	5.33 2.84
	313393	Al674685	Hs.200141	ESTs	1.36 2.58	5.26
	313399	AW376889	Hs.194097	ESTs ESTs	6.57	15.07
	313414 313417	Al241540 AA741151	Hs.132933 Hs.137323	ESTs	0.63	3.01
60	313457	AA576052	Hs.193223	Homo sapiens cDNA FLJ11646 fis, clone HE	2.78	4.70
00	313499	Al261390	Hs.146085	KIAA1345 protein	0.91	2.37
	313516	AA029058	Hs.135145	ESTs	3.41	7.08
	313556	AA628517	Hs.118502	ESTs	0.23	0.70
	313569	Al273419	Hs.135146	hypothetical protein FLJ 13984	1.88	1.00
65	313570	AA041455	Hs.209312	ESTs	0.73	2.27
	313638	Al753075	Hs.104627	Homo sapiens cDNA FLJ10158 fls, clone HE	1.00 0.20	1.72 1.42
	313662	AA740151	Hs.130425		1.00	1.00
	313671	W49823	Hs.104613	RP42 homolog	3.46	5.80
70	313672 313690	AW468891 AI493591	Hs.122948 Hs.78146	ESTs platelet/endoihelial cell adhesion molec	0.51	0.97
70	313711	AA398070	Hs.133471	ESTs	0.18	1.01
	313723	AA070412		gb:zm68c10.s1 Stratagene neuroepithelium	1.08	1.03
	313726	AI744687	Hs.257806	ESTs	2.13	2.99
	313774	AW136836		ESTs	1.38	1.19
75	313784	AA910514	Hs.134905	ESTs	3.88	5.78
	313790	AW078569	Hs.177043	ESTs	0.22	2.06
	313832	AW271022		ESTs	1.15	0.91
	313834	AW418779		ESTs	0.68 5.74	3.14 8.88
QΛ	313835		Hs.159087	ESTs	5.74 0.16	1.14
80	313852		Hs.123641	protein tyrosine phosphatase, receptor t	2.09	4.06
	313854 313865		Hs.275002 Hs.163839	ESTs ESTs	3.41	4.09
	313865 313871	AW471088		ESTs	5.28	6.83
	313883			abmu76d01.st NCI_CGAP_Alv1 Homo sapiens	2.90	10.91
85	313915		Hs.163443	Homo saplens cDNA FLJ11576 fis, clone HE	1.00	1.00

	w	O 02/08	6443			
	313926	AW473830	Hs.171442	ESTs	3.40	4.11
	313948	AW452823	Hs.135268	ESTs	5.77	9.15
	313978	AI870175	Hs.13957	ESTs	0.46 4.10	0.75 6.40
5	313983 314035	Al829133 AA164199	Hs.226780 Hs.270152	ESTs ESTs	5.88	7.90
,	314037	AW300048	Hs.275272	ESTS	1.00	3.79
	314040	AA166970	Hs.118748	ESTs	7.60	11.33
	314067	AW293538	Hs.51743	KIAA1340 protein	1.86	1.21
10	314103	A1028477	Hs.132775	ESTs	2.90	5.29
10	314107	AA806113	Hs.189025	ESTs	2.00	1.66
	314113	AA218986	Hs.118854	ESTS	0.91 2.53	4.17 3.32
	314124 314126	AW118745 AA226431	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr gb:nc18b12.s1 NCI_CGAP_Pr1 Homo sapiens	3.13	5.08
	314128	AA935633	Hs.194628	ESTs	2.90	6.35
15	314151	AA236163	Hs.202430	ESTs	4.15	6.45
	314184	AW081795	Hs.233465	ESTs	3.44	4.65
	314192	AW290975	Hs.118923	ESTs	1.00	1.23
	314244	AL036450	Hs.103238	ESTs	2.88	3.67
20	314253	AA278679	Hs.189510	ESTs	4.98	7.16 1.94
20	314262	AW086215	Hs.246096 Hs.275809	ESTs ESTs	0.38 3.34	5.66
	314320 314332	AA811598 AL037551	Hs.95612	ESTs	2.85	2.09
	314335	AA287443	Hs.142570	Homo saplens clone 24629 mRNA sequence	4.35	4.78
	314340	AW304350	Hs.130879	ESTs, Moderately similar to putative p15	0.77	0.86
25	314351	AA292275	Hs.193746	ESTs	3.07	3.77
	314376	AI628633	Hs.324679	ESTs	4.10	6.11
	314443	AA827125	Hs.192043	ESTs .	6.20 0.58	13.67 2.49
	314458 314466	Al217440 AA767818	Hs.143873 Hs.122707	ESTs ESTs	2.53	2.62
30	314478	AJ521173	Hs.125507	DEAD-box protein	3.94	5.65
50	314482	AL043807	Hs.134182	ESTs	1.30	1.44
	314506	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	3.28	3.47
	314519	R42554	Hs.210862	T-box, brain, 1	3.12	6.16
25	314529	AL046412	Hs.202151	ESTs	3.43	6.87
35	314546	AW007211	Hs.16131	hypothetical protein FLJ12876	1.38 2.29	1.00 5.27
	314562 314579	Al564127 AW197442	Hs.143493 Hs.116998	ESTs ESTs	3.87	5.75
	314580	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	0.10	0.71
	314585	AA918474	Hs.216363	ESTs	1.08	1.40
40	314589	AW384790	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	1.00	1.00
	314592	AA435761	Hs.192148	ESTs	0.90	2.60
	314603	AA418024	Hs.270670	ESTs	4.56 3.42	6.29 3.92
	314604	AA946582	Hs.8700	deleted in liver cancer 1 ESTs	3.42 2.97	3.52 4.55
45	314606 314648	AA418241 AA878419	Hs.188767	gb:EST391378 MAGE resequences, MAGP Homos		1.36
	314699	Al038719	Hs.132801	ESTs	3.66	4.97
	314701	Al754634	Hs.131987	ESTs	0.03	0.90
	314710	AI669131	Hs.290989	EST	3.40	7.52
50	314750	Al095005	Hs.135174	ESTs	2.80	6.54 4.26
50	314767	AW135412	Hs.164002 Hs.109045	ESTs hypothetical protein FLJ10498	3.20 1.00	1.00
	314801 314817	AA481027 Al694139	Hs.192855	ESTs	0.91	0.99
	314835	Al281370	Hs.76064	ribosomal protein L27a	5.75	7.44
	314852	Al903735		gb:MR-BT035-200199-031 BT035 Homo saplen	1.68	4.34
55	314853	AA729232	Hs.153279	ESTs	0.60	1.85
	314940	AW452768	Hs.162045	ESTs	10.10	16.20
	314941	AA515902	Hs.130650	ESTs	0.31 2.18	1.02 0.37
	314943 314955	AI476797 AA521382	Hs.184572 Hs.192534	cell division cycle 2, G1 to S and G2 to ESTs	2.59	3.90
60	314973	AW273128	Hs.300268	ESTs	1.05	1.25
	315004	AA527941	Hs.325351	EST	5.64	13.63
	315006	Al538613	Hs.298241	Transmembrane protease, serine 3	0.52	1.78
	315033	A1493046	Hs.146133	ESTs	2.46	1.00
65	315035	AI569476	Hs.177135	ESTs	0.34	1.33 2.64
UJ	315056	AI202703	Hs.152414 Hs.105866	ESTs ESTs	2.10 1.00	1.30
	315069 315071	Al821517 AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	1.78	1.00
	315073	AW452948	Hs.257631	ESTs	1.17	1.52
	315078	AA568548	Hs.190616	ESTs	3.00	3.79
70	315080	AA744550	Hs.136345	ESTs	1.00	1.00
	315120	AA564991	Hs.269477	ESTs	0.64	1.44
	315175	Al025842	Hs.152530	ESTs	0.61	1.91
	315193	AI241331	Hs.131765	ESTs Homo sapiens clone TCCCTA00151 mRNA sequ	1.06 0.48	0.97 1.96
75	315196 315200	AA972756 AI808235	Hs.44898 Hs.307686	EST	3.76	9.40
, ,	315254	A1474433	Hs.179556	ESTs	5.37	9.36
	315353	AW452608	Hs.279610	hypothelical protein FLJ10493	1.00	1.30
	315397	AA218940	Hs.137516	fidgetin-like 1	3.38	2.24
00	315403	AW362980	Hs.163924	ESTs	2.04	5.23
80	315431	AA622104	Hs.184838	ESTS	2.36	8.04
	315454	Al239473	11- 450040	gb:qh36f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.46 2.79	7.64 5.76
	315455	AW393391	Hs.156919 He 313671	ESTs ESTs, Moderately similar to OVCA1	3.78 0.89	2.15
	315473 315483	Al681671 AW512763	Hs.312671 Hs.222024	transcription factor BMAL2	2.32	1.96
85	315526	Al193048	Hs.128685	ESTs	1.67	1.78
-						

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	315530	AI200852	Hs.127780	ESTs	1.05	1.01
	315541	Al168233	Hs.123159	sperm associated antigen 4	0.85	0.56
	315552 315562	AW445034 AA737415	Hs.256578 Hs.152826	ESTs ESTs	1.00 2.66	2.22 2.48
5	315577	AW513545	Hs.17283	hypothetical protein FLJ10890	2.20	2.25
_	315587	Al268399	Hs.140489	ESTs	1.00	1.04
	315589	AW072387	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	0.14	1.05 12.56
	315623 315634	AA364078 AA837085	Hs.258189 Hs.220585	ESTs ESTs	7.44 0.50	1.40
10	315668	AA912347	Hs.136585	ESTs	0.43	1.22
	315677	Al932662	Hs.164073	ESTs	0.60	1.39
	315706	AW440742	Hs.155556	hypothetical protein FLJ20202	2.18	3.77
	315707	Al418055	Hs.161160 Hs.201591	ESTs ESTs	2.88 0.11	2.63 0.60
15	315730 315745	H25899 Al821759	Hs.191856	ESTs	3.50	7.25
	315791	AA678177	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gb:zi15a05.s1 Soares_fetal_liver_spleen_	1.78	2.63
	315801	AA827752	Hs.266134	ESTs	4.31	6.23
	315820 315878	Al652022 AA683336	Hs.258785 Hs.189046	ESTs ESTs	2.35 2.12	3.01 2.64
20	315905	AJ821911	Hs.209452	ESTs	1.03	1.97
	315923	Al052789	Hs.133263	ESTs	2.63	5.06
	315954	AW276810	Hs.254859	ESTs, Moderately similar to ALU5_HUMAN A	1.21 3.09	0.85 3.41
	315978 316001	AA830893 Al248584	Hs.119769 Hs.190745	ESTs Homo sapiens cDNA: FLJ21326 fis, clone C	2.20	6.82
25	316011	AW516953	Hs.201372	ESTs	0.35	1.63
	316012	AA764950	Hs.119898	ESTs	6.56	8.13
	316040	Al983409	Hs.189226	ESTs	5.69 2.84	10.69 10.45
	316048 316076	A1720759 AW297895	Hs.224971 Hs.116424	ESTs ESTs	0.30	1.05
30	316124	Al308862	Hs.167028	ESTs	1.00	1.43
	316151	Al806016	Hs.156520	ESTs	5.80	9.03
	316187	AW518299	Hs.192253	ESTs	1.20 4.92	3.96 6.94
	316204 316232	AA731509 AW297853	Hs.120257 Hs.251203	ESTs ESTs	1.48	1.60
35	316275	Al671041	Hs.292611	ESTs, Moderately similar to ALU1_HUMAN A	5.86	12.14
	316291	AW375974	Hs.156704	ESTs	2.73	2.69
	316303	AA740994	Hs.209609 Hs.120610	ESTs ESTs	1.53 3.66	1.26 8.34
	316344 316346	AA744518 Al028478	Hs.157447	ESTs	3.51	6.69
40	316365	AI627845	Hs.210776	ESTs	2.50	4.33
	316380	A1393378	Hs.164496	ESTs	1.16	2.16 10.34
	316470 316509	AA809902 AA767310	Hs.243813 Hs.291766	ESTs ESTs	5.40 2.46	2.89
	316514	AA768037	Hs.291671	ESTs ·	4.70	6.04
45	316519	A1929097		gb:od10c11.s1 NCI_CGAP_GCB1 Homo sapiens	4,41	9.70
	316609 316633	AW292520 Al125586	Hs.122082 Hs.127955	ESTs ESTs	1.00 2.61	2.89 3.72
	316700	AW172316	Hs.252961	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.46	4.64
~~	316711	Al743721	Hs.285316	ESTs, Moderately similar to ALU7_HUMAN A	4.45	6.95
50	316713	AI090671	Hs.134807	hypothetical protein FLJ12057	0.30 0.20	2.40 1.45
	316715 316787	Al440266 AW369770	Hs.170673 Hs.130351	ESTs, Weakly similar to AF126780 1 retin	4.05	5.53
	316809	AA825839	Hs.202238	ESTs	2.25	3.82
<i></i>	316811	AA922060	Hs.132471	ESTs	1.00	1.32
55	316812	AW135045	Hs.232001	ESTs ESTs	3,28 0.67	4.70 1.81
	316818 316824	AA827176 AA837416	Hs.124316 Hs.124299	ESTs	3.53	6.00
	316827	Al380429	Hs.172445	ESTs	0.72	1.56
C O	316891	AW298119	Hs.202536	ESTs	1.64	2.97
60	316951	AA134365	Hs.57548	ESTs ·	1.45 1.00	1.08 1.53
	316970 316971	AA860172 AA860212	Hs.132406 Hs.170991	ESTS ESTS	1.08	1.96
	316990	AA861611	Hs.130643	ESTs	5.44	10.04
65	317001	AI627917	Hs.233694	hypothetical protein FLJ11350	3.56	4.37
65	317008 317051	AW051597 AA873253	Hs.143707 Hs.126233	ESTs ESTs	0.69 6.18	1.37 12.72
	317128	AA971374	Hs.125674	ESTs	1.87	2.66
	317129	H12523	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone C	4.12	6.64
70	317137	AW341567	Hs.125710	ESTS	2.82 1.98	5.12 2.51
70	317196 317212	A1348258 A1866468	Hs.153412 Hs.148294	ESTs ESTs	1.86	2.83
	317223	AW297920	Hs.130054	ESTs	0.83	1.57
	317224	D56760	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	2.74	0.86
75	317266	AA906289	Hs.203614	ESTs	1.00 2.60	1.00 4.21
75	317282 317285	AI807444 AW370882	Hs.176101 Hs.222080	ESTs ESTs	1.96	3.49
	317302	AA908709	Hs.135564	ESTs	7.16	8.32
	317304	AW449899	Hs.130184	ESTs	1.38	2.28
80	317320	AA927151	Hs.130452	ESTs ESTs	3.58 2.08	8.13 4.92
SV	317413 317417	AW341701 AA918420	Hs.126622 Hs.145378	ESTs ESTs	3.06	4.79
	317452	AA972965	Hs.135568	ESTs	4.22	9.21
	317519	A1859695	Hs.126860	ESTs	1.88	4.15 4.55
85	317521 317529	A1824338 A1916517	Hs.126891 Hs.126865	ESTs ESTs	3.12 2.73	4.55 3.34
00	011025	A10011	113.120000			

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	317570	Al733361	Hs.127122	ESTs	1.00	2.43
	317571	AA938663	Hs.199828	ESTs	5.20 0.33	11.95 1.56
	317598 317627	AW206035 Al346110	Hs.192123 Hs.132553	ESTs ESTs	1.50	1.39
5	317650	Al733310	Hs.127346	ESTs	0.48	1.46
•	317659	AA961216	Hs.127785	ESTs	4.18	7.14
	317674	AW294909	Hs.132208	ESTs	2.92	3.20
	317686		Hs.187319 Hs.174794	ESTs ESTs	1.00 5.33	1.01 9.59
10	317692 317701	Al307659 Al674774	Hs.128014	ESTs	1.00	1.00
10	317711	AI733015	Hs.272189	ESTs	5.13	7.81
	317722	A1733373	Hs.128119	ESTs	2.50	6.03
	317756	AA973667	Hs.128320	ESTs	1.59 1.00	1.30 2.48
15	317777 317799	Al143525 Al498273	Hs.47313 Hs.128808	KIAA0258 gene product ESTs	1.78	2.11
13	317803	AA983251	Hs.128899	ESTs	0.80	1.06
	317821	Al368158	Hs.70983	PTPL1-associated RhoGAP 1	0.17	0.68
	317848	AI820575	Hs.129086	Homo sapiens cDNA FLJ12007 fis, clone HE	5.30	8.16 2.28
20	317850	N29974	Hs.152982 Hs.129119	hypothetical protein FLJ13117 ESTs	1.30 2.18	5.93
20	317861 317865	AW341064 Al298794	Hs.129130	ESTs	4.48	8.20
	317869	AW295184	Hs.129142	deoxyribonuclease II beta	0.44	0.99
	317881	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.06	2.23
25	317890	Al915599	Hs.129225	ESTs ESTs, Weakly similar to ALU4_HUMAN ALU S	4.68 3.14	7.48 3.37
23	317899 317986	Al952430 Al005163	Hs.150614 Hs.201378	ESTs, Weakly similar to T12545 hypotheti	0.28	1.66
	318001	AW235697	Hs.130980	ESTs	5.12	9.97
	318016	AI016694	Hs.256921	ESTs	1.86	4.50
20	318023	AW243058	Hs.131155	ESTS	2.92 3.92	5.22 6.37
30	318054 318068	AW449270 Al024540	Hs.232140 Hs.131574	ESTs ESTs	1.21	1.27
	318117	Al208304	Hs.250114	ESTs	0.86	1.17
	318187	Al792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN IIII	5.90	6.98
25	318223	Al077540	Hs.134090	ESTs	1.05	0.90 2.40
35	318240	A1085377 A1082692	Hs.143610 Hs.134662	ESTs ESTs	3.10 0.02	1.05
	318255 318266	AI554341	Hs.271443	ESTs	6.12	10.55
	318330	AI093840	Hs.143758	ESTs	4.98	7.90
40	318369	Al493501	Hs.170974	ESTs	2.46 0.77	5.62 0.45
40	318428 318458	Al949409 Al149783	Hs.194591 Hs.158438	ESTs ESTs	3.54	4.92
	318467	A1151395	Hs.144834	ESTs	4.56	5.62
	318473	Al939339	Hs.146883	ESTs	2.08	4.05
45.	318476	AI693927	Hs.265165	ESTs	4.22	8.07
45	318487	AI167877	Hs.143716 Hs.144709	ESTs ESTs	1.47 1.40	1.05 4.14
	318488 318491	Al217431 - T26477	Hs.22883	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.84	1.90
	318499	T25451		gb:PTHI188 HTCDL1 Homo sapiens cDNA 5/3	2.58	5.20
~ 0	318537	AA377908	Hs.13254	ESTs	3.26	4.18
50	318538	N28625	Hs.74034	Homo saplens clone 24651 mRNA sequence	0.35 3.22	1.07 4.60
	318547 318552	R20578 R18364	Hs.90431 Hs.90363	ESTs ESTs	4.87	9.06
	318575	R55102	Hs.107761	ESTs, Wealty similar to unnamed protein	1.91	1.98
	318580	T34571	Hs.49007	poly(A) polymerase alpha	2.74	6.22
55	318587	AA779704	Hs.168830	Homo saptens cDNA FLJ12136 fis, clone MA EST	0.85 4.88	2.46 4.93
	318596 318622	A1470235 T48325	Hs.172698 Hs.237658	apolipoprotein A-II	4.80	12.51
	318629	N25163	Hs.8861	ESTs	0.39	1.04
~	318637	AA243539	Hs.9196	hypothetical protein	1.72	3.57
60	318648	T77141	Hs.184411	albumin hypothetical protein EDAG-1	6.27 3.96	9.91 8.84
	318650 318671	AA393302 AA188823	Hs.176626 Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	1.53	0.81
	318679	T58115	Hs.10336	ESTs	1.00	2.19
~=	318711	Al936475	Hs.101282	Homo sapiens cDNA: FLJ21238 fis, clone C	3.05	3.18
65	318725	AI962487	Hs.242990	ESTs ESTs, Wealdy similar to ALU1_HUMAN ALU S	1.08 0.77	2.46 1.33
	318728 318740	Z30201 NM_002543	Hs.291289 Hs.77729	oxidised low density lipoprotein (lectin	0.25	1.49
	318776	R24963	Hs.23766	ESTs	1.00	3.01
~ ^	318784	H00148	Hs.5181	proliferation-associated 2G4, 38kD	2.70	3.86
70	318816	F07873	Hs.21273	ESTs ab:ym04f10.r1 Soares infant brain 1NIB H	3.90 2.25	7.13 3.56
	318865 318879	H10818 R56332	Hs.18268	go:ymu410.r1 Soales illialit crais 1116 H adenylate kinase 5	1.78	5.00
	318881	Z43224	Hs.124952	ESTs	4.79	14.13
	318894	F08138	Hs.7387	DKFZP564B116 protein	5.31	7.00
75 .	318901	AW368520	Hs.301528	L-kynurenine/alpha-aminoadipate aminotra	1.03 2.23	0.91 3.80
	318925 318936	Z43577	Hs.21470 Hs.308298	ESTs ESTs	1.86	7.16
	318982	Al219221 Z44140	Hs.269622	ESTs	5.84	9.79
•	318986	Z44186	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.00	1.00
80	319041	Z44720	Hs.98365	ESTs, Weakly similar to weak similarity	3.38	6.11
	319103	H05896	Hs.4993	KIAA1313 protein putative selenocysteine lyase	1.00 3.79	1.07 5.03
	319170 319196	R13678 F07953	Hs.285306 Hs.16085	putative G-protein coupled receptor	1.00	2.98
	319199	F07361	Hs.13306	ESTs	3.53	5.66
85	319242		Hs.12839	ESTs	5.87	7.26

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	319263	T65331	Hs.81360	Homo sapiens cDNA: FLJ21927 fis, clone H	1.81	1.57
	319267	F11802	Hs.6818	ESTs	1.10	4.72
	319270 319279	R13474 T65094	Hs.290263 Hs.12677	ESTs CGI-147 protein	4.80 1.50	10,40 2.11
5	319282	AA461358	Hs.12876	ESTs	1.00	1.00
•	319289	W07304	Hs.79059	transforming growth factor, beta recepto	0.18	0.68
	319291	W86578	Hs.285243	hypothetical protein FLJ22029	0.26	0.62
	319293	F12119	Hs.12583	ESTs	3.13	4.50
10	319312	Z45481	11- 205022	gb:HSC2QE041 normalized infant brain cDN	1.10 0.16	1.00 0.73
10	319370 319391	H54254 R06304	Hs.325823 Hs.13911	ESTs, Moderately similar to ALU5_HUMAN A ESTs	1.26	2.43
	319396	H67130	Hs.301743	ESTs	0.70	0.76
	319398	AA359754	Hs.191196	ESTs	2.45	3.59
1.5	319407	R05329		gb:ye91b04.r1 Soares fetal liver spleen	2.00	3.54
15	319425	T82930	11- 404400	gb:yd39f07.r1 Soares fetal liver spleen	4.28	8.81
	319433 319437	R06050 AA282420	Hs.191198 Hs.111991	ESTs ESTs, Wealdy similar to Y48A5A.1 [C.eleg	6.15 3.26	14.13 5.68
	319466	AI809937	Hs.116417	ESTs	1.76	5.65
	319471	R06546	Hs.19717	ESTs	4.29	4.84
20	319480	R06933	Hs.184221	ESTs	1.00	1.00
	319484	T91772		gb:yd52a10.s1 Soares fetal liver spleen	2.81	4.88
	319486	A1382429	Hs.250799	ESTS	2.08 2.80	2.82 4.39
	319508 319523	T99898 T69499	Hs.270104 Hs.191184	ESTs, Moderately similar to ALUB_HUMAN A ESTs	1.55	3.25
25	319545	R83716	Hs.14355	Homo saplens cDNA FLJ13207 fis, clone NT	1.65	1.19
	319546	R09692		gb:yf23b12.r1 Soares fetal liver spleen	5.11	8.54
	319552	AA096106	Hs.20403	ESTs	1.89	3.36
	319582	T82998	Hs.250154	hypothetical protein FLJ12973	3.48	4.82
30	319586	D78808	Hs.283683	chromosome 8 open reading frame 4	0.26	0.82
30	319604 319609	R11679 AW247514	Hs.297753 Hs.12293	vimentin hypothetical protein FLJ21103	1.68 3.06	3.41 4.24
	319611	H14957	115.12230	gb:ym19c10.r1 Soares infant brain 1NIB H	2.76	4,24
	319653	AA770183	Hs.173515	uncharacterized hypothalamus protein HT0	2.51	3,55
~ ~	319657	R19897	Hs.106604	ESTs	5.32	7.68
35	319658	R13432	Hs.167481	syntrophin, gamma 1	3.35	5.00
	319661	H08035	Hs.21398	ESTs, Moderately similar to A Chain A, H	5.18	12.55
	319662 319708	H06382 R15372	Hs.21400 Hs.22664	ESTs ESTs	1.58 1.00	1.56 1.22
	319742	T77668	Hs.21162	ESTs	2.48	3.13
40	319748	R18178	Hs.295866	Homo sapiens mRNA; cDNA DKFZp434N1923 (f	3.02	4.85
	319772	R76633	Hs.22646	ESTs	4.36	11,61
	319788	AA321932	Hs.117414	KIAA1320 protein	2.56	3.68
	319805	R92857	Hs.271350	likely ortholog of mouse polydom	4.63 0.63	6.56 1.32
45	319812 319834	N74880 AA071267	Hs.264330	N-acylsphingosine amidohydrolase (acid c gb:zm61g01.r1 Stratagene fibroblast (937	0.63	0.94
43	319878	T78517	Hs.13941	ESTs	3.99	6.44
	319882	AA258981	Hs.291392	ESTs ·	5.09	7.36
	319912	T77559	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	3.24	3.21
50	319935	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.40 3.31	9.42 5.39
50	319944 319947	179248 AA160967	Hs.133510 Hs.14479	ESTs Homo saplens cDNA FLJ14199 fis, clone NT	2.90	4.95
	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	1.81	1.57
	320007	AA336314		gb:EST40943 Endometrial tumor Homo saple	3.42	6.29
~ ~	320018	T83263		gb:yd40h09.r1 Soares fetal liver spleen	2.77	5.14
55	320030	H63789	Hs.296288	ESTs, Wealdy similar to KIAA0638 protein	4.10 3.27	6.69 3.27
	320032 320040	AI699772 AA233671	Hs.292664 Hs.87164	ESTs, Weakly similar to A46010 X-linked hypothetical protein FLJ14001	1.81	1.64
	320040	T86564	Hs.302256	EST	3.38	7.36
	320063	AA074108	Hs.120844	FOXJ2 forkhead factor	5.90	16.73
60	320096	H58138	Hs.117915	ESTs	2.08	4.47
	320099	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.00	1.00
	320112 320140	T92107	Hs.188489 Hs.119023	ESTs SMC2 (structural maintenance of chromoso	2.27 1.00	2.06 1.00
	320188	H94179 AW419200	Hs.172318	ESTs	1.26	1.00
65	320193	AA831259	Hs.17132	ESTs	2.58	6.23
	320195	R62203	Hs.24321	Homo saplens cDNA FLJ12028 fis, clone HE	2.85	4.53
	320199	R78659	Hs.29792	ESTs	0.40	0.94
	320203	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	0.84	1.18
70	320219	AA327564	Hs.127011	tubulointerstitial nephritis antigen	1.00 0.18	1.17 1.09
70	320220 320225	AF054910 AF058989	Hs.127111 Hs.128231	tektin 2 (testicular) G antigen, family B, 1 (prostate associa	5.26	13.75
	320231	H03139	Hs.24683	ESTs	1.59	1.93
	320260	NM_003608	Hs.131924	G protein-coupled receptor 65	1.38	4.56
96	320267	AL049337	Hs.132571	Homo saplens mRNA; cDNA DKFZp564P016 (fr	1.00	1.92
75	320268	H06019	Hs.151293	Homo sapiens cDNA FLJ10664 ffs, clone NT	5.58	5.70
	320322	AF077374	Hs.139322	small proline-rich protein 3	1.41 0.05	1.01 0.67
	320325 320330	AI167978 AF026004	Hs.139851 Hs.141660	caveolin 2 chloride channel 2	2.17	1.26
	320339	H10807	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.81	2.32
80	320388	H16065	Hs.31286	ESTs	1.00	3.22
-	320402	R22291	Hs.23368	Homo saplens clone FLC0578 PRO2852 mRNA,	1.41	1.36
	320413	AA203711	Hs.173269	ESTs	2.31	3.61
	320432	R62786	Hs.124136	ESTs ESTs	11.25 2.22	20.78 3.49
85	320436 320438	AA253352 W24548	Hs.293663 Hs.5669	ESTS	3.53	8.14
	J25400	*********		_		

	W	O 02/086	5443			
	320448	AJ240233	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	1.42	3.46
	320451	R26944	Hs.180777	Homo saplens mRNA; cDNA DKFZp564M0264 (f	0.87	0.81
	320484	AA094436	Hs.296267	follistatin-like 1	0.65	1.18
_	320499	R32555	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	3.44	7.15
5	320514	AB007978	Hs.158278	KIAA0509 protein	6.44	13.62
	320521	N31464	Hs.24743	hypothetical protein FLJ20171	1.48	1.04
	320526	AW374205	Hs.111314	ESTs	3.66	7.87
	320527	R34672	Hs.324522	ESTs	3.16	5.63
	320536	AA331732	Hs.137224	ESTs	2.83	5.83
10	320556	AF054177	Hs.14570	hypothetical protein FLJ22530	1.28	1.00
	320564	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.22	0.81
	320587	Z44524	Hs.167456	Homo saplens mRNA full length insert cDN	1.84	2.44
	320635	R54159	Hs.80506	small nuclear ribonucleoprotein polypept	1.00	6.25
	320639	AA243258	Hs.7395	hypothetical protein FLJ23182	2.60	2.30
15	320648	N48521	Hs.26549	Homo sapiens mRNA for KIAA1708 protein,	1.00	1.53
13	320651	AA489268	Hs.111334	ferritin, light polypeptide	0.14	0.79
	320664	A1904216	Hs.91251	hypothetical protein FLJ11198	5.02	8.84
		AA132650	Hs.300511	ESTs	3.63	5.37
	320676	R59291	Hs.26638	ESTs, Weakly similar to unnamed protein	0.37	1.31
20	320683		Hs.171929	ESTs, Weakly similar to A54849 collagen	1.27	1.02
20	320689	AA334609			3.53	4.60
	320696	AW135016	Hs.172780	ESTs	1.06	0.85
	320714	Al445591	11-404405	gb:yq04a10.r1 Soares fetal liver spleen	1.35	1.49
	320727	U96044	Hs.181125	immunoglobulin tambda locus	0.04	
25	320771	Al793266	Hs.117176	poly(A)-binding protein, nuclear 1		0.82
25	320794	AA281993	Hs.91226	ESTs	2.96	4.33
	320822	AF100780	Hs.194679	WNT1 inducible signaling pathway protein	0.10	0.79
	320824	AF120274	Hs.194689	artemin	1.16	1.11
	320830	AJ132445	Hs.266416	claudin 14	1.06	1.75
20	320843	AA317372	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.36	1.47
30	320849	D60031	Hs.34771	ESTs	5.30	7.49
	320853	Al473796	Hs.135904	ESTs	1.00	1.00
	320896	AB002155	Hs.271580	uroplakin 1B	5.90	2.55
	320921	R94038	Hs.199538	inhibin, beta C	2.20	1.17
	320927	A1205786	Hs.213923	ESTs	0.18	1.46
35 .	320957	AJ878933	Hs.92023	core histone macroH2A2.2	1.67	2.18
	320997	H22544		gb:yn69f11.r1 Soares adult brain N2b5HB5	3.26	3.62
	321045	W88483	Hs.293650	ESTs	2.25	4.55
	321046	H27794	Hs.269055	ESTs	2.69	4.25
	321052	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	2.14	2.56
40	321059	Al092824	Hs.126465	ESTs	1.69	0.53
	321062	R87955	Hs.241411	Homo sapiens mRNA full length insert cDN	2.76	5.20
	321067	AF131782	Hs.241438	Homo saplens clone 24941 mRNA sequence	4.79	7.41
	321102	AA018306		gb:ze40d08.r1 Soares retina N2b4HR Homo	1.79	4.27
	321130	H43750	Hs.125494	ĒSTs	1.00	3.14
45	321142	AI817933	Hs.298351	ASPL protein	8.73	15.36
	321155	AA336635	Hs.99598	hypothetical protein MGC5338	3.04	5.03
	321158	AA700289		gb:yu76f11.r1 Soares fetal liver spleen	4.62	8.39
	321170	N53742	Hs.172982	ESTs	2.21	4.46
	321199	AW385512		gb:yy56d10.s1 Soares_multiple_sclerosis_	5.69	8.01
50	321206	H54178	Hs.226469	Homo sapiens cDNA FLJ12417 fis, clone MA	4.00	7.32
-	321225	AL080073	Hs.251414	Homo sapiens mRNA; cDNA DKFZp564B1462 (f	4.17	4.63
	321236	AW371941	Hs.18192	Ser/Arg-related nuclear matrix protein (1.00	1.00
	321244	AF068654		gb:Homo saplens Isolate AN.1 immunoglobu	2.18	9.13
	321270	R83560		gb:yv76c06.s1 Soares fetal liver spleen	3.80	5.26
55	321317	AI937060	Hs.6298	KIAA1151 protein	1.81	1.65
	321318	AB033041	Hs.137507	KIAA1215 protein	1.00	1.00
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	0.44	0.93
	321342	AA127984	Hs.222024	transcription factor BMAL2	4.94	4.93
	321356	R93443	Hs.271770	ESTs	3.10	4.66
60	321418	AJ739161	Hs.161075	ESTs	2.28	2.54
00	321420	Al368667	Hs.132743	ESTs	1.13	0.97
	321430	U05890		gb:H.sapiens (DIG3) mRNA for immunoglobu	2.42	3.35
	321453	N50080	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	1.60	3,11
	321467	X13075	10.02010	gb:Human 2a12 mRNA for kappa-immunoglobu	0.42	0.72
65	321468	AA514198	Hs.38540	ESTs	2.46	6,50
05	321491	H70665	Hs.292549	ESTs	1.00	1.25
	321498	AW295517	Hs.255436	ESTs	3.19	6.24
	321504	W02356	Hs.268980	ESTs	2.28	3.86
	321510	AA703650	Hs.255748	ESTs	2.14	3.94
70		H84972	Hs.108551	ESTs	2.78	5.37
70	321513			ESTs	3.06	7.19
	321516 321565	Al382803 Al525773	Hs.159235 Hs.266514	hypothetical protein FLJ11342	4.89	7.82
			NS.200314	gbrys90g04.r1 Soares retina N2b5HR Homo	1.00	1.73
	321577	H84260	Hs.28803		4.88	6.73
75	321581	AA019964		ESTs	1.00	2.08
75	321582	AA143755	Hs.21858	trinucleotide repeat containing 3	2.26	4.52
	321587	H95531	11- 00000	gb:ys76e02.r1 Soares retina N2b4HR Homo	1.95	3.83
	321626	AA295430	Hs.96322	hypothetical protein FLJ23560		
	321628	H87064	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN A	0.47	1.02
οΛ	321642	AW085917	Hs.247084	ESTs	1.52	1.38
80	321669	H95404	Hs.294110	ESTS	2.17	2.45
	321687	AA625149		gb:af70c12.r1 Soares_NhHMPu_S1 Homo sapi	4.31	6.95
	321688	H97646	Hs.123158	Homo sapiens cDNA FLJ12830 fis, clone NT	2.82	3.28
	321693	AA700017	Hs.173737	ras-related C3 botulinum toxin substrate	0.51	1.08
O.F	321700	N55160	Hs.167260	ESTs	4.57	7.46
85	321701	AW390923	Hs.42568	ESTs	1.00	1.00

	w	O 02/08	6443			
	321709	N25847	Hs.108923	RAB38, member RAS oncogene family	1.00	1.00
	321710	N35682	Hs.259743	ESTs	2.97	5.26
	321775	Al694875	Hs.202312	Homo sapiens cione N11 NTera2D1 teratoca	1.00	1.00
_	321777	A1637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	1.68	0.45
5	321779	N42729	Hs.163835	ESTs	0.90	0.90
	321829	D81993	Hs.8966	turnor endothelial marker 8	2.69	3.89
	321846	AA281594	Hs.87902	ESTs	5.11	7.64
	321879	AL109670	Hs.302809	ESTs	6.49 0.28	9.58 0.95
10	321883	AA426494	Hs.46901	KIAA1462 protein	0.26	0.95
IO	321899	N55158	Hs.29468	ESTs	6.20	10.76
	321911	AF026944 R49202	Hs.293797	ESTs EST	4.62	10.70
	321949		Hs.181694 Hs.195689	ESTs	2.89	5.47
	321955 321956	Al651866 AL110177	Hs.132882	ESTs	0.32	1.25
15	321987	AL133612	Hs.272759	KIAA1457 protein	1.00	1.83
13	321991	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	4.00	6.47
	322002	AA328801	Hs.84522	ESTs	2.10	3.48
	322035	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.00	1.90
	322044	AW340926	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	gbxy51b10.x1 NCI_CGAP_Lu34.1 Homo sapie	3.20	9.67
20	322057	N92197	Hs.154679	synaptotagmin 1	1.55	1.07
	322060	Al341937		gb:qt10e03.x1 NCI_CGAP_GC4 Homo saplens	4.59	7.68
	322070	U80769	Hs.210322	Homo sapiens mRNA for KIAA1766 protein,	2.78	4.52
	322083	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	3.10	5.52
	322091	AI819863	Hs.106243	ESTs	1.59	1.75
25	322125	R93901		gb:yq16c12.r1 Soares fetal liver spleen	2.06	5.27
	322130	R98978	Hs.117767	ESTs	10.12	16.49
	322147	AF085919	Hs.114176	ESTs	0.94	0.64
	322166	AF085958		gb:yr88b03.r1 Soares fetal liver spleen	4.09	6.67
20	322173	H52567		gb:yt85d04.r1 Soares_pineal_gland_N3HPG	3.46	4.85
30	322178	H56535		gb:yt88g03.r1 Soares_pineal_gland_N3HPG	0.44	2.54
	322179	H92891		gb:yt94c02.s1 Soares_plneal_gland_N3HPG	4.52	7.50
	322186	H67346	Hs.269187	ESTs	0.15	0.98
	322196	W87895	Hs.211516	ESTs	2.20 3.42	5.04 4.84
25	322212	AF087995	Hs.134877	ESTs	3.42 0.82	2.14
35	322221	A1890619	Hs.179662	nucleosome assembly protein 1-like 1	3.62	3.98
	322277	A1640193	Hs.226389	ESTs gb:zd46f01.r1 Soares_fetal_heart_NbHH19W	1.00	1.00
	322278	AF086283 Al792140	Hs.49265	ESTs	0.66	2.76
	322284 322288	AL037273	Hs.7886	pellino (Drosophila) homolog 1	0.71	0.70
40	322320	AF086419	113.7000	gb:zd78d03.r1 Soares_fetal_heart_NbHH19W	2.02	2.76
70	322336	AA308526	Hs.76152	decorin	2.92	4.44
	322339	W17348	113.70102	gb:zb18c07.x5 Soares_fetal_lung_NbHL19W	8.50	11.56
	322366	AW404274	Hs.122492	hypothetical protein	0.61	1.34
	322372	W25624	Hs.153943	ESTs	7.37	12.07
45	322374	AJ394663	Hs.122116	ESTs, Moderately similar to Osf2 [M.musc	4.78	10.50
	322378	AF064819	Hs.201877	DESC1 protein	1.00	1.00
	322388	AI815730	Hs.247474	hypothelical protein FLJ21032	7.09	8.49
	322416	AA223183	Hs.298442	adaptor-related protein complex 3, mu 1	3.20	5.80
	322419	AA248987	Hs.14084	ring finger protein 7	1.64	1.57
50	322425	W37943	Hs.34892	KIAA1323 protein	0.83	1.00
	322431	AA069222	Hs.141892	ESTs	3.96	5.22
	322450	AA040131	Hs.25144	ESTs .	5.18	12.67
	322465	AA137152	Hs.286049	phosphoserine aminotransferase	3.41	2.23
c c	322467	AF116826	Hs.180340	putative protein-tyrosine kinase	1.00	1.30
55	322473	AA744286	Hs.266935	tRNA selenocysteine associated protein	1.75	2.03
	322509	T52172	Hs.302213	ESTs	1.00	2.27 5.49
	322523	W80398	Hs.193197	ESTs	2.75 1.25	1.27
	322527	AF147359	Un 270047	gb:Homo saplens full length insert cDNA	4.57	8.81
60	322560	Al916847 W87285	Hs.270947	ESTS	1.00	1.42
UU	322566		Hs.269587	ESTs gb:zh69c01_r1 Soares_fetal_liver_spleen_	4.18	6.94
	322585	AA837622 AA679084		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.40	4.85
	322635	AA007352	Hs.256042	ESTs	2.94	4.64
	322641		Hs.258538	striatin, calmodulin-binding protein	0.48	0.38
65	322653 322664	A1828854 AA011522	HS.200000	gb:zi03g07.r1 Soares_fetal_liver_spleen_	1.92	2.18
05	322687	Al110759	•	gb:AF074666 Human fetal liver cDNA libra	4.14	6.75
	322692	AA018117	Hs.60843	potassium voltage-gated channel, shaker-	3.50	5.00
	322694	AI110872	Hs.279812	PRO0327 protein	1.80	1.72
	322708	AF113674	Hs.283773	clone FLB1727	1.00	3.43
70	322712	AA021328	Hs.23607	hypothetical protein FLJ11109	3.28	3.86
	322766	AW068805	Hs.288467	Homo saplens cDNA FLJ12280 fis, clone MA	1.63	1.53
	322770	AA045796	Hs.122682	ESTs	1.53	1.06
	322794	Al608591	Hs.38991	S100 calcium-binding protein A2	12.06	1.94
	322810	Al962276	Hs.127444	ESTs	4.09	6.90
75	322818	AW043782	Hs.293616	ESTs	1.20	1.63
	322820	Al377755	Hs.120695	ESTs	0.21	1.93
	322872	AA827228	Hs.126943	ESTs	2.04	1.63
	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	5.26	1.22
00	322887	Al986306	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.80	2.24
80	322913	A1733737	Hs.68837	ESTs	2.38	6.61
	322926	AI825940	Hs.211192	ESTs	4.02	5.79
	322929	Al365585	Hs.146246	ESTs	0.30	1.14
	322968	A1905228	Hs.83484	SRY (sex determining region Y)-box 4	2.06	1.13
05	322971	C15953	Hs.212760	hypothetical protein FLJ13649	1.18 2.28	2.00 2.61
85	322981	AA493252	Hs.159577	ESTs	2.20	2.01

	W	O 02/086	0443			
	322988	C18727	Hs.171941	ESTs	0.39	2.00
	323003	AI733859	Hs.149089	ESTs	3.28	1.00
	323013	AA134042	Hs.191451	ESTs	3.38	5.68
_	323025	AL157565	Hs.315369	Homo saplens cDNA: FLJ23075 fis, clone L	0.06	1.10
5	323032	AW244073	Hs.145946	ESTs	10.18	21.27
	323052	R21124	Hs.85573	Homo sapiens DC29 mRNA, complete cds	1.46	1.90
	323064	AL119341	Hs.49359	Homo sapiens mRNA; cDNA DKFZp547E052 (fr	3.08	5.64
	323098	A1700025	Hs.270471	ESTs	2.31	4.49
10	323102	AL119913	Hs.163615	ESTs	5.38	11.64
10	323155	AL135041		gb:DKFZp762K2310_1 762 (synonym: hmel2)	2.38	5.56
	323176	AW071648	Hs.82101	pleckstrin homology-like domain, family	1.06	1.41
	323191	AA195600	Hs.301570	ESTs	0.73	1.24
	323225	AA205654	Hs.24790	KIAA1573 protein	5.25	11.95
4.5	323232	AA148722	Hs.224680	ESTs	0.45	1.35
15	323266	AW003362	Hs.243886	nuclear autoantigenic sperm protein (his	1.71	1.83
	323281	A1697556	Hs.292659	ESTs	1.24	3.21
	323283	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	12,68	15.05
	323314	AA226310	Hs.191501	ESTs	4.42	9.61
••	323316	AL134620	Hs.280175	ESTs	2.98	5.93
20	323334	Al336501	Hs.77273	ras homolog gene family, member A	1.98	3.30
	323338	R74219	Hs.23348	S-phase kinase-associated protein 2 (p45	1.62	1.00
	323348	AA233056	Hs.191518	ESTs	1.00	1.07
	323351	AA704103	Hs.24049	ESTs	1.43	1.68
	323359	AA234172	Hs.137418	ESTs	0.34	1.18
25	323360	AA716061	Hs.161719	ESTs	3.01	3.71
	323405	AW139550	Hs.115173	ESTs	1.90	8.81
	323420	A1672386	Hs.263780	ESTs	0.29	1.01
	323434	AW081455	Hs.120219	E\$Ts	2.27	1.92
	323445	AA253103	Hs.135569	ESTs, Weakly similar to NEUROD (H.sapien	0.43	0.80
30	323449	AA282865	Hs.284153	Fanconi anemia, complementation group A	3.19	3.85
	323492	H00978	Hs.20887	hypothetical protein FLJ 10392	2.70	3.20
	323501	AA182461	Hs.84520	ESTs	2.04	3.31
	323505	AI652287		gb:EST382593 MAGE resequences, MAGK Homo:		3.08
	323515	AA282274	Hs.256083	ESTs	2.69	3.40
35	323541	Al185116	Hs.104613	RP42 homolog	1.20	1.09
	323545	AI814405	Hs.224569	ESTs	1.25	1.55
	323635	R63117	Hs.9691	Homo sapiens cDNA: FLJ23249 fis, clone C	0.27	0.72
	323675	AA984759	Hs.272168	turnor differentially expressed 1	3.70	5.80
	323678	AL042121	Hs.20880	ESTs	3.33	5.10
40	323691	AA317561	Hs.145599	ESTs	1.00	1.00
	323693	AW297758	Hs.249721	ESTs	2.01	1.54
	323746	AW298611	Hs.12808	MARK	4.11	5.53
	323774	AA329806	Hs.321056	Homo sapiens mRNA; cDNA DKFZp586F1322 (f	2.06	3.70
4.5	323856	AA355264	Hs.267604	hypothetical protein FLJ 10450	3.42	8.13
45	323857	T18988	Hs.293668	ESTs	5.97	12.51
	323870	AA341774	Hs.129212	ESTs	3.17	4.52
	323876	AL042492	Hs.147313	ESTs	0.36	1.00
	323885	AA344308	Hs.128427	Homo sapiens BAC clone RP11-335J18 from	2.31	3.33
~ ^	323911	AL043212	Hs.92550	ESTs	4.38	5.41
50	323919	AA862973	Hs.220704	ESTs	5.80	10.20
	323972	Al869964	Hs.182906	ESTs	3.10	5.14
	324005	AA610011	Hs.208021	ESTs	5.34	10.07
	324036	Al472078	Hs.303662	ESTs	1.00	5.03
<i>E E</i>	324055	AA528794	Hs.128644	ESTs	0.86	1.00
55	324063	AW292740	Hs.272813	dual oxidase 1	0.45 2.82	0.91 5.12
	324072	AA381829		gb:EST94855 Activated T-cells I Homo sap	2.40	2.52
	324092	AW269931	Hs.202473	Homo sapiens cDNA: FLJ22278 fis, clone H	1.32	4.30
	324095	AW377983	Hs.298140	Homo sapiens cDNA: FLJ22502 fis, clone H	1.40	1.77
60	324129	Al381918	Hs.285833	Homo saplens cDNA: FLJ22135 fis, clone H	4.24	6.21
UU	324132	AW504860	Hs.288836	hypothetical protein FUJ12673	6.96	10.69
	324214	AA412395	Hs.225740	ESTs Homo sapiens cDNA: FLJ22141 fis, clone H	0.81	0.53
	324227	AA295552	Hs.28631		2.42	4.05
	324266	AL047634	Hs.231913	ESTs ESTs	3.62	5.38
65	324275	AA429088	Hs.98523	ESTs, Weakly similar to T14742 hypotheti	0.14	0.70
UJ	324281	AL048026 AA432032	Hs.124675		3.71	4.34
	324290		Hs.304420	ESTs gb:DKFZp761P1910_r1 761 (synonym: hamy2)	0.95	0.91
	324303	AL118754	U- 420472		4.06	5.91
	324312	Al198841	Hs.128173	ESTs	5.88	8.25
70	324325	AL138153	Hs.300410	ESTs regulator of differentiation (in S. pomb .	0.87	1.25
70	324338	AL138357	Hs.145078	ESTs, Weakly similar to unnamed protein	1.28	1.00
	324341	AW197734	Hs.99807		2.54	3.46
	324343	AW452016	Hs.293232	ESTs	5.85	8.36
	324371	AA452305	Hs.270319	ESTS	0.76	1.64
75	324382	AW502749	Hs.24724	MFH-amplified sequences with feucine-ric	2.88	5.69
75	324384	AA453396	Hs.127656	KIAA1349 protein	1.81	1.99
	324385	F28212	Hs.284247	KIAA1491 protein	1.00	1.00
	324388	AI924963	Hs.306206	hypothetical protein FLJ11215	2.73	2.17
	324432	AA464510 AW152624	Hs.152812	ESTs ESTs, Weakly similar to unnamed protein	0.71	1.90
80	324497		Hs.136340	Homo saplens cDNA FLJ11569 fis, clone HE	1.00	1.00
00	324510	Al148353 AA492588	Hs.287425	gb:ng99c08.s1 NCI_CGAP_Thy1 Homo saplens	2.18	3.50
	324580	AA492366 AA506935	Hs.132036	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.96	11.36
	324582	AA572994	Hs.325489	ESTS VERMY SIMILAR OF ALCO INTO MANY ALCO S	2.92	4.22
	324633	AW295832	Hs.134798	ESTs, Moderately similar to TTL MOUSE TU	5.48	11.74
85	324640	AW014734	Hs.157969	ESTs Moderately similar with two doc 10	0.39	0.73
0.5	324675	A11014134	113.101303	2010		

	W	O 02/08	6443			
	324699	AW504732	Hs.21275	hypothetical protein FLJ11011	0.93	0.93
	324747	AA603532	Hs.130807	ESTs	1.57	1.81
	324748	AA657457	Hs.292385	ESTs	1.55	1.34
	324801	Al819924	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	6.56
5	324804	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	1.00	7.53
•	324828	AA843926	Hs.124434	ESTs	2.00	3.25
	324855	AW152305	Hs.122364	ESTs	2.74	3.43
	324866	Al541214	Hs.46320	Small proline-rich protein SPRK (human,	1.07	0.95
	324871	AW297755	Hs.271923	Homo saniens cDNA: FLJ22785 fis, clone K	1.68	1.21
10	324886	AA806794	Hs.131511	ESTs	2.56	5.61
10	324889	D31010	1.0.101011	gb:HUML12147 Human fetal lung Homo saple	2.20	4.65
	324948	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	5.28	7.05
	324953	Al264628	Hs.125428	ESTs	3.37	5.51
	324958	AA625076	Hs.132892	protocadherin 20	5.12	9.81
15	324988	T06997	Hs.121028	hypothetical protein FLJ10549	2.52	1.08
13			Hs.78672	laminin, alpha 4	5.24	10.22
	325024	F13254		ESTs	1.00	1.00
	325105	H97109	Hs.105421	ESTS	1.99	2.14
	325108	AA401863	Hs.22380		2.73	3.17
20	325114	D83901	Hs.315562	ESTs	1.86	3.41
20	325146	Al064690	Hs.171176	ESTs	0.42	0.93
	325149	D61117	Hs.187646	ESTs	6.50	11,31
	325187	A1653682	Hs.197812	ESTs		
	325228				6.18	15.76
25	325235				2.64	4.12 4.42
25	325328				2.87	
	325340				0.29	0.33
	325367				16.56	24.29
	325373				0.63	1.22
20	325389				0.88	1.05
30	325436				5.75	14.14
	325471				8.46	17.82
	325498				3.32	6.42
	325557				5.51	8.28
	325559				7.48	21.40
35	325560				4.08	6.25
	325569				4.20	5.24
	325585				1.10	1.13
	325587				1.00	1.00
	325597				2.98	13.40
40	325639				0.78	0.78
	325685				0.46	0.66
	325686				0.95	1.55
	325735				4.48	9.20
	325739				0.59	0.88
45	325740				2.42	6.61
-1.5	325792				7.88	9.83
	325819				4.74	7.18
	325883				2.02	2.64
	325895		•		7.78	15.98
50	325925				2.04	10.60
-	325932				4.18	7.36
	325941				3.66	9.03
	325969				0.61	0.80
	325971			1	4.88	7.42
55	326025				0.55	1.07
33	326046				7,21	14.72
	326099				3.60	5.98
	326108				1.27	1.06
	326163				3.27	5.70
60					0.45	1.11
00	326165				0.43	0.45
	326189				5.60	9.00
	326204				7.00	12.01
	326230				1.00	8.09
65	326274				9.86	15.35
UJ	326360				0.52	0.77
	326393					
	326505				1.00	1.42
	326515				1.24	5.84 13.49
70	326589				9.20	
70	326592				2.77	4.01
	326605				2.01	2.53
	326692				1.00	1.00
	326693				1.00	1.31
75	326720				0.19	0.65
75	326742				2.34	7.20
	326770				0.25	0.83
	326818				3.09	4.56
	326936				2.08	3.45
00	326964	•			0.41	1.70
80	326983				2.02	3.80
	326991				1.09	1.20
	327036				1.00	8.04
	327040				3.05	4.22
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85	327075				1.59	1.40

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	327085		2.50	12.57
	327130		5.38	8.04
	327156	•	3.74	6.58
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5	327224		1,20 £ ££	
,			6.56	12.91
	327288		2.61	5.40
	327321		2.42	3.11
	327332		6.62	10.58
• •	327361		2.69	4.41
10	327377		2.04	6.72
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	327414		1.00	8.01
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	327483		4.08	8.87
	327562		0.68	2.86
	327568		1.00	2.00
	327606		2.06	3.61
20	327611		5.90	14.26
	327642		4.06	8.74
	327654	•		
			1.05	2.08
	327734		1.00	1.00
25	327775		1.46	11.79
25	327796		3.47	5.65
	327840		3.26	6.64
	327940		5.84	15.58
	327984		0.36	1.50
	328004		1.87	1.42
30	328021		0.42	0.59
-	328068		2.83	4.68
		•		
	328100		3.04	5.39
	328101		3.54	5.20
25	328113		0.72	0.91
35	328157		5.58	5.16
	328196		√5.76	11.13
	328197		5.98	10.58
	328264		3.11	4.88
	328299		2.20	3.06
40	· 328342		1.49	1.94
70				
	328365		1.00	1.00
	328369		4.40	7.36
	328381		1.86	4.93
4 =	328451		5.51	7.56
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	328530	•	5.41	7.62
	328600		3.14	10.68
	328608			
50			4.56	8.17
50	328616		2.24	11.91
	328623		3.04	5.46
	328632		0.70	1.19
	328664		3.48	6.80
	328666		10.42	26.47
55	328698		9.68	14.56
	328700		2.74	10.22
	328708		0.15	0.57
	328735		6.23	8.91
	328743			0.51
60			3.62	6.54
OO	328806		0.22	0.78
	328861		3.68	10.54
	328908		5.42	16.36
	328933		2.02	5.29
	328934		1.73	4.45
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	329005		2.88	7.26
	329011	•	2.52	3.72
	329033		1.00	1.03
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70	329067		1.98	2.41
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	329157		2.30	11.04
	329178		2.64	5.02
	329192		6.41	15.27
75	329194		0.31	0.79
	329204		1.60	3.75
	220224			3.75 6.11
	329224		2.99	0.11
	329228		0.83	0.83
00	329288		0.63	1.01
80	329337		1.00	1.00
	329541		0.76	1,68
	329560		1.34	1.68 2.02
	329588		1.68	2.22
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85	320703			
0.5	329703		1.00	1.00

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	329764				5.78	15.50
	329816			•	2.09	5.44
	329860				3.13	10.77
	329993				7.83	14.21
5	330020				5.58	13.12
_	330036				3.32	5.57
	330052				4.31	7.97
	330085				1.34	1.76
	330088				4.70	12.46
10	330093				0.44	1.06
10	330100				3.47	4.83
	330106				2.14	3.61
	330107				3.17	6.87
	330120				5.61	11.89
15	330120				4.50	12.74
13					1.55	7.62
	330208				13.10	23.38
	330263 330300				2.81	4.98
	330313				3.00	4.41
20					0.67	0.76
20	330366				4.76	11.82
	330372	44440740	11- 400074	leaveshada alaba 6 ilamedia alaba 61		2.15
	330385	AA449749	Hs.182971	karyopherin alpha 5 (importin alpha 6)	2.14 0.40	1.15
	330397	D14659	Hs.154387	KIAA0103 gene product		
25	330468	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.11	0.94
25	330472	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.67	1.17
	330478	L38486	Hs.296049	microfibrillar-associated protein 4	0.46	1.07
	330493	M27826	Hs.267319	endogenous retroviral protease	1.07	0.95
	330495	M31328	Hs.71642	guanine nucleotide binding protein (G pr	0.97	0.96
•	330506	M61906	Hs.6241	phosphoinositide-3-kinase, regulatory su	0.17	3.66
30	330512	M80563	Hs.81256	S100 calcium-binding protein A4 (calcium	0.60	1.06
	330537	U19765	Hs.2110	zinc finger protein 9 (a celtular retrov	2.81	2.07
	330547	U32989	Hs.183671	tryptophan 2,3-dloxygenase	3.91	1.49
	330551	U39840	Hs.299867	hepatocyte nuclear factor 3, alpha	1.15	1.03
	330568	U56244		(NONE)	2.83	4.79
35	330599	U90437		gb:Human RP1 homolog mRNA, 3'UTR region	2.08	1.54
	330601	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.89	1.35
	330605	X02419	Hs.77274	plasminogen activator, urokinase	1.87	1.55
	330609	X04741	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.83	1.30
	330617	X53587	Hs.85266	integrin, beta 4	1.54	1.15
40	330630	X78669	Hs.79088	reticulocalbin 2, EF-hand calcium bindin	1.39	1.19
	330644	Y07755	Hs.38991	S100 calcium-binding protein A2	3.83	1.13
	330650	Z68228	Hs.2340	junction plakoglobin	1.25	0.95
	330660	AA347868	Hs.139293	ESTs, Weakly similar to ALU7_HUMAN ALU S	15.50	29.07
	330692	AA017045	Hs.6702	ESTs	1.00	1.00
45	330707	AA133891	Hs.293690	ESTs	0.20	1.35
	330715	AA233707	Hs.11571	Homo sapiens cDNA FLJ11570 fis, clone HE	0.12	1.40
	330717	AA233926	Hs.52620	integrin, beta 8	6.62	5.42
	330722	AA243560	Hs.34382	ESTs	1.40	1.65
	330740	AA297746	Hs.22654	Homo sapiens voltage-gated sodium channe	0.27	2.04
50	330742	AA400979	Hs.25691	receptor (calcitonin) activity modifying	0.44	0.90
50	330744	AA406142	Hs.12393	dTDP-D-glucose 4,6-dehydratase	0.71	3.23
	330751	AA428286	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.66	1.52
	330760	AA448663	Hs.30469	ESTs	0.52	0.90
	330763	AA450200	Hs,274337	hypothetical protein FLJ20666	0.37	0.97
55	330786	D60374	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	0.78	0.84
55	330790	T48536	Hs.105807	ESTs	0.23	3.17
	330814	AA015730	Hs.265398	ESTs, Weakly similar to transformation-r	0.37	2.07
	330827	AA040332	Hs.12744	ESTs	1.60	1.00
	330844	AA063037	Hs.66803	ESTs	0.93	1.16
60			Hs.267319		1.02	1.03
00	330901 330931	AA157818 F01443	Hs.284256	endogenous retroviral protease hypothetical protein FLJ14033 similar to	0.24	0.88
	330952	H02855	Hs.29567	ESTs	0.08	1.31
	330961	H10998	Hs.7164	a disintegrin and metalloproteinase doma	1.29	1.26
			Hs.23748	ESTs	0.48	0.96
65	330968	H16568		hypothetical protein KIAA1165	0.29	0.74
05	331014	H98597	Hs.30340		0.99	8.56
	331046	N66563	Hs.191358	ESTs	1.24	1.00
	331060	N75081	Hs.157148	Homo saplens cDNA FLJ11883 fis, clone HE		1.03
	331099	R36671	Hs.83937	hypothetical protein	0.75	
70	331108	R41408	Hs.21983	ESTS	1.00 6.04	2.75 10.68
70	331131	R54797	U- 4407	gb:yg87b07.s1 Soares infant brain 1NiB H		0.96
	331135	R61398	Hs.4197	ESTs	0.80	
	331170	T23461	Hs.159293	ESTS	2.63	4:29
	331180	T32446	Hs.6640	Human DNA sequence from PAC 75N13 on chr	1.78	2.71
75	331183	T40769	Hs.8469	ESTs	1.00	3.01
75	331203	T82310	11-00000	(NONE)	1.70	3.80
	331271	AA059347	Hs.82226	glycoprotein (transmembrane) nmb	1.20	3.19
	331306	AA252079	Hs.63931	dachshund (Drosophila) homolog	0.31	1.30
	331327	AA281076	Hs.109221	ESTs	2.09	2.41
00	331341	AA303125	Hs.23240	Homo sapiens cDNA FLJ13496 fis, clone PL	0.72	2.43
80 .	331359	AA416979	Hs.46901	KIAA1462 protein	0.09	0.91
	331363	AA421562	Hs.91011	anterior gradient 2 (Xenepus laevis) hom	1.02	0.87
	331378	AA448881	Hs.49282	hypothetical protein FLJ11088	1.03	1.23
	331384	AA456001	Hs.93847	NADPH oxidase 4	1.40	1.00
0.5	331402	AA505135	Hs.44037	ESTs	1.80	3.93
85	331422	F10802	Hs.163628	ESTs, Moderately similar to ALU7_HUMAN	1.65	1.89

	W	O 02/08	6443			
	331490	N32912	Hs.26813	CDA14	2.48	1.73
	331531 331547	N51343 N54811		gb:yz15g04.s1 Soares_multiple_sclerosis_ gb:od74f04.s1 NCI_CGAP_Ov2 Homo saplens	0.98 3.80	1.68 5.75
	331578	N67960	Hs.249989	ESTs	0.11	0.67
5	331589	N71027	Hs.152618	ESTs	1.09	1.38
	331608	N89861	Hs.112110	PTD007 protein	0.93	0.76
	331614 331668	N92293 W69707	Hs.240272 Hs.58030	EST EST	0.17 2.24	1.34 3.82
	331671	W72033	Hs.194695	ras homolog gene family, member I	1.00	1.24
10	331676	W79834	Hs.58559	ESTs, Wealdy similar to rhotekin [M.musc	0.08	1.07
	331681	W85712 W93592	Hs.119571 Hs.152213	collagen, type III, alpha 1 (Ehlers-Danl wingless-type MMTV integration site fami	8.72 0.94	4.27 0.54
	331692 331717	AA190888	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	1.57	1.34
	331718	AA191404	Hs.104072	ESTs	6.80	11.77
15	331811	AA404500	Hs.301570	ESTs	1.10	1.00
	331820 331831	AA405970 AA412031	Hs.97996 Hs.97901	transcription termination factor, mitoc EST	0.73 2.77	0.59 4.08
	331852	AA418988	Hs.98314	Homo saplens mRNA; cDNA DKFZp586L0120 (f	0.23	0.93
	331943	AA453418	Hs.21275	hypothetical protein FLJ11011	0.36	1.88
20	331969	AA460702	Hs.82772	collagen, type XI, alpha 1	1.00	1.00
	331990 332002	AA478102 AA482009	Hs.139631 Hs.105104	ESTs ESTs	3.04 1.19	3.87 0.78
	332027	AA489671	Hs.65641	hypothetical protein FLJ20073	1.27	1.03
25	332029	AA489697	Hs.145053	ESTs	0.30	1.62
25	332033 332048	AA489840 AA496019	Hs.251014 Hs.201591	EST ESTs	2.30 0.17	3.70 0.52
	332071	AA598594	Hs.205293	KIAA1211 protein	1.35	1.23
	332074	AA599012		gb:ae41e11.s1 Gessler Wilms tumor Homo s	0.19	2.00
20	332083	AA600200	Hs.155546	KIAA1080 protein; Golgi-associated, gamm	0.31	1.18
30	332085 332125	AA600353 AA609861	Hs.173933 Hs.312447	nuclear factor I/A ESTs	0.30 0.22	1.50 0.62
	332177	F10812	Hs.101433	ESTs	8.21	18.03
	332180	H03348	Hs.7327	claudin 1	2.27	1.57
25	332185	H10356	Hs.101689	ESTs	0.09	1.18
35	332203 332232	H49388 N48891	Hs.317769 Hs.101915	EST Stargardt disease 3 (autosomal dominant)	8.05 0.78	5.02 0.85
	332240	N54803	Hs.324267	ESTs, Weakly similar to putative p150 [0.96	1.23
	332261	N70294	Hs.269137	ESTs	2.40	3.74
40	332275	R08838	Hs.26530	serum deprivation response (phosphatidy)	0.27	0.75
40	332280 332299	R38100 R69250	Hs.146381 Hs.21201	RNA binding motif protein, X chromosome nectin 3; DKFZP566B0846 protein	0.39 5.24	1.88 12.76
	332304	R74041	Hs.101539	ESTs	1.44	3.18
	332314	T25862	Hs.101774	hypothetical protein FLJ23045	0.68	1.32
45	332384	M11433	Hs.101850	retinol-binding protein 1, cellular	1.71	0.88 0.86
43	332434 332445	N75542 T63781	Hs.289068 Hs.11112	Homo saplens cONA FLJ11918 fis, clone HE ESTs	0.43 0.68	1.00
	332453	L00205	Hs.111758	keratin 6A	31.54	1.00
	332458	M33493	Hs.250700	tryptase bela 1	0.51	1.00
50	332504	AA053917 M17252	Hs.15106 Hs.278430	chromosome 14 open reading frame 1 cytochrome P450, subfamily XXIA (steroid	0.79 0.98	1.24 1.70
50	332525 332530	M31682	Hs.1735	inhibin, beta B (activin AB beta polypep	0.88	0.66
	332535	N20284	Hs.19280	cysteine-rich motor neuron 1	0.22	1.46
	332539	AA412528	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	0.93	1.49
55	332559 332563	M13955 N92924	Hs.166189 Hs.274407	cytokeratin 2 protease, serine, 16 (thyrnus)	0.35 1.00	1.13 1.00
55	332565	AA234896	Hs.25272	E1A binding protein p300	0.36	1.05
	332594	AA279313	Hs.3239	methyl CpG binding protein 2 (Rett syndr	0.53	0.59
	332634	S38953	Hs.283750	tenascin XA	0.38	1.16 1.70
60	332638 332640	AA283034 AA417152	Hs.50640 Hs.5101	JAK binding protein protein regulator of cytokinesis 1	1.00 6.15	1.16
00	332654	AA001296	Hs.288217	hypothetical protein MGC2941	1.50	2.73
	332665	AA223335	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.20	0.91
	332692 332716	AA496035 L00058	Hs.247926 Hs.79070	gap junction protein, alpha 5, 40kD (con v-myc avian myelocytomatosis viral oncog	0.17 1.00	1.12 1.44
65	332736	L13773	Hs.114765	myeloid/lymphold or mixed-lineage leukem	1.00	1.81
-	332758	X93921	Hs.296938	dual specificity phosphatase 7	0.53	0.78
	332781	AA233258	Hs.247112	hypothetical protein FLJ 10902	1.44	1.56
	332792 332816				1.70 1.85	1.19 2.47
70	332858				1.04	1.57
	332906				3.48	8.04
	332911				1.00	1.00
	332912 332922				1.06 1.00	4.40 1.00
75	332956				0.42	0.88
	332959				1.96	6.34
	332982			•	0.56	0.99
	332984 332998				0.30 1.47	0.78 2.01
80	333058				0.47	1.38
	333097				2.14	3.19
	333121				2.76	3.70
	333122 333123				1.92 1.85	1.21 1.39
85	333138				0.47	0.52

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	WUUZ	2/080443		
	333139		1.88	0.84
			0.21	0.64
	333140			1.11
	333221		1.51	1.11
	333260		0.75	1.01
5	333380		6.68	15.75
•			4.56	12.61
	333387			
	333512		5.05	8.01
	333524		2.28	3.98
			2.31	1.53
10	333585		2.07	4.47
10	333603		2.23	1.17
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	333618		1.44	1.36
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	333628		1.90	1.90
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IJ			1.85	2.35
	333678		1.03	2.33
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	333763		1.99	2.60
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	333777		1.00	
	333846		2.9 9	4.50
25	333884		0.47	0.94
23			0.50	1.00
	333887			
	333891		0.43	0.89
	333892	• • • • • • • • • • • • • • • • • • •	0.51	0.91
			0.26	1.13
~~	333904		0.20	1.13
30	333906		0.55	0.98
	333948		1.70	2.15
			0.37	1.09
	333954		0.01	
	333966		8.10	14.30
	333968		0.63	1.38
35			4.24	12.30
33	334061		1.30	12.03
	334094		1.30	
	334113		4.55	8.63
	334161		0.82	1.59
			0.47	0.76
40	334183			0.70
40	334187		1.36	3.70
	334219		0.69	1.04
			1.88	1.70
	334222		4.70	
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	334239		0.79	0.62
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	334382		1.50	1.31
			3.59	4.75
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	334588		8.14	19.53
	334616		1.55	1.56
			5.16	8.07
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	334648		0.59	2.13
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55			8.13	10.60
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	334891		0.32	1.14
	334933		1.00	3.84
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05			0.38	1.97
	335125			
	335179		1.24	1.98
	335188		0.46	1.47
			1.61	1.42
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70	335288			0.31
	335289		0.20	0.26
	335361		2.18	1.58
		•	0.50	0.71
	335379			
	335414		3.64	14.94
75	335416		2.93	3.98
, ,			0.96	0.91
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	335497		1.71	1.92
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WO 02/086443			PCT/US02/12476
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15	335995	0.37 1.04	1.17
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	336038	1.19	1.21
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	336331	1.00	1.00
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	336633 336634	2.55 2.19	2.23 2.03
	336635	2.69	2.48
	336636	2.13	1.83
30	336637	2.43	2.24
	336638	2.31	2.03
	336659	0.60 0.31	1.31 1.18
	336675 336684	1.50	1.14
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	336716	4.43	6.37
	336721	2.20 1.64	0.74
	336798 336900	6.14	2.14 12.73
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	337028	1.30	2.09
	337043	4.01	11.53
	337046	1.67 2.78	1.84 7.35
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	337183	5.72	11.41
	337184	3.72	5.90 1.06
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50	337229	0.22	1.03
	337268	1.00	3.31
	337299	3.23	5.14
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<i>J</i> .J	337389 337493	2.06	6.30
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	337755	1.54	0.92
65	337786	5.07	9.73 12.87
65	337809	6.18 3.78	12.97
	337862 337871	2.66	8.16
	337958	0.26	1.34
=-	338008	1.48	1.12
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	338083 338110	0.65 1.00	2.16 1.61
	338112	5.86	8.25
	338145	1.70	1.97
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	338158	1.30 2.58	4.55 3.57
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	338215 338279	6.01 0.53	0.95
85	338316	20.58	38.66
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	338418		6.12	13.86
	338469		3.09	5.11
	338501		6.28	10.32
10	338506		6.97	12.41
	338523		3.10	5.84
	338549		1.70	2.70
	338561		0.79	0.81
	338662		1.72	1.46
15	338671		0.17	0.91
	338676		2.10	15.86
	338726		1.20	1.09
	338779		0.12	0.57
	338804		0.99	1.67
20	338836		1.00	1.00
	338871		4.30	9.81
	338872		5.02	12.81
	338879	•	0.23	1.12
	338937		6.55	12.26
25	338966		1.76	5.42
	338993		1.00	2.40
	339047		5.26	10.81
	339100		5.10	6.88
	339114		1.00	1.70
30	339121		1.00	3.75
	339170		10.36	19.67
	339229		4.08	13.48
	339264		2.64	3.83
	339293		1.73	1.94
35				

40

TABLE 8B shows the accession numbers for those Pkeys in Table 8A lacking unigenelD's. For each probeset we have listed the gene cluster number from which the ofigonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence strillarly using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

CAT number. Gene cluster number Accession: Genbank accession numbers 45 Pkey **CAT number Accessions** 322044 187363_1 AW340926 AA249063 N86075 322060 44320_1 Al341937 AW003063 U34725 AA904742 50 321430 42705_1 X57414 X57415 X13075 X13076 R93901 AF075073 R93902 321467 322125 43034_1 46779_1 322166 46861_1 H69434 AF085958 H69846 H52567 H52557 AF085970 H52164 H56535 AF085980 H56712 322173 46873_1 55 322178 322179 46882_1 46885_1 H92891 AF085982 H92777 321577 1615102_1 H84849 H84252 H84260 H86664 H85320 H95531 H95521 H84529 AA070412 AA102346 AA081885 H22544 H46842 AI204929 321587 1615333_1 313723 320997 111953_1 627492_1 60 322278 47271_1 W69304 AF086283 W69200 AA625149 AA313030 AA313052 H97463 AA665089 AA135130 AA484059 AA102419 AW877765 W79150 AF086419 218439_1 129439_1 47422_1 321687 313883 322320 A1668646 A1734214 W17348 AW979268 AA878419 AA431342 AA431628 A1308300 A1308296 65 322339 814584_1 314648 300201 293660_1 682222 1 A1093967 306897 25196_-2 AL120701 AL135041 AL121524 AF147359 T58511 T58560 W88919 W89125 323155 979809_1 70 38927_1 473768_2 322527 322585 1574395_1 Z42308 H23514 300362 AA005129 AA679084 AA694399 AA011522 AA702841 AA011691 AA330797 AI239464 AI239473 AA625812 AI208703 322635 82296_1 322664 85042_1 75 380580_1 315454 322687 37372_1 327472_1 AF074666 Al110759 AF090902 AI903735 AA491283 AI694953 AW976903 AA761362 314852 Al347274 AW844024 AA381722 AA381829 AW963906 AW963902 AA381242 307783 324072 697809_1 269032_1 AA381722 AA381829 AW953905 AW953902 AA381242 AA488472 W27363 AA317053 BE082689 AW967036 BE079872 AW970512 AA280251 Al652287 BE466438 Al650725 AA551854 AA281574 AW571481 AA678177 AA677034 AL118754 AA333202 H38001 AA847835 AA768378 80 300627 221345_1 323505 196389_1 403558_1 233842_1 315791 324303 316519 442885_1 85 300926 333127_1 AA504860 AA504911

Unique Eos probeset identifier number

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TABLE 8C shows the genomic position for those Pkeys in Table 8A lacking unigene ID's and accession numbers. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons. 5 Pkey: Ref:

Strand: Nt position:

10	Nt_position:	Indicates nucleotide p	ositions of predi	cted exons.
10	Pkey	Ref Strand	Nt_position	
	rkey	rei Silaliu	исрояции	
	332792	Dunham, I. et.al.	Plus	73381-73768
1.5	332816	Dunham, I. et.al.	Plus	359844-360030
15	332906	Dunham, I. et.al.	Plus	1923101-1923205
	332911 332912	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	1961767-1961858 1962120-1962246
	332922	Dunham, I. et.al.	Plus	2009620-2009738
	332956	Dunham, I. et.al.	Plus	2510528-2510658
20	332959	Dunham, I. et.al.	Plus	2518145-2518213
	333138	Dunham, I. et.al.	Plus	3369205-3369323
	333139	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	3369495-3369571
	333221 333380	Dunham, I. et.al.	Plus Plus	3978070-3978187 4904775-4904846
25	333387	Dunham, I. et.al.	Plus	4910935-4910997
	333512	Dunham, I. et.al.	Plus	5560510-5560564
	333524	Dunham, I. et.al.	Plus	5612620-5612780
	333585	Dunham, I. et.al.	.Plus	6234778-6234894
30	333618 333627	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	6582391-6562566 6620584-6620903
50	333628	Dunham, I. et.al.	Plus	6629004-6629233
	333650	Dunham, I. et.al.	Plus	6796852-6797128
	333678	Durham, 1. et.al.	Plus	7068223-7068288
35	333750	Dunham, I. et.al.	Plus	7608165-7608234
22	333763 333767	Ounham, I. et.al. Dunham, I. et.al.	Plus Plus	7692491-7692630 7694407-7694623
	333768	Dunham, I. et.al.	Plus	7695440-7695697
	333769	Dunham, I. et.al.	Plus	7696625-7696707
40	333772	Dunham, I. et.al.	Plus	7706773-7706902
40 -	333777	Dunham, I. et.al.	Plus	7746805-7746916
	333846 333884	Dunham, i. et.al.	Plus Plus	8008623-8008757 8153960-8154161
	333887	Dunham, I. et.al. Dunham, I. et.al.	Plus	8154882-8155025
	333891	Dunham, I. et.al.	Plus	8156437-8156709
45	333892	Dunham, I. et.al.	Plus	8156825-8157001
	333948	Dunham, I. et.al.	Plus	8583497-8583627
	333954 333966	Dunham, I. et.al. Dunham, I. et.al.	Pius Pius	6563186-6563335 8655643-8655826
	333968	Dunham, I. et.al.	Plus	8681004-8681241
50	334061	Dunham, I. et.al.	Plus	9686941-9687077
	334094	Dunham, I. et.al.	Plus	9889953-9890105
	334113 334161	Dunham, I. et.al.	Plus Plus	10282459-10282597 10599033-10599180
	334219	Dunham, I. et.al. Dunham, I. et.al.	Plus	12716160-12716384
55	334239	Dunham, I. et.al.	Plus	13056569-13056693
	334333	Dunham, I. et.al.	Plus	13603544-13603657
	334378	Dunham, I. et.al.	Plus	13907239-13907370
	334382 334562	Dunham, I. et.al. Dunham, I. et.al.	Plus Plus	13915866-13916036 14987847-14987940
60	334588	Dunham, I. et.al.	Plus	15032740-15032817
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<i>(</i>	332984	Dunham, I. et.al.	Minus	2632606-2632457
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	325569		Pius	79927-802	
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) =	325597	5866992	Plus	1065020-1	065089
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	330123	6671869	Minus	35311-35406
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33	326983 326991	5867657 5867660	Minus Plus	16023-16581 18147-18339
	326936	6004446	Minus	10217-10357
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60	327053	6531965	Plus	2247267-2247437
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	327036	6531965	Plus	319951-320040
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	327332	5867516	Minus	56361-56532
	327220 327224	5867525 5867534	Minus Plus	65701-65781 188468-188544
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	327377 327562	5867793 5867804	Minus Minus	37610-37676 343989-344474
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	327606 327611	6004463 5867868	Plus Minus	200262-200495 175063-175392
	327642	5867891	Minus	2513-2743
85	327654 327734	5867910 5867940	Minus Minus	97564-97710 31003-31583
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	327796	5867982	Plus	85267-85405
	327840	6249578	Minus	73065-73206
_	330208	6013599	Plus	66517-66931
5	330263	6671884	Minus	101503-101634
	328004	5867993	Minus	157407-157887
	328101	5868020	Plus	289920-290014
	328100	5868020	Minus	263545-263635
10	328113	5868024	Minus	80378-80491
10	328157	5868064	Plus	73326-73615
	328196	5868080	Minus	16551-16729
	328197	5868081	Minus	42133-42438
	327940	5868197	Minus	95240-95428
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13	328021	5902482	Plus	713478-714590
	328068	6117819	Plus	253903-254022
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	328735	5868289	Plus	89389-89455
	328743	5868289	Plus	274638-274726
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	328342	5868383	Plus	59955-60094
	328365	5868387	Minus	270724-270798
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	328908	5868493	Plus	117002-117059
	328933	5868500	Plus	771755-771889
	328934	5868500	Plus	846342-846448
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	330313	6042030	Minus	33642-33775
	329005	5868542	Plus	85470-85673
	330366	2944106	Plus	151837-151914
	330372	6580495	Minus	317461-317688
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	329037	5868562	Minus	32466-32562
	329067	5868591	Minus	146417-147652
	329134	5868679	Plus	29959-30018
55	329157	5868687	Minus	145940-146155
22	329178	5868704	Plus	179177-179463
	329192	5868716	Plus	166936-167020
	329194	5868716	Minus	304450-304559
	329204	5868720	Minus	3050-3190 27422-27664
60	329224 329228	5868728 5868728	Plus Minus	50118-50287
0 0	329288	5868771	Plus	25554-26299
	329337	5868806	Minus	467155-467222
	329011	6682532	Plus	48658-48741

TABLE 9A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer

Table 9A shows about 1312 genes up-regulated in lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) relative to normal body tissues. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 9B show the accession numbers for those Pkey's lacking UnigenelD's for table 9A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Table 9C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 9A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Pkey: ExAccn:

UnigenelD: Unigene number Unigene Title: Unigene gene title

5

10

Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the average of normal lung samples

Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, aslhma) divided by the average of normal lung samples R1:

20

R2:

	RZ:	VAGIS	e or non-many	litarit ittiig disease sampies (moddong tronomias, empriyo	orna, narvors, arc	NCC10313, ESUN
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
	400195		g	NM_007057*:Homo sapiens ZW10 interactor	1.00	1.00
25	400205			NM_006265*:Homo sapiens RAD21 (S. pombe)	15.80	396.00
	400220			Eos Control	2.28	2.84
	400277			Eos Control	7.68	9.72
	400285			Eos Control	1.00	1.00
~~	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.04	2.24
30	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	132.45	4.00
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	43.86	74.00
	400301	X03635	Hs.1657	estrogen receptor 1	1.00	1.00
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.75	1.65
25	400328	X87344	Hs.180062	transporter 2, ATP-binding cassette, sub	0.87	1.80
35	400419	AF084545		Target	156.55	253.00 2.00
	400512	A F040000		NM_030878*:Homo sapiens cytochrome P450,	1.00 3.67	2.00 87.00
	400517	AF242388		lengsin NM_030878*:Homo sapiens cytochrome P450,	1.00	1.00
	400560 400664			NM_002425:Homo sapiens matrix metallopro	20.26	45.00
40	400665			NM_002425:Homo sapiens matrix metallopro	1.36	1.07
70	400666			NM_002425:Homo sapiens matrix metallopro	3.26	3.22
	400749			NM_003105*:Homo sapiens sortilin-related	1.00	91.00
	400763			Target Exon	7.63	24.00
	401027			Target Exon	1.00	1.00
45	401093			C12000586*:gij6330167[dbj]BAA86477.1] (A	1.00	155.00
	401203			Target Exon	1.00	86.00
	401212			C12000457*:gi[7512178[pir][T30337 polypr	1.00	400.00
	401411			ENSP00000247172*:HYPOTHETICAL 126.2 kDa	1.00	72.00
	401435			C14000397*:gi]7499898[pid][T33295 hypoth	1.00	64.00
50	401464	AF039241		histone deacetylase 5	3.82	49.00
	401714			ENSP00000241802*:CDNA FLJ11007 FIS, CLON	2.02	40.00
	401747			Homo sapiens keratin 17 (KRT17)	128.43	68.00
	401760			Target Exon	1.74	35.00
<i>E E</i>	401780			NM_005557*:Homo sapiens keratin 16 (foca	26.47	10.50
55	401781			Target Exon	10.33	4.61
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	4.13 1.44	2.70 2.10
	401797			Target Exon	1.41	1.86
	401961 401985	AF053004		NM_021626:Homo sapiens serine carboxypep class I cytokine receptor	1.00	177.00
60	401994	AF053004		Target Exon	61.84	47.00
OO	402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00
	402260			NM_001436*:Homo saplens fibrillarin (FBL	1.58	1.39
	402265			Target Exon	2.09	35.00
	402297			Target Exon	1.00	92.00
65	402408			NM_030920*:Homo sapiens hypothetical pro	28.87	13.00
	402420			C1000823*:gi]10432400[emb]CAC10290.1] (A	1.00	1.44
	402674			Target Exon	7.44	243.00
	402802			NM_001397:Homo sapiens endothelin conver	1.00	70.00
=0	402994			NM_002463*:Homo sapiens myxovirus (Influ	1.37	1.43
70	403137			NM_005381*:Homo saplens nucleolin (NCL),	1.00	19.00
	403306	NM_006825		transmembrane protein (63kD), endoplasmi	1.00	43.00
	403329			Target Exon	1.60	61.00
	403381			ENSP00000231844*:Ecotropic virus integra	1.00 28.13	119.00 136.00
75	403478			NM_022342:Homo sapiens kinesin protein 9	20.13	76.00
13	403485			C3001813*:gi 12737279 ref XP_012163.1 k	6.30	29.33
	403627 403715			Target Exon Target Exon	1.30	35.00
	404044			ENSP00000237855*:DJ398G3.2 (NOVEL PROTE)	1.00	54.00
	404076			NM_016020°:Homo sapiens CGI-75 protein (14.29	91.00
80	404076			C8000950:gi[423560]pir [A47318 RNA-bindi	1.00	1.00
00	404140			NM_006510:Homo sapiens ret finger protei	1.42	1.44
	404165			ENSP00000244562:NRH dehydrogenase [quino	1.00	54.00
	404185			Target Exon	1.00	117.00
	404210			NM 005936:Homo sapiens myeloid/lymphoid	5.93	13.77
85	404253			NM_021058*:Homo sapiens H2B histone fami	1.00	1.00
				- ·		

	W	U U2/U804	443			
	404287		•	C6001909:gij704441]dbjjBAA18909.1] (D298	29.71	42.00
	404298			C6001238*:gi 121715 sp P26697 GTA3_CHICK	1.30	1.00
	404347			Target Exon	1.00	1.00
	404440			NM_021048:Homo sapiens melanoma antigen,	1.00	15.00
5					1.00	
,	404721			NM_005596*:Homo sapiens nuclear factor I		60.00
	404794	NM_000078		cholesteryl ester transfer protein, plas	1.07	1.38
	404854			Target Exon	1.61	2.01
	404877			NM_005365:Homo sapiens melanoma antigen,	1.00	1.00
	404927			Target Exon	1.00	1.00
10	404996			Target Exon	1.00	1.00
	405449			CY000047*:gi[11427234 ref[XP_009399.1] z	1.00	1.00
	405568			NM_031413*:Homo sapiens cat eye syndrome	1.00	78.00
					0.76	
	405572			Target Exon		1.14
1 5	405646			C12000200:gi 4557225 ref NP_000005.1 al	1.01	1.28
15	405676	BE336714		cytochrame c-1	1.13	2.89
	405770			NM_002362:Homo saplens melanoma antigen,	45.52	37.00
	405932			C15000305:gij3806122 gbjAAC69198.1] (AF0	1.99	1.99
	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.77	2.38
	406360			Target Exon	1.00	35.00
20	406399			NM_003122*:Homo sapiens serine protease	1.00	39.00
20					1.00	1.00
	406467		11. 404400	Targel Exon		
	406621	X57809	Hs.181125	immunoglobulin lambda tocus	1.41	1.74
	406642	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.16	3.91
	406663	U24683	Hs.293441	Immunoglobulin heavy constant mu	2.07	2.93
25	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	15.00	51.00
	406673	M34996	Hs.198253	major histocompatibility complex, class	0.98	3.09
	406676	X58399	Hs.81221	Human L2-9 transcript of unrearranged Im.	1.30	1.53
	406678	U77534	1.0.0 (22.1	gb:Human clone 1A11 immunoglobulin varia	1.33	1.45
					1.46	2.85
20	406685	M18728	11- 070000	gb:Human nonspecific crossreacting antig		
30	406687	M31126	Hs.272822	pregnancy specific beta-1-glycoprotein 9	8.61	8.50
	406690	M29540	Hs.220529	carcincembryonic antigen-related cell ad	226.37	350.00
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.01	2.52
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	20.25	32.00
	406851	AA609784		major histocompatibility complex, class	0.75	1.91
35	406964	M21305		gb:Human elpha satellite and satellite 3	38.15	1114.00
55	406967	M24349		gb:Human parathyroid hormone-like protel	1.00	1.00
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	1.77	1.10
40	407128	R83312	Hs.237260	EST	1.00	1.00
40	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	142.70	135.00
	407168	R45175	Hs.117183	ESTs	2.16	18.00
	407239	AA076350	Hs.67846	teukocyte immunoglobutin-like receptor,	1.10	1.57
	407242	M18728	1.0.0.0	gb:Human nonspecific crossreacting antig	1.12	2.85
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	3.24	15.38
45					3.53	3.68
43	407289	AA135159	Hs.203349	Homo saplens cDNA FLJ12149 ffs, clone MA		
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	19.74	73.00
	407366	AF026942	Hs.271530	gb:Homo sapiens cig33 mRNA, partial sequ	0.06	8.25
	407378	AA299264	Hs.57776	ESTs, Moderately similar to 138022 hypot	1.00	26.00
	407430	AF169351		gb:Homo sapiens protein tyrosine phospha	1.00	25.00
50	407453	AJ132087		gb:Homo sapiens mRNA for axonemal dynein	1.00	75.00
	407577	AW131324	Hs.246759	hypothetical protein MGC12538	1.00	1.00
	407634	AW016569	Hs.136414	UDP-GicNAc:betaGal beta-1,3-N-acetylgluc	111.20	228.00
	407710	AW022727	Hs.23616	ESTs	1.00	28.00
	407720				1.89	1.31
55		AB037776	Hs.38002	KIAA1355 protein	1.00	1.00
22	407746	AK001962		hypothetical protein FLJ11100		
	407756	AA116021	Hs.38260	ublquitin specific protease 18	4.51	5.00
	407758	D50915	Hs.38365	KIAA0125 gene product	1.00	28.00
	407782	AA608956	Hs.112619	ESTs, Moderately similar to PURKINJE CEL	0.97	1.14
	407788	BE514982	Hs.38991	S100 calcium-bloding protein A2	7.88	3.83
60	407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	3.63	42.00
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	89.96	109.00
	407839	AA045144	Hs.161566	ESTs	173,91	108.00
	407944	R34008	Hs.239727	desmocollin 2	111.30	70.00
					151,17	8.00
65	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kO)		
03	408031	AA081395	Hs.42173	Homo saplens cDNA FLJ10366 fls, clone NT	9.91	93.00
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	195.78	231.00
	. 408070	AW148852		gb:xf05d05.x1 NCI_CGAP_Brn35 Homo sapien	1.00	1.00
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	37.84	61.00
	408122	AJ432652	Hs.42824	hypothetical protein FLJ10718	0.85	1.71
70	408212	AA297567	Hs.43728	hypothetical protein	5.88	7.91
	408243	Y00787	Hs.624	interleukin 8	4.27	9.98
	408349	BE546947	Hs.44276	homeo box C10	3.79	3.46
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.88	1.65
75	408354	Al382803	Hs.159235	ESTs	1.00	73.00
75	408369	R38438	Hs.182575	solute carrier family 15 (H??? transport	1.41	16.50
	408380	AF123050	Hs.44532	diubiquitin	15.19	37.22
	408482	NM_000676	Hs.45743	adenosine A2b receptor	1.65	1.19
	408522	Al541214	Hs.46320	Small proline-rich protein SPRK (human,	1.98	1.24
	408536	AW381532	Hs.135188	ESTs	1.55	1.50
80	408545	AW235405	Hs.253690	ESTs	1.00	1.00
00					1.00	44.00
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A		56.00
	408633	AW963372	Hs.46677	PRO2000 protein	107.16	
	408660	AA525775		ESTs, Moderately similar to PC4259 ferri	1.00	1.00
0.5	408761	AA057264	Hs.238936	ESTs, Weakly similar to (defline not ava	52.24	141.00
85	408771	AW732573	Hs.47584	potassium voltage-galed channel, delayed	3.05	109.00
Ų.						

WO 02/086443 AF192522 Hs.47701 NPC1 (Niemann-Pick disease, type C1, gen 1.02 1.07 408783 neurotrophic tyrosine kinase, receptor, vaccinia related kinase 1 61.00 408790 AW580227 Hs.47860 41.19 Hs.48269 45.00 408805 H69912 24.67 AW438865 Hs.256862 1.00 58.00 408841 **ESTs** 5 408873 AL046017 Hs.182278 calmodulin 2 (phosphorylase kinase, delt 1.00 89.00 serine/threonine kinase 15 guanine nucleotide binding protein (G pr glycoprotein (transmembrane) nmb 408908 BE296227 Hs.250822 7.76 1.00 Hs.71642 1.00 408992 408996 AA059325 1.00 Hs.344096 3.71 Al979168 NM_004553:Homo sapiens NADH dehydrogenas 409015 BE389387 Hs.49767 1.44 1.24 small inducible cytokine subfamily A (Cy Hypothetical protein, XP_051860 (KIAA119 10 409038 T97490 Hs.50002 4.2B 5 32 195.00 Hs.50081 112.42 409041 409077 AR033025 AA401369 Hs.190721 **ESTs** 1.00 17.00 BE243834 Hs.50441 CGI-04 protein 2.02 1.93 409093 40.00 409103 AF251237 Hs.112208 XAGE-1 protein 80 44 15 14.87 SMC4 (structural maintenance of chromoso 6.00 409142 AL136877 Hs.50758 409187 carbamoyl-phosphate synthetase 1, mitoch ESTs, Weakly similar to 2109260A B cell 1.00 1.00 AF154830 Hs.50966 Al654298 Hs.271695 1.22 409228 1.00 AJ879419 Hs.27206 1.00 1.00 409234 23.00 409268 AA625304 Hs.187579 **ESTs** 11.90 20 hypothetical protein FLJ13352 1.00 1.00 409269 AA576953 Hs.22972 NM 005982 Hs.54416 sine oculis homeobox (Drosophila) homolo 168.91 35.00 409361 409404 BE220053 Hs.129056 1.00 1.00 laminin, gamma 2 (nicein (100kD), kalini splicing factor, arginine/serine-rich 5 409420 Z15008 Hs.54451 Hs.346735 79.74 96.00 1.45 2.10 409430 R21945 25 ESTs 409446 Al561173 Hs.67688 1.00 409506 NM_006153 Hs.54589 NCK adaptor protein 1 3.97 28.00 AA075382 AA401369 gb:zm87b03.s1 Stratagene ovarian cancer ESTs 15.98 141.00 409522 Hs.190721 17.00 1.00 409582 Hs.55279 W74001 serine (or cysteine) proteinase inhibito 292.12 79.00 409632 30 Hs.56023 brain-derived neurotrophic factor 1.00 82.00 409705 M37762 Homo sapiens brain tumor associated prot 409719 A1769160 Hs.108681 1.00 1.00 thymosin, beta, identified in neuroblast 0.12 18.12 AA125985 Hs.56145 409731 Homo saplens mRNA; cDNA DKFZp586P2321 (f 409744 AW675258 Hs.56265 20.75 51.00 22.46 1.00 409757 NM_001898 Hs.123114 15.80 35 AW502152 AW247090 gb:UI-HF-BR0p-air-f-11-0-UI.r1 NIH_MGC_5 minichromosome maintenance deficient (S. 1.00 409866 Hs.57101 1.50 1.09 409893 409902 Al337658 Hs.156351 **ESTs** 25.92 50.00 409935 AW511413 Hs.278025 **ESTs** 2.63 2.11 2.17 4.01 inhibin, beta A (activin A, activin AB a 409956 AW103364 Hs.727 40 Hs.57697 NM_001523 hyaluronan synthase 1 2.07 409958 AB041036 Hs.57771 kallikrein 11 1.04 2.28 410001 gb:RC3-BT0319-120200-014-a09 BT0319 Homo 1.00 58.00 410032 BE085985 Hs.58009 KIAA0918 protein 1.00 34.00 AB020725 410037 highly expressed in cancer, rich in leuc 1.00 410044 BE566742 Hs.58169 45 410048 W76467 Hs.58218 profine oxidase homolog 1 03 1 44 1.50 1.12 410076 T05387 Hs.7991 FSTs AW248508 Hs.279727 Homo sapiens cDNA FLJ14035 fis, clone HE 1.00 410102 410153 BE311926 Hs.15830 hypothetical protein FLJ12691 1.00 1.00 hypothetical protein FLJ10514 zinc finger protein 281 hypoxia-inducible protein 2 410166 AK001376 Hs.59346 1.00 1.00 50 42.01 51.00 410193 AJ132592 Hs.59757 410274 AA381807 Hs.61762 1.72 1.00 410309 BE043077 Hs.278153 2.00 75.00 410340 AW182833 Hs.112188 hypothetical protein FLJ13149 32.08 410348 410407 1.00 1.00 AW182663 Hs.95469 Hs.63287 FSTs. 55 carbonic anhydrase IX X66839 410418 D31382 transmembrane protease, serine 4 4.30 2.03 Hs.63325 hypothetical protein KIAA1335 hypothetical protein MGC14128 1.00 18.00 410438 AB037756 Hs.45207 1.34 1.04 410553 AW016824 Hs.255527 a disintegrin and metalloproteinase doma 1.41 410555 W27235 Hs.64311 60 Homo sapiens cDNA: FLJ22044 fis, clone H 410561 BE540255 Hs.6994 10.04 1.00 10.88 18.92 410681 AW246890 Hs.65425 calbindin 1, (28kD) Hs.165028 1.00 57.00 Al375672 **ESTs** 410781 411027 AF072099 Hs.67846 teukocyte immunogłobulin-like receptor, 3.78 adenylate cyclase activating polypeptide cell division cycle 2-like 1 (PTSLRE pr gb:QV3-BT0379-010300-105-g03 BT0379 Homo 411074 X60435 Hs.68137 1 00 1.15 65 411089 AA456454 1.56 1.58 BE069199 1.00 84.00 411152 Hs.334605 Homo sapiens cONA FLJ14408 fis, clone HE 1.82 1.45 411248 AA551538 7.32 3.44 12.74 411252 AB018549 Hs.69328 MD-2 protein kinesin-like 6 (mitotic centromere-assoc 2.55 411263 BE297802 Hs.69360 70 GM2 ganglioside activator protein 1.35 2.02 Hs.289082 411365 M76477 411402 BE297855 Hs.69855 NRAS-related gene 1.00 46.00 411573 AB029000 Hs.70823 KIAA1077 protein 11.40 11.35 Hs.70830 Hs.90063 U6 snRNA-associated Sm-like protein LSm7 1.08 1.90 411579 ACCODS 258 411617 AA247994 neurocalcin della 2.57 75 411732 AA059325 Hs.71642 guanine nucleotide binding protein (G pr 1.02 1.00 411773 NM_006799 AF245505 Hs.72026 protease, serine, 21 (testisin) 2.19 2.19 2.79 Hs.72157 Adlican 411789 microtubule-associated protein 18 23.34 34.00 411800 N39342 Hs.103042 411945 AL033527 Hs.92137 v-myc avian myelocytomatosis viral oncog 1.00 8.00 80 hypothetical protein FLJ10901 1.64 412115 AK001763 Hs.73239 2.07 RAB6 interacting, kinesin-like (rabkines macrophage migration inhibitory factor (118.48 92.00 Hs.73625 Hs.73798 412140 AA219691 BF262621 1.98 1.49 412276 Hs.22826 ESTs, Wealthy similar to 155214 salivary 1.16 1.34 412464 T78141 AA766268 Hs.266273 hypothetical protein FLJ13346 41.52 84.00 412530 85 nuclear transcription factor Y, alpha 412537 AL031778 17.90 55.00

	W	O 02/0864	443			
	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	14.65	47.00
	412719 412723	AW016610	Hs.816	ESTs hypothetical protein AF301222	382.46 54.90	128.00 1.00
	412723	AA648459 H06382	Hs.335951	ESTs	1.00	11.00
5	412817	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	1.63	1.42
	412863	AA121673	Hs.59757	zinc finger protein 281	17.63 1.00	56.00 22.00
	412924 413004	BE018422 T35901	Hs.75258 Hs.75117	H2A histone family, member Y interleukin enhancer binding factor 2, 4	2.19	2.05
	413011	AW068115	Hs.821	biglycan	1.22	1.88
10	413048	M93221	Hs.75182	mannose receptor, C type 1	0.30	6.23
	413063 413129	AL035737 AF292100	Hs.75184 Hs.104613	chitinase 3-like 1 (cartilage glycoprote RP42 homolog	3.43 4.67	8.71 4.77
	413142	M81740	Hs.75212	ornithine decarboxylase 1	1.92	2.59
1.5	413223	AI732182	Hs.191866	ESTs	5.73	27.00
15	413248	T64858 U75679	Hs.21433 Hs.75257	hypothetical protein OKFZp547J036 stem-loop (histone) binding protein	0.99 1.00	1.06 18.00
	413273 413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.10	1.09
	413281	AA861271	Hs.222024	transcription factor BMAL2	95.94	69.00
20	413364	BE536218	Hs.137516 Hs.840	fidgetin-like 1 indoleamine-pyrrole 2,3 dioxygenase	1.00 0.95	1.00 2.09
20	413385 413409	M34455 Al638418	Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.00	1.00
	413453	AA129640	Hs.128065	ESTs	1.00	31.00
	413527	BE250788	Hs.179882	hypothetical protein FLJ12443	1.08 79.15	1.46 114.00
25	413554 413573	AA319146 AI733859	Hs.75426 Hs.149089	secretogranin II (chromogranin C) ESTs	1.00	1.00
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	8.80	10.00
	413597	AW302885	Hs.117183	ESTS	1.00 1.00	1.00 1.00
	413690 413691	BE157489 AB023173	Hs.75478	gb:RC1-HT0375-120200-011-e06 HT0375 Homo ATPase, Class VI, type 11B	3.16	2.32
30	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	2.88	9.52
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	144.10 1.00	108.00 17.00
	413801 413833	M62246 Z15005	Hs.35406 Hs.75573	ESTs, Highly similar to unnamed protein centromere protein E (312kD)	1.00	1.00
	413882	AA132973	Hs.184492	ESTs	64.24	148.00
35	413926	AA133338	Hs.54310	ESTs	1.00 43.42	67.00
	413943 413995	AW294416 BE048146	Hs.144687 Hs.75671	Homo sapiens cDNA FLJ12981 fis, clone NT syntaxin 1A (brain)	45.42 1.23	42.00 1.11
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.02	2.51
40	414142	AW368397	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.00	102.00
40	414180 414245	A1863304 BE148072	Hs.120905 Hs.75850	Homo saplens cDNA FLJ11448 fis, done HE WAS protein family, member 1	6.92 1.00	77.00 1.00
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.00	59.00
	414317	BE263280	Hs.75888	phosphogluconate dehydrogenase	1.52	1.73
45	414334 414341	AA824298 D80004	Hs.21331 Hs.75909	hypothetical protein FLJ10036 KIAA0182 protein	1.78 33.90	1.72 151.00
7.5	414368	W70171	Hs.75939	uridine monophosphate kinase	171.60	97.00
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.32 226.15	1.85 66.00
	414430 414570	Al346201 Y00285	Hs.76118 Hs.76473	ubiquitin carboxyl-terminal esterase L1 insulin-like growth factor 2 receptor	1.64	1.98
50	414618	A1204600	Hs.96978	hypothetical protein MGC10764	1.87	72.00
	414675	R79015	Hs.296281	Interleuidn enhancer binding factor 1	1.51 43.61	1.39 64.00
	414683 414696	S78296 AF002020	Hs.76888 Hs.76918	hypothetical protein MGC12702 Niemann-Pick disease, type C1	28.63	71.00
	414711	Al310440	Hs.288735	Homo sapiens cDNA FLJ13522 fis, clone PL	14.86	42.00
55	414718	H95348	Hs.107987	ESTs	1.00 1.64	5.00 1.44
	414732 414747	AW410976 U30872	Hs,77152 Hs,77204	minichromosoma maintenance deficient (S. centromere protein F (350/400kD, mitosin	65.01	74.00
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	130.35	121.00
60	414774	X02419	Hs.77274	plasminogen activator, urokinase	2.24 1.63	2.19 1.53
60	414806 414809	D14694 Al434699	Hs.77329 Hs.77358	phosphatidylserine synthase 1 transferrin receptor (p90, CD71)	1.97	2.60
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.48	10.60
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian DNA (cytosine-5-)-methyltransferase 1	103.22 1.80	143.00 1.69
65	414839 414883	X63692 AA926960	Hs.77462	CDC28 protein kinase 1	14.29	10.06
0.5	414907	X90725	Hs.77597	poto (Drosophia)-like kinase	1.95	2.20
	414914	U49844	Hs.77613	ataxia telangiectasia and Rad3 related	3.00 1.02	2.90 1.21
	414945 414972	BE076358 BE263782	Hs.77667 Hs.77695	lymphocyte antigen 6 complex, locus E KIAA0008 gene product	1.02	1.00
70	415014	AW954064	Hs.24951	ESTs	1.42	2.84
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00 107.00
	415138 415227	C18356 AW821113	Hs.295944 Hs.72402	tissue factor pathway inhibitor 2 ESTs	34.72 1.87	49.00
	415238	R37780	Hs.21422	ESTs	1.00	1.00
75	415263	AA948033	Hs.130853	ESTs	1.00	1.00
	415295	R41450 NM_015156	Hs.6546 Hs.78398	ESTs KIAA0071 protein	1.00 51.18	1.00 166.00
	415339 415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	30.84	63.00
00	415674	BE394784	Hs.78596	proleasome (prosome, macropain) subunit,	1.48	1.39
80	415709 415735		Hs.278558 Hs.120811	ESTs ESTs, Wealdy similar to 138022 hypotheti	1.00 1.00	1.00 72.00
	415799		Hs.225841	DKFZP434D193 protein	6.23	31.00
	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t	24.30	1.00
85	415857 415989	AA866115 Al267700	Hs.127797	Homo sapiens cONA FLJ11381 fis, clone HE ESTs	32.51 78.89	35.00 1.00
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	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin t	1.00	1.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.35	2.32
	416111 416177	AA033813 AA174069	Hs.79018 Hs.187607	chromatin assembly factor 1, subunit A (ESTs	39.03 1.00	3.00 9.00
5	416178	AI808527	Hs.192822	serologically defined breast cancer anti	3.83	3.76
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	416209 416239	AA236776 AL038450	Hs.79078 Hs.48948	MAD2 (mitotic arrest deficient, yeast, h ESTs	9.70 83.87	1.00 129.00
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	1.96	2.12
10	416322	BE019494	Hs.79217	pyrroline-5-carboxytate reductase 1	2.08	1.73
	416423 416448	H54375 L13210	Hs.268921 Hs.79339	ESTs lectin, galactoside-binding, soluble, 3	1.00 1.28	89.00 1.54
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	27.29	67.00
1.5	416658	U03272	Hs.79432	fibrilln 2 (congenital contractural ara	53.29	51.00
15	416661	AA634543 AA354604	Hs.79440 Hs.122546	IGF-II mRNA-binding protein 3 hypothetical protein FLJ23017	9.96 3.68	5.00 33.00
	416722 416819	U77735	Hs.80205	pim-2 oncogene	1.59	1.84
	416936	N21352	Hs.42987	ESTs, Wealdy similar to S21348 probable	1.00	1.00
20	417034	NM_006183	Hs.80962	neurotensin	1.00 32.95	1.00 156.00
20	417061 417079	A1675944 U65590	Hs.188691 Hs.81134	Homo sapiens cDNA FLJ12033 fis, clone HE interleukin 1 receptor antagonist	3.91	4.93
	417218	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	1.00	51.00
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	3.38	2.05
25	417308 417315	H60720 Al080042	Hs.81892 Hs.180450	KIAA0101 gene product ribosomal protein S24	82.94 106.61	25.36 121.00
	417324	AW265494	1,0,,,,,,,	ESTs	1.20	1.28
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comifin)	8.97	3.27
	417389 417428	BE260964 N87579	Hs.82045 Hs.278871	midkine (neurite growth-promoting factor gb:LL2030F Human fetal heart, Lambda ZAP	2.59 1.00	1.82 52.00
30	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	304.75	173.00
	417466	A1681547	Hs.59457	hypothetical protein FLJ22127	1.24	1.34
	417512 417515	A1979168 L24203	Hs.344096 Hs.82237	glycoprotein (transmembrane) nmb ataxia-telangiectasia group D-associated	2.14 2.66	5.50 1.68
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
35	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	42.76	51.00
	417715 417720	AW969587 AA205625	Hs.86366 Hs.208067	ESTs ESTs	6.35 113.31	2.75 56.00
	417791	AW965339	Hs.111471	ESTs	39.98	16.00
40	417830	AW504786	Hs.122579	hypothetical protein FLJ 10461	2.61	31.00
40	417866 417900	AW067903 BE250127	Hs.82772 Hs.82906	collagen, type XI, alpha 1 CDC20 (cell division cycle 20, S. cerevi	2.35 1.52	2.44 1.11
	417933	X02308	Hs.82962	thymidylate synthetase	4.74	2.55
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.61	5.21
45	417975	AA641836	Hs.30085	hypothetical protein FLJ23186 ESTs	12.49 1.00	38.00 26.00
73	417991 418004	AA731452 U37519	Hs.190008 Hs.87539	aldehyde dehydrogenase 3 family, member	3.02	2.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	187.59	1.00
	418054	NM_002318	Hs.83354 Hs.83363	lysyl oxidase-like 2 coagulation factor VIII-associated (intr	2.85 1.54	2.63 1.69
50	418057 418113	NM_012151 Al272141	Hs.83484	SRY (sex determining region Y)-box 4	6.82	5.22
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	1.26	1.46
	418203 418207	X54942 C14685	Hs.83758 Hs.34772	CDC28 prolein kinase 2 ESTs	134.19 1,00	144.00 1.00
	418216	AA662240	Hs.283099	AF15q14 protein	64.66	61.00
55	418236	AW994005	Hs.337534	ESTs	18.53	147.00
	418249 418281	H89226 U09550	Hs.34892 Hs.1154	KIAA1323 protein oviductal glycoprotein 1, 120kD (mucin 9	30.53 1.00	106.00 3.00
	418283	S79895	Hs.83942	cathepsin K (pycnodysoslosis)	3.96	5.16
60	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.18	2.91
60	418322 418327	AA284166 U70370	Hs.84113 Hs.84136	cyclin-dependent kinase Inhibitor 3 (CDK paired-like homeodomain transcription fa	11.96 9.23	6.68 2.22
	418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	1.00	1.00
	418379	AA218940	Hs.137516	fidgetin-like 1	21.68	44.00
65	418397 418403	NM_001269 D86978	Hs.84746 Hs.84790	chromosome condensation 1 KIAA0225 protein	1.00 16.91	8.00 18.98
05	418462	BE001596	Hs.85266	Integrin, beta 4	1.56	1.16
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.22	2.38
	418506 418526	AA084248 BE019020	Hs.85339 Hs.85838	G protein-coupled receptor 39 solute carrier family 16 (monocarboxylic	2.66 2.04	2.22 2.21
70	418538	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor	1.33	37.00
	418543	NM_005329	Hs.85962	hyaturonan synthase 3	1.04	1.23
	418574 418592	N28754 X99226	Hs.284153	M-phase phosphoprotein 9 Fanconi anemia, complementation group A	48.60 18.24	85.00 26.00
	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.19	1.41
75	418661	NM_001949	Hs.1189	E2F transcription factor 3	29.05	43.00
	418663	AK001100 NM 001327	Hs.41690 Hs.87225	desmocollin 3 cancerflestis antigen	112.17 1.18	19.00 1.10
	418678 418686	NM_001327 Z36830	Hs.87268	annexin A8	1.54	1.10
00	418689	Al360883	Hs.274448	hypothetical protein FLJ11029	1.19	1.04
80	418712	Z42183	Lie Danna	gb:HSC0BF041 normalized Infant brain cDN	1.00	12.00
•	418727 418738	AA227609 AW388633	Hs.94834 Hs.6682	ESTs solute carrier family 7, (cationic amino	1.00 49.85	49.00 1.00
	418819	AA228776	Hs.191721	ESTs	1.00	140.00
85	418830	BE513731	Hs.88959	hypothetical protein MGC4816	20.97 57.09	23.00 35.00
O)	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	80.10	33.00

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	418971	AA360392	Hs.87113	ESTs	1.00	12.00
	418973 419078	AA233056 M93119	Hs.191518 Hs.89584	ESTs insulinoma-associated 1	4.89 1.00	28.00 10.00
_	419079	AW014836	Hs.18844	ESTs	1.09	1.98
5	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	2.06 15.60	1.68 51.00
	419088 419092	AI538323° J05581	Hs.52620 Hs.89603	integrin, beta 8 mucin 1, transmembrane	1.11	1,83
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00
10	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	1.10 1.00	1.14 1.00
10	419183 419216	U60669 AU076718	Hs.89663 Hs.164021	cytochrome P450, subfamily XXIV (vitamin small inducible cytokine subfamily B (Cy	3.18	2.43
	419288	AA256106	Hs.87507	ESTs	1.00	34.00
	419335	AW950146	Hs.284137	hypothetical protein FLJ12888	1.00 22.63	8.00 54.00
15	419354 419359	M62839 Alo43202	Hs.1252 Hs.90073	apolipoprotein H (beta-2-glycoprotein I) chromosome segregation 1 (yeast homolog)	2.50	1.98
	419423	D26488	Hs.90315	KIAA0007 protein	1.00	7.00
	419443	D62703	11- 00570	gb:HUM316G108 Clontech human aorta polyA	1.00 1.64	12.00 1.84
	419452 419474	U33635 AW968619	Hs.90572 Hs.155849	PTK7 protein tyrosine kinase 7 ESTs	13.63	62.00
20	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	4.27	2.26
	419488 419502	AA316241 AU076704	Hs.90691	nucleophosmin/nucleoplasmin 3 fibrinogen, A alpha polypeptide	3.66 13.05	3.63 115.00
	419539	AF070590	Hs.90869	Homo saplens clones 24622 and 24623 mRNA	74.60	117.00
25	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	1.47	4.98
25	419569 419594	AI971651 AA013051	Hs.91143 Hs.91417	jagged 1 (Alagille syndrome) topolsomerase (DNA) II binding protein	1.00 94.30	4.00 94.00
	419703	Al793257	Hs.128151	ESTs	15.26	50.00
	419721	NM_001650	Hs.288650	aquaporin 4	1.00 1.00	191.00 59.00
30	419729 419741	AA586442 NM_007019	Hs.21411 Hs.93002	gb:no53a03.s1 NCI_CGAP_SS1 Homo sapiens ubiquitin carrier protein E2-C	2.02	1.08
-	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	1.00	1.00
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z phospholipase A2, group VII (platelet-ac	29.87 50.99	77.00 214.00
	419839 419936	U24577 Al792788	Hs.93304	gb:ol91d05.y5 NCI_CGAP_Kid5 Homo sapiens	1.00	1.00
35	419937	AB040959	Hs.93836	DKFZP434N014 protein	1.64	2.47
	419983 420005	W55956 AW271106	Hs.94030 Hs.133294	Homo sapiens mRNA; cDNA DKFZp586E1624 (f ESTs	15.72 3.15	94.00 1.43
	420047	A1478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	12.45	39.00
40	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	1.00	117.00 1.21
40	420162 420251	BE378432 AW374968	Hs.95577 Hs.348112	cyclin-dependent kinase 4 Human DNA sequence from clone RP5-1103G7	1.43 2.35	3.23
	420259	AF004884	Hs.96253	catcium channel, voltage-dependent, P/Q	0.77	1.15
	420281	A1623693	Hs.323494	ESTs ESTs, Weakly similar to ALU5_HUMAN ALU S	45.04 49.22	54.00 31.00
45	420309 420332	AW043637 NM_001756	Hs.21766 Hs.1305	serine (or cysteine) proteinase inhibito	0.05	2.82
	420380	AA640891	Hs.102406	ESTs	0.99	2.74
	420462 420520	AF050147 AK001978	Hs.97932 Hs.98510	chondromodulin 1 precursor similar to rab11-binding protein	1.00 49.74	1.00 133.00
	420552	AK000492	Hs.98806	hypothetical protein	94.65	88.00
50	420560	AW207748	Hs.59115	ESTs distal-less homeo box 5	1.00 1.00	17.00 13.00
	420610 420689	Al683183 H79979	Hs.99348 Hs.88678	ESTs	50.09	95.00
	420721	AA927802	Hs.159471	ZAP3 protein	1.00	31.00
55	420759 420783	T11832 Al659838	Hs.127797 Hs.99923	Homo saplens cDNA FLJ11381 fis, clone HE lectin, galactoside-binding, soluble, 7	1.00 3.04	48.00 1.25
33	420900	AL045633	Hs.44269	ESTs	2.24	7.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00 27.00
	421002 421027	AF116030 AA761198	Hs.100932 Hs.55254	transcription factor 17 ESTs	1.00 2.87	38.00
60	421037	AI684808	Hs.197653	ESTs	1.00	46.00
	421041	N36914	Hs.14691	ESTs, Moderately similar to 138022 hypot	1.00 1.34	98.00 1.46
	421073 421110	NM_004689 AJ250717	Hs.101448 Hs.1355	metastasis associated 1 cathepsin E	119.47	427.00
~~	421133	AA401369	Hs.190721	ESTs	1.10	17.00
65	421150	AI913562	Hs.189902	ESTs	1.45 1.00	1.63 15.00
	421155 421307	H87879 BE539976	Hs.102267 Hs.103305	lysyl oxidase Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.37	1.10
	421316	AA287203	Hs.324728	SMA5	1.00	21.00 3.94
70	421379 421451	Y15221 AA291377	Hs.103982 Hs.50831	small inducible cytoldne subfamily B (Cy ESTs	1.92 5.89	14.00
, 0	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	1.56 5.11	1.08 5.23
	421508 421515	NM_004833 Y11339	Hs.105115 Hs.105352	absent in melanoma 2 GalNAc alpha-2, 6-slalyltransferase I, I	1.00	3.00
75	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	2.63	10.58
	421526	AL080121	Hs.105460	DKFZP56400823 protein secreted frizzled-related protein 4	1.46 30.21	1.88 50.32
	421552 421574		Hs.105700 Hs.105924		1.67	1,74
90	421582	AI910275		trefoil factor 1 (breast cancer, estroge	1.23	1.00
80	421633 421659		Hs.106260 Hs.106511	sorting nexin 10 protocadherin 17	1.00 0.05	116.00 6.33
	421677	H64092	Hs.38282	ESTs	1.31	1.42
	421753	BE314828	Hs.107911	ATP-binding cassette, sub-family B (MDR/	1.41 1.12	1.20 1.14
85	421773 421777		Hs.112457 Hs.108196		1.12	1.29

WO 02/086443 421800 AA298151 Hs.222969 1.03 1.30 ATP-binding cassette, sub-family C (CFTR 1.59 421817 AF146074 Hs.108660 1.88 22.80 11.84 421896 N62293 Hs 45107 **ESTs** 90.00 AF013758 Hs.109643 polyadenylate binding protein-interactin 421928 5 gamma-aminobutyric acid (GABA) A recepto 421931 NM_000814 Hs.1440 1.13 1.49 20.25 keratin 6A 421948 L42583 Hs.334309 51.83 hypothetical protein FLJ11856 AW961017 U80736 1.17 1.15 421975 Hs.6459 trinucleotide repeat containing 9 Hs.110826 422026 Hs.272027 F-box only protein 5 67.61 62.00 422094 AF129535 resolventy protein FLJ22704 gastrin-releasing peptide gb:QV0-OT0033-010400-182-a07 OT0033 Homo 10 2.34 422095 AI868872 Hs.282804 4.37 95.50 4.18 422109 S73265 Hs.1473 AW881145 71.00 422128 422129 AU076635 serine (or cysteine) proteinase inhibito 1.13 1.38 Hs.1478 mitochondrial ribosomal protein L42 protease inhibitor 3, sidn-derived (SKAL S100 calcium-binding protein A7 (psorias 96.00 422134 AW179019 Hs.112110 41.59 15 L10343 AA586894 2.37 1.10 422158 Hs.112341 Hs.112408 1.68 422168 422278 AF072873 Hs.114218 frizzled (Drosophila) homolog 6 4.93 5.73 apolipoprotein L CDC45 (cell division cycle 45, S.cerevis cytochrome P450, subfamily IIS, polypept 422282 AF019225 Hs.114309 1 49 171 25.99 10.91 422283 AW411307 Hs.114311 20 1.54 Hs.98370 1.41 422310 AA316622 Hs.114948 cytokine receptor-like factor 1 1.15 1.78 AF073515 422311 422330 D30783 Hs.115263 1.00 112.00 C-type (calcium dependent, carbohydrate-Opa-interacting protein 5 prostate differentiation factor 60.00 Hs.115515 Hs.116206 9.39 422364 AF067800 18.33 53.00 422406 AF025441 25 Hs.296638 3.21 422424 A1186431 Hs.116724 32.00 422440 NM_004812 aldo-keto reductase family 1, member 810 47.53 73.68 35.54 mucin 4, tracheobronchial 422487. AJ010901 Hs.198267 collagen, type XVII, alpha 1 173.97 26,00 Hs.117938 AU076442 422511 AW500470 Hs.117950 multifunctional polypeptide similar to S 2.92 422515 mutuinctional polypepuoe similar to S LIM homeobox protein 2 collagen, type III, alpha 1 (Ehlers-Danl glycoprotein hormones, alpha polypeptide baculoviral IAP repeat-containing 5 (sur hypothetical protein FLJ 10549 cartilage oligomeric matrix protein (pse centromere protein A (17KD) 30 422656 1.00 1.00 AI870435 Hs.1569 Hs.119571 3.89 4.55 422737 M26939 Hs.119689 AA441787 422756 422765 AW409701 Hs.1578 3.88 1.53 Hs.121028 53.00 422809 AK001379 99.56 35 1.69 3.17 422867 L32137 Hs.1584 Hs.1594 70.46 61.00 NM_001809 42293B ECT2 protein (Epithelial cell transformi Hs.122579 77 74 3.00 422956 8.55 cadherin 13, H-cadherin (heart) 5.88 AW890487 AA401369 422960 Hs.63984 171.41 17.00 Hs.190721 **ESTs** 422963 40 AU076657 chaperonin containing TCP1, subunit 5 (e 2.12 1.62 422976 Hs.1600 35.00 422981 AF026445 Hs.122752 TATA box binding protein (TBP)-associate 10.49 Hs.221974 12.40 32.47 422986 AA319777 ESTs gb:DKFZp761A092_r1 761 (synonym: hamy2) 60.00 AL 119930 423034 ESTs, Moderately similar to HXDA_HUMAN H sperm associated antigen 4 423049 X59373 Hs.188023 1.00 1.00 45 423081 AF262992 Hs.123159 1.82 2.96 1.53 423184 NM_004428 NM_000094 Hs 1624 enhrin-A1 Hs.1640 collagen, type VII, alpha 1 (epidermolys 2.14 1.69 423217 Hs.125845 ribulose-5-phosphate-3-epimerase 7.18 14.00 423248 21.90 sushi-repeat protein 64.00 423309 BE006775 Hs.126782 50 1.00 423361 423453 AW170055 **ESTs** Hs.47628 Hs.128791 CGI-09 protein 55.52 66.00 AW450737 423511 AF036329 Hs.129715 gonadotropin-releasing hormone 2 0.88 1.17 1.76 5.40 ligand of neuronal nitric oxide synthase 423516 AB007933 Hs.129729 Hs.233785 423551 AA327598 ESTs 55 1.00 50.00 M90516 Hs.1674 glutamine-fructose-6-phosphate transamin 423554 423575 Hs.163443 Homo sapiens cDNA FLJ11576 fis, clone HE 38 88 70.00 C18863 1.00 67.00 Hs.166368 Hs.1690 423624 AI807408 1.00 AW959908 heparin-binding growth factor binding pr 423634 Hs.157148 hypothetical protein MGC13204 19.14 5B.00 423642 AW452650 60 13.57 423662 AA642452 Hs.130881 B-cell CLL/lymphoma 11A (zinc finger pro 3.61 matrix metalloproteinase 12 (macrophage DKFZp434J1813 protein 240.73 40.00 423673 BE003054 AA329796 Hs.1695 59.00 Hs.1098 423698 hypothetical protein LOC57822 paired box gene 9 4.20 1.00 AJ403108 Hs.132127 1.00 423725 1.00 423761 NM_006194 Hs.132576 nuclear pore complex protein 65 7.18 6.64 A 1295745 423787 Hs.236204 44.00 hypothetical protein 1.00 AF151064 423816 cocaine- and amphetamine-regulated trans 'Homo saplens mRNA; cDNA DKFZp761J1324 (f U20325 Hs.1707 1.00 1.00 423826 Hs.133315 Hs.134585 Hs.159234 1.00 423849 AL157425 1.00 DKFZP434G232 protein forkhead box E1 (thyroid transcription f 1.00 1.00 423887 423934 AL080207 70 U89995 31.00 KIAA1632 protein osteoblast specific factor 2 (fasciclin 423954 AW753164 Hs.288604 5.81 10.87 3.30 423961 D13666 Hs.136348 3.55 tumor protein 63 kDa with strong homolog 233.42 68.00 424012 424016 AW368377 Hs.137569 hypothetical protein MGC15730 0.93 1.01 AW163729 Hs.6140 75 424028 AF055084 Hs.153692 Homo saplens cDNA FLJ14354 fis, clone Y7 21.30 52.00 1.00 serine (or cysteine) proteinase inhibito 1.00 424046 AF027866 Hs.138202 21.91 70.00 Hs.102267 lysyl oxidase 424086 A1351010 424098 AF077374 Hs.139322 small proline-rich protein 3 137.82 54.00 Hs.290270 1.00 1.00 424120 T80579 80 1.00 AW582904 34.00 islet amylold polypeptide gb:EST41944 Endometrial tumor Homo sapie 424165 Hs.142255 48.00 AA337221 L29306 13.06 424200 1.00 Hs.171814 tryptophan hydroxylase (tryptophan 5-mon 424279 AW975531 87.00 302.00 Hs.154443 minichromosome maintenance deficient (S. 164,58 424308 424326 NM_014479 Hs.145296 disintegrin protease 53.72 85 0.88 1.15

AA339036

424340

FSTs

Hs.7033

	W	O 02/086	443			
	424351	BE622117	Hs.145567	hypothetical protein	0.93	1.03
	424364 424381	AW383226 AA285249	Hs.201189 Hs.146329	ESTs, Weakly similar to G01763 atrophin- protein kinase Chk2	7.02 95.55	3.24 92.00
_	424411	NM_005209	Hs.146549	crystallin, beta A2	1.63	3.25
5	424420	BE614743	Hs.146688	prostaglandin E synthase	1.63	1.33
	424441 424502	X14850	Hs.147097 Hs.149585	H2A histone family, member X	1.82 1.00	1.29 1.00
	424502	AF242388 X06256	Hs.149509	lengsin Integrin, alpha 5 (fibronectin receptor,	1.02	2.24
10	424513	BE385864	Hs.149894	mitochondrial translational initiation f	1.00	17.00
10	424539	L02911	Hs.150402	Activin A receptor, type 1 (ACVR1) (ALK	32.46	108.00 2.58
	424568 424602	AF005418 AK002055	Hs.150595 Hs.151046	cytochrome P450, subfamily XXVIA, polype hypothetical protein FLJ11193	3.40 31.87	25.00
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.58	2.37
15	424645	NM_014682	Hs.151449	KIAA0535 gene product	1.00	1.00
15	424687 424717	J05070 AW992292	Hs.151738 Hs.152213	matrix metalloproteinase 9 (gelatinase B wingless-type MMTV integration site fami	2.12 1.00	2.23 1.00
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ 10570 fis, clone NT	56.19	12.00
	424840	D79987	Hs.153479	extra spindle poles, S. cerevislae, homo	2.65	1.30
20	424867 424905	A1024860 NM_002497	Hs.153591 Hs.153704	Not56 (D. melanogaster)-like protein NIMA (never in mitosis gene a)-related k	1.23 21.35	1.05 1.00
20	424979	D87989	Hs.154073	UDP-galactose transporter related	1.36	1.35
	424999	AW953120		gb:EST365190 MAGE resequences, MAGB Horno	1.24	1.41
	425048 425057	H05468 AA826434	Hs.164502 Hs.1619	ESTs achaete-scute complex (Drosophila) homol	1.00 7.46	11.00 87.00
25	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	2.52	3.82
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase	4.84	4.03
	425159 425202	NM_004341 AW962282	Hs.154868 Hs.152049	carbamoyl-phosphate synthetase 2, aspart ESTs, Wealdy similar to 138022 hypotheti	3.62 1.00	2.73 53.00
	425202	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	100.77	44.00
30	425236	AW067800	Hs.155223	stanniocatcin 2	3.30	2.90
	425245	A1751768 NM_005940	Hs.155314 Hs.155324	KIAA0095 gene product matrix metalloproteinase 11 (stromelysin	1.91 1.41	2.32 1.49
	425247 425266	J00077	Hs.155421	alpha-fetoprotein	1.00	68.00
25	425274	BE281191	Hs.155462	minichromosoma maintenance deficient (mi	1.97	1.63
35	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	141.49 1.00	123.00 84.00
	425349 425371	AA425234 D49441	Hs.79886 Hs.155981	ribose 5-phosphate isomerase A (ribose 5 mesothelin	0.87	1.59
	425397	J04088	Hs.156346	topoisomerase (DNA) li alpha (170kD)	14.90	5.76
40	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00	1.00 9.74
40	425424 425483	NM_004954 AF231022	Hs.157199 Hs.158159	ELKL motif kinase FAT tumor suppressor (Drosophila) homolo	10.58 1.74	1.40
	425566	AW162943	Hs.250618	UL16 binding protein 2	1.49	1.14
	425580	L11144	Hs.1907	galanin	53.29 33.45	233.00 1.00
45	425650 425692	NM_001944 D90041	Hs.1925 Hs.155956	desmoglein 3 (pemphigus vulgaris antigen N-acetyltransferase 1 (arylamine N-acety	1,00	55.00
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-recept	1.00	10.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	1.00 1.00	41.00 48.00
	425776 425810	U25128 Al923627	Hs.159499 Hs.31903	parathyrold hormone receptor 2 ESTs	27.39	98.00
50	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.99	1.58
	425849	AI077288	Hs.296323 Hs.159651	serum/glucocorticold regulated kinase death receptor 6, TNF superfamily member	71.16 1.35	3.42 1.34
	425852 426067	AK001504 AA401369	Hs.190721	ESTs	1.01	17.00
~ ~	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	26.26	47.00
55	426215 426227	AW067800 U67058	Hs.155223 Hs.154299	stannlocatcin 2 Human proteinase activated receptor-2 mR	1.91 22.40	2.90 25.00
	426269	H15302	Hs.168950	Homo saplens mRNA; cDNA DKFZp566A1046 (f	1.00	1.00
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	91.39	229.00
60	426329 426427	AL389951 M86699	Hs.271623 Hs.169840	nucleoporin 50kD TTK protein kinase	4.34 7.02	4.08 1.00
00	426432	AF001601	Hs.169857	paraoxonase 2	1.16	1.68
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.59	1.71
	426459 426471	AF151812 M22440	Hs.169992 Hs.170009	hypothatical 43.2 Kd protein transforming growth factor, alpha	1.56 20.60	1.66 26.00
65	426496	D31765	Hs.170114	KIAA0061 protein	9.81	22.00
	426501	AA401369	Hs.190721	ESTs	19.23	17.00
	426514 426536	BE616633 Al949749	Hs.170195 Hs.44441	bone morphogenetic protein 7 (osteogenic ESTs	103.74 4.65	41.00 23.00
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	1.00	43.00
70	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	160.06	8.00
	426691	NM_006201 J03626	Hs.171834 Hs.2057	PCTAIRE protein kinase 1 uridine monophosphate synthetase (orotat	1.51 2.13	1.35 1.68
	426746 426752	X69490	Hs.172004	titin	0.02	5.14
76	426784	U03749	Hs.172216	chromogranin A (parathyrold secretory pr	1.72	1.71
75	426807 426812	AA385315 AF105365	Hs.156682	ESTs solute carrier family 12 (potassium/chlo	1.30 1.47	1.64 1.53
	426814	AF036943	Hs.172613 Hs.172619	myelin transcription factor 1-like	1.00	1.00
	426831	BE296216	Hs.172673	S-adenosythomocysteine hydrolase	1.51	1.25
80	426897 426925	AA401369 NM_001196	Hs.190721 Hs.315689	ESTs Homo sapiens cDNA: FLJ22373 fis, clone H	141.56 32.61	17.00 38.00
30	426925 426935	NM_000088	Hs.172928	collagen, type I, alpha 1	2.65	3.16
	426964	AA393739	Hs.287416	Homo sapiens cDNA FLJ11439 fis, clone HE	1.97	3.49
	426966 426991	Al493134 AK001536		sclerostin Homo sapiens cDNA FLJ10674 fis, clone NT	1.00 3.39	1.00 2.28
85	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00

	W	O 02/0864				
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.58 1.34	1.05 1.60
•	427260 427281	AA663848 AA906147	Hs.102869	gb:ae70b06.s1 Stratagene schizo brain S1 ESTs	1.00	66.00
	427335	AA448542	Hs.251677	Gantigen 7B	51.83	4.00
5	427354	T57896	Hs.191095	ESTs	1.17	1.95
	427356	AW023482	Hs.97849	ESTs	7.31 1.00	41.00 57.00
	427376 427383	AA401533 NM_005411	Hs.19440 Hs.177582	ESTs surfactant, pulmonary-associated protein	0.42	1.32
	427427	AF077345	Hs.177936	lectin, superfamily member 1 (cartilage-	1.00	20.00
10	427441	AA412605	Hs.343879	SPANX family, member C	1.00	1.00
	427445	X80818	Hs.178078 Hs.178761	glutamate receptor, metabolropic 4 26S proteasome-associated pad1 homolog	0.97 4.60	1.03 4.04
	427505 427510	AA361562 Z47542	Hs.179312	small nuclear RNA activating complex, po	22.00	45.00
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	97.45	92.00
15	427546	AA188763	Hs.36793	hypothetical protein FLJ23188	1.50 6.81	3.24 40.00
	427562 427585	R56424 D31152	Hs.26534 Hs.179729	ESTs collagen, type X, alpha 1 (Schmid metaph	69.91	62.00
	427660	Al741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.70	49.00
20	427666	Al791495	Hs.180142	calmodulin-like skin protein	1.37	1.88 67.00
20	427668	AA298760 NM_007045	Hs.180191 Hs.180296	hypothetical protein FLJ14904 FGFR1 oncogene partner	29.55 3.52	2.63
	427677 427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.84	70.00
25	427719	Al393122	Hs.134726	ESTs	7.03 2.92	4.52 1.74
25	427722 427747	AK000123 AW411425	Hs.180479 Hs.180655	hypothetical protein FLJ20116 serine/threonine kinase 12	1.76	1.26
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfami	9.63	59.00
	427961	AW293165	Hs.143134	ESTs	41.97 23.82	118.00 1.00
30	428004 428023	AA449563 AL038843	Hs.151393	glutamate-cysteine ligase, catalytic sub Homo sapiens cDNA: FLJ23602 fis, clone L	1,40	1.33
30	428046	AW812795	Hs.337534	ESTs, Moderately similar to 138022 hypot	96.28	167.00
	428093	AW594506	Hs.104830	ESTs	1.25	1.29
	428098	AU077258	Hs.182429 Hs.26912	protein disulfide isomerase-related prot ESTs	1.86 1.00	1.60 42.00
35	428129 428169	Al244311 Al928984	Hs.182793	golgi phosphoprotein 2	2.76	2.11
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00
	428227	AA321649	Hs.2248 Hs.2250	small Inducible cytokine subfamily B (Cy leukemia inhibitory factor (chollnergic	85.59 8.57	181.00 21.64
	428242 428330	H55709 L22524	Hs.2256	matrix metalloproleinase 7 (matrilysin,	7.77	15.90
40	428434	A1909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	0.58	1.43
	428450	NM_014791	Hs.184339	KIAA0175 gene product	237.53 6.00	204.00 4.60
	428471 428479	X57348 Y00272	Hs.184510 Hs.334562	stratifin cell division cycle 2, G1 to S and G2 to	56.54	16.00
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.53	2.15
45	428505	AL035461	Hs.2281	chromogranin B (secretogranin 1)	1.00 1.00	1.00 58.00
	428532 428645	AF157326 AA431400	Hs.184786 Hs.98729	TBP-interacting protein ESTs, Weakly similar to 2017205A dihydro	1.00	16.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.00	1.00
50	428698	AA852773	Hs.334838	KIAA1866 protein	187.37 47.24	255.00 80.00
50	428728 428748	NM_016625 AW593206	Hs.191381 Hs.98785	hypothetical protein Ksp37 protein	1.00	87.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	428771	AB028992	Hs.193143	KIAA1069 protein	1.98 4.67	92.00 6.15
55	428801 428810	AW277121 AF068236	Hs.254881 Hs.193788	ESTs nitric oxide synthase 2A (inducible, hep	1.67 1.03	1.27
55	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	124.17	43.00
	428845	AL157579	Hs.153610	KIAA0751 gene product	1.00	1.00
	428959	AF100779 AF120274	Hs.194680 Hs.194689	WNT1 inducible signaling pathway protein artemin	15.16 1.36	27.00 1.24
60	428969 429038	AL023513	Hs.194766	seizure related gene 6 (mouse)-like	0.97	3.31
	429065	A1753247	Hs.29643	Homo sapiens cONA FLJ13103 fis, clone NT	6.82	16.47
	429164 429170	Al688663 NM_001394	Hs.116586 Hs.2359	ESTs dual specificity phosphatase 4	19.08 16.18	67.00 105.00
	429183	AB014604	Hs.197955	KIAA0704 protein	79.72	104.00
65	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.00	1.00
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3 ESTs	1.33 1.00	1.09 7.00
	429220 429228	AW207206 Al553633	Hs.326447	ESTs	39.47	29.25
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18
70	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07 3.70	1.00 142.00
	429276 429359	AF056085 W00482	Hs.198612 Hs.2399	G protein-coupled receptor 51 matrix metalloproteinase 14 (membrane-in	1.30	1.94
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	94.09	86.00
75	429413	NM_014058	Hs.201877	DESC1 protein	41.91 12.19	10.00 1.00
75	429486 429504	AF155827 X99133	Hs.203963 Hs.204238	hypothetical protein FLJ10339 lipocalin 2 (oncogene 24p3)	1.61	1.08
	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90
	429547	AA401369	Hs.190721	ESTs	1.06	17.00
80	429551 429563	AW450624 BE619413	Hs.220931 Hs.2437	ESTs eukaryotic translation initiation factor	2.8 9 1.49	65.00 1.37
JU	429597		Hs.2442	a disinlegrin and metalloproteinase doma	61.86	100.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	429612		Hs.252587 Hs.120845	pituitary tumor-transforming 1 ESTs	2.78 1.00	1.74 1.00
85	429616 429656		Hs.211584	neurofilament, light polypeptide (68kD)	1.00	4.00

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	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	69.95	104.00
	429736 429782	AF125304 NM_005754	Hs.212680 Hs.220689	tumor necrosis factor receptor superfami Ras-GTPase-activating protein SH3-domain	1.25 1.00	1.21 7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00
5	429918	AW873986	Hs.119383	ESTs	1.00	78.00
	429978 429986	AA249027	Hs.227277	ribosomal protein S6 sine oculis homeobox (Drosophila) homolo	1.98 1.00	3.09 48.00
	429900	AF092047 AA464510	Hs.152812	ESTs	69.27	59.00
4.0	430114	AA847744	Hs.99640	ESTs	1.00	1.00
10	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.00 1.10	51.00 2.22
	430147 430287	R60704 AW182459	Hs.234434 Hs.125759	hairy/enhancer-of-split related with YRP ESTs, Weakly similar to LEU5_HUMAN LEUKE	1.00	127.00
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.80	1.47
15	430300	U60805	Hs.238648	oncostatin M receptor	1.00 92.31	35.00 28.00
15	430315 430337	NM_004293 M36707	Hs.239147 Hs.239600	guanine deaminase calmodulin-like 3	1.18	1.08
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	5.28	66.00
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	16.76 1.63	38.00 1.50
20	430393 430439	BE185030 AL133561	Hs.241305	estrogen-responsive B box protein DKFZP434B061 protein	1.00	1.00
20	430451	AA836472	Hs.297939	cathepsin B	1.64	2.12
	430454	AW469011	Hs.105635	ESTs CONTACT OF THE PARTY OF TH	63.35 2.47	44.00 1.91
	430466 430481	AF052573 AA479678	Hs.241517 Hs.203269	polymerase (DNA directed), theta ESTs, Moderately similar to ALU8_HUMAN A	1.00	31.00
25	430486	BE052109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00
	430508	Al015435	Hs.104637	ESTs	4.75	7.27
	430533 430563	AA480895 AF146074	Hs.57749 Hs.108660	ESTs, Weakly similar to T17288 hypotheti ATP-binding cassette, sub-family C (CFTR	1.00 1.00	1.00 1.59
	430677	Z26317	Hs.94560	desmoglein 2	1.72	1.30
30	430678	AA401369	Hs.190721	ESTs	0.90	17.00
	430686 430788	NM_001942 Al742925	Hs.2633 Hs.7179	desmoglain 1 ESTs, Weakly similar to 2004399A chromos	1.00 1.62	1.00 1.84
	430890	X54232	Hs.2699	glypican 1	1.58	1.40
25	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	90.28	132.00
35	430985 431009	AA490232 BE149762	Hs.27323 Hs.48956	ESTs, Weakly similar to 178885 serine/th gap junction protein, beta 6 (connexin 3	0.94 60.25	1.28 28.00
	431089	BE041395	113.40330	ESTs, Weakly similar to unknown protein	23.32	941.00
	431092	Al332764	Hs.125757	ESTs	13.46	63.00
40	431124	AF284221	Hs.59506	doublesex and mab-3 related transcriptio Homo sapiens cDNA: FLJ23494 fis, clone L	49.43 0.44	62.00 2.20
40	431164 431211	AA493650 M86849	Hs.94367 Hs.323733	gap junction protein, beta 2, 26kD (conn	182.26	101.00
	431221	AW207837	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	4.15	13.97
	431277	AA501806	Hs.345824	ESTs gb:EST382704 MAGE resequences, MAGK Homo	1.00 40.55	86.00 200.00
45	431322 431342	AW970622 AW971018	Hs.21659	ESTs	1.00	53.00
	431384	BE158000	Hs.285026	gb:MR2-HT0377-150200-202-e03 HT0377 Homo	0.94	1.14
	431462	AW583672	Hs.256311 Hs.298312	grantn-like neuroendocrine peptide precu hypothetical protein DKFZp434A1315	1.30 3.90	1.25 26.00
	431494 431515	AA991355 NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.41	1.87
50	431548	AI834273	Hs.9711	novel protein	5.66	15.00
	431630 431745	NM_002204 AW972448	Hs.265829 Hs.163425	integrin, alpha 3 (antigen CD49C, alpha ESTs	0.99 0.99	1.44 3.51
	431770	BE221880	Hs.268555	5-3' exoribonuclease 2	67.12	91.00
e e	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.36	4.71
55	431846 431890	BE019924 X17033	Hs.271580 Hs.271986	uroplakin 1B integrin, alpha 2 (CD49B, alpha 2 subuni	4.49 2.20	2,51 3,32
	431934	AB031481	Hs.272214	STG protein	1.01	1.04
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	51.17 0.94	46.35 1.65
60	432006 432023	AL137382 R43020	Hs.272320 Hs.236223	Homo sapiens mRNA; cDNA DKFZp434L1226 (f EST	0.94	47.00
00	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	1.10	2.24
	432210	Al567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.42 1.00	1.45 1.00
	432226 432239	AW182766 X81334	Hs.273558 Hs.2936	phosphate cytidylyltransferase 1, cholin matrix metalloproteinase 13 (collagenase	18.67	1.00
65	432265	8E382679	Hs.285753	SCG10-like-protein	1.09	1.21
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	40.98	58.00 214.00
	432365 432374	AK001106 W68815	Hs.274419 Hs.301885	hypothetical protein FLJ10244 Homo saplens cDNA FLJ11346 fis, clone PL	1.00 157.34	37.00
	432375	8E536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
70	432407	AA221036	11 400404	gb:zr03f12.r1 Stratagene NT2 neuronal pr	73.71	75.00 72.00
	432441 432489	AW292425 A1804855	Hs.163484 Hs.207530	ESTs ESTs	56.35 1.00	24.00
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	137.72	98.00
75	432552	A1537170	Hs.173725	ESTs, Weakly similar to ALUS_HUMAN ALU S	1.00	31.00 35.18
75	432583 432606	AW023624 NM_002104	Hs.162282 Hs.3066	potassium channel TASK-4; potassium chan granzyme K (serine protease, granzyme 3;	0.27 2.87	6.22
	432625	Al243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	26.63	56.00
	432653	N62096	Hs.293185	ESTs, Wealthy similar to JC7328 amino aci	1.92	5.29
80	432677 432715	NM_004482 AA247152	Hs.278611 Hs.200483	UDP-N-acetyl-alpha-D-galactosamine:polyp ESTs, Wealdy similar to KIAA1074 protein	1.00 45.13	48.00 31.00
00	432753	NM_014075	Hs.336938	Homo sapiens PRO0593 mRNA, complete cds	1.00	68.00
	432788	AA521091	Hs.178499	Homo saplens cDNA: FLJ23117 fts, clone L	2.69	3.67
	432842 432867	AW674093 AW016936	Hs.334822 Hs.233364	hypothetical protein MGC4485 ESTs	1.22 1.00	1.34 1.00
85	432917	NM_014125	Hs.241517	PRO0327 protein	10.25	6.62
		_				

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	432920	U37689	Hs.3128 Hs.279905	polymerase (RNA) II (DNA directed) polyp clone HQ0310 PRO0310p1	1.44 154.79	1.30 85.64
	433001 433023	AF217513 AW864793	Hs.87409	thrombospondin 1	20.96	100.00
_	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	1.00	10.00
5	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.20 13.82	1.09 39.00
	433159 433183	AB035898 AF231338	Hs.150587 Hs.222024	kinesin-like protein 2 transcription factor BMAL2	1.00	69.00
	433258	AA622788	Hs.203613	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.00	1.25
10	433409	A1278802	Hs.25661	ESTs	44.81 70.39	117.00 105.00
10	433437 433485	U20536 Al493076	Hs.3280 Hs.201967	caspase 6, apoptosis-related cysteine pr aldo-keto reductase family 1, member C2	11.55	2.00
	433537	Al733692	Hs.112488	ESTs	8.66	55.00
	433547	W04978	Hs.303023	beta tubulin 1, class VI calcium/calmodulin-dependent protein kin	25.16 1.00	83.00 19.00
15	433556 433647	W56321 AA603367	Hs.111460 Hs.222294	ESTs	20.30	49.00
10	433658	L03678	Hs.156110	immunoglobulin kappa constant	5.92	10.03
	433800	AI094221	Hs.135150	lung type-I cell membrane-associated gly	2.29 3.71	2.22 8.00
	433819 433862	AW511097 D86960	Hs.112765 Hs.3610	ESTs KIAA0205 gene product	62.08	104.00
20	433980	AA137152	Hs.286049	phosphoserine aminotransferase	108.91	47.00
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	1.00
	434094 434105	AA305599 AW952124	Hs.238205 Hs.13094	hypothetical protein PRO2013 presentiins associated rhombold-like pro	121.27 1.22	87.00 1.23
	434217	AW014795	Hs.23349	ESTs	14.11	57.00
25	434340	Al193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.10	2.56
	434360 434414	AA401369 Al798376	Hs.190721	ESTs gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	40.98 1.48	17.00 1.56
	434424	AI811202	Hs.325335	Homo saplens cDNA: FLJ23523 fis, clone L	1.00	64.00
20	434467	BE552368	Hs.231853	Homo sapiens cDNA FLJ13445 fls, clone PL	54.91	85.00
30	434551 434627	BE387162 Al221894	Hs.280858 Hs.39311	ESTs, Highly similar to A35661 DNA excls ESTs	2.46 1.00	2.00 1.00
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1.00	23.00
	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	7.08	56.00
35	434792 434808	AA649253 AF155108	Hs.132458 Hs.256150	ESTs Homo sapiens, Similar to RIKEN cDNA 2810	8.52 11.33	44.00 1.00
55	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	· 1.00	1.00
	434876	AF160477	Hs.61460	ig superfamily receptor LNIR	1.25 1.00	1.29 6.00
	434891 434928	AA814309 AW015595	Hs.123583 Hs.4267	ESTs Homo sapiens ciones 24714 and 24715 mRNA	1.00	1.00
40	435013	H91923	Hs.110024	Target CAT	1.26	1.10
	435066	8E261750	Hs.4747	dyskeratosis congenita 1, dyskerin	1.69 1.00	1.37 1.00
	435087 435099	AW975241 AC004770	Hs.23567 Hs.4756	ESTs flap structure-specific endonuclease 1	2.90	1.93
	435159	AA668879	Hs.116649	ESTs	1.00	1.00
45	435205	X54136	Hs.181125	immunoglobulin lambda locus	1.02 2.04	1.46 2.70
	435232 435304	NM_001262 H10709	Hs.4854 Hs.269524	cyclin-dependent klnase inhibitor 2C (p1 ESTs	27.58	139.00
	435313	AI769400	Hs.189729	ESTs	1.00	14.00
50	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	1.00 1.00	38.00 1.00
50	435509 435525	A1458679 A1831297	Hs.181915 Hs.123310	ESTs ESTs	1.00	56.00
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	1.00	2.00
	435550	AI224456	Hs.324507	H.saplens polyA site DNA	3.42 3.95	3.92 1.80
55	435602 435766	AF217515 R11673	Hs.283532 Hs.186498	uncharacterized bone marrow protein BM03 ESTs	1.00	28.00
-	435793	AB037734	Hs.4993	KIAA1313 protein	23.68	42.00
	436069	A1056879	Hs.263209	ESTs	1.00 1.00	58.00 18.00
	436170 436211	AW450381 AK001581	Hs.14529 Hs.334828	ESTs hypothetical protein FLJ10719; KIAA1794	5.84	22.00
60	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	1.42	1.27
	436217	T53925	Hs.107 Hs.301724	fibrinogen-like 1 hypothetical protein FLJ11301	57.97 2.51	31.00 1.71
	436238 436251	AK002163 BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.33	1.64
~~	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	108.99	52.00
65	436302	AL355841 AW992292	Hs.99330 Hs.152213	hypothetical protein FLJ23588 wingless-type MMTV integration site fami	0.75 60.01	2.81 1.00
	436396 436414	BE264633	Hs.143638	WD repeat domain 4	2.50	2.19
	436419	AI948626	Hs.171356	ESTs	0.95	1.33
70	436443 436474	AW138211	Hs.128746 Hs.199887	ESTs ESTs	1.12 1.00	9.26 1.00
70	436481	AJ270693 AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.28	1.56
	436486	AA742221	Hs.120633	ESTs	1.00	19.00
	436511 436553	AA721252 X57809	Hs.291502 Hs.181125	ESTs immunoglobulin lambda locus	16.76 1.08	14.00 1.74
75	436557	W15573	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	19.20	9.75
	436608	AA628980		down syndrome critical region protein DS	33.92	25.00 4 10
	436667	AW025183	Hs.127680 Hs.292979	ESTs ESTs	0.89 1.00	1.19 10.00
	436771 436839	AW975687 AA401369	Hs.190721	ESTS	1.00	17.00
80	436887	AW953157	Hs.193235	hypothetical protein DKFZp547D155	1.06	1.15
	436944	AW268614	Hs.5840 Hs.156704	ESTs ESTs	1.00 25.13	1.00 25.00
	436961 436972	AW375974 AA284679	Hs.25640	claudin 3	1.59	1.46
0.5	437016	AU076916	Hs.5398	guanine monphosphate synthelase	2.35	1.78
85	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	1.34	1.13

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	437181	Al306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	1.00	17.00
	437204	AL110216	Hs.22826	ESTs, Weakly similar to 155214 salivary	40.55	82.00
	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (f	1.00	112.00
_	437259	Al377755	Hs.120695	ESTs	1.00	205.00
5	437270	R18087	Hs.323769	cisplatin resistance related protein CRR	1.56	1.54
	437271	AL137445	Hs.28646	Homo sapiens mRNA; cDNA DKFZp5660134 (fr	113.25 1.82	125.00 4.57
	437370 437390	AL359567 Al125859	Hs.161962 Hs.112607	Homo sapiens mRNA; cDNA DKFZp547D023 (fr ESTs	1.35	1.75
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.58	3.20
10	437435	Al306152	Hs.27027	hypothetical protein DKFZp762H1311	3.03	1.08
	437444	H46008	Hs.31518	ESTs	1.00	39.00
	437568	Al954795	Hs.156135	ESTs	1.00	19.00
	437623	063880	Hs.5719	chromosome condensation-related SMC-asso	1.95 1.00	1.57 3.00
15	437789 437814	Al581344 Al088192	Hs.127812 Hs.135474	ESTs, Weakly similar to T17330 hypotheti ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.00	45.00
13	437840	AA884836	Hs.292014	ESTs	1.07	1.78
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.68	3.26
	437879	BE262082	Hs.5894	hypothetical protein FLJ10305	1.87	2.52
20	437915	AJ637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	74.05	35.00
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	23.15 1.00	89.00 1.00
	437937 437942	Al917222 Al888256	Hs.121655 Hs.307526	ESTs ESTs	12.28	31.00
	438091	AW373062	110.001020	nuclear receptor subfamily 1, group 1, m	1.53	10.85
	438113	AJ467908	Hs.8882	ESTs	1.80	2.39
25	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	22.67	36.90
	438274	Al918906	Hs.55080	ESTs	1.00	1.00
	438378	AW970529	Hs.86434	hypothetical prolein FLJ21816	38.92	38.00
	438403	AA806607	Hs.292206 Hs.130183	ESTs ESTs	1.00 2.05	1.00 80.00
30	438494 438546	AA908678 AW297204	Hs.125811	ESTs	1.00	131.00
20	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	1.43	1.45
	438702	AI879064	Hs.54618	ÉSTs	1.00	34.00
	438724	AW612553	Hs.114670	Human DNA sequence from clone RP11-16L21	1.33	1.10
35	438746	A\885815	Hs.184727	Human melanoma-associated antigen p97 (m	2.42	1.59
33	438779	NM_003787	Hs.6414	nucleolar protein 4 ESTs	1.00 2.03	18.00 2.57
	438821 438885	AA826425 A1886558	Hs.192375 Hs.184987	ESTS	6.42	88.00
	438898	AA401369	Hs.190721	ESTs	22.41	17.00
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
40	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	2.20	1.88
	439000	AW979121		gb:EST391231 MAGE resequences, MAGP Homo	2.78	4.81
	439023	AA745978	Hs.28273 Hs.35598	ESTs ESTs	1.17 1.00	1.31 28.00
	439024 439128	R96696 Al949371	Hs.153089	ESTs	1.00	67.00
45	439146	AW138909	Hs.156110	immunoglobulin kappa constant	1.38	1.41
	439223	AW238299	Hs.250618	UL16 binding protein 2	1.93	1.64
	439285	AL133916	u	hypothetical protein FLJ20093	46.23 2.00	139.00 2.20
	439318 439343	AW837046 AF086161	Hs.6527 Hs.114611	G protein-coupled receptor 56 hypothetical protein FLJ11808	6.10	7.37
50	439394	AA401369	Hs.190721	ESTs	3.39	17.00
-	439410	AA632012	Hs.188746	ESTs	1.83	3.07
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23,28	52.00
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	18.76	122.00
55	439453	BE264974	Hs.6566 Hs.58042	thyroid hormone receptor interactor 13 ESTs, Moderately similar to GFR3_HUMAN G	2.78 1.22	1.58 1.44
55	439477 439492	W69813 AF086310	Hs. 103159	ESTs	7.46	39.00
	439523	W72348	Hs.185029	ESTs	1.00	1.19
	439592	AF086413	Hs.58399	ESTs	1.00	1.00
C O	439606	W79123	Hs.58561	G protein-coupled receptor 87	33.61	1.00
60	439670	AF088076	Hs.59507	ESTs, Weakly similar to AC004858 3 U1 sm	1.00 4.30	1.00 10.00
	439702 439706	AW085525 AW872527	Hs.134182 Hs.59761	ESTs ESTs, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	2.36	1.88
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length Insert cDN	2.02	6.08
65	439759	AL359055	Hs.67709	Homo saplens mRNA full length insert cDN	1.00	21.00
	439780	AL109688		gb:Homo sapiens mRNA full length insert	7.27	25.00
	439840	AW449211	Hs.105445	GDNF family receptor alpha 1	1.00 32.58	1.00 71.00
	439926 439963	AW014875 AW247529	Hs.137007 Hs.6793	ESTs platelet-activating factor acetylhydrola	21.28	9.55
70	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	68.83	61.00
. •	440006	AK000517	Hs.6844	hypothelical protein FLJ20510	1.83	4.02
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	1.42	2.54
	440106	AA864968	Hs.127699	KIAA1603 protein	1.00	54.00
75	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	24.18 3.21	52,00 4.72
13	440273 440289	A1805392 AW450991	Hs.325335 Hs.192071	Homo saplens cDNA: FLJ23523 fis, clone L ESTs	38.63	113.00
	440325	NM_003812	Hs.7164	a disintegrin and metalioproteinase doma	62.88	147.00
	440492	R39127	Hs.21433	hypothetical protein DKFZp547J036	2.35	3.62
00	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	10.84	57.00
80	440659	AF134160	Hs.7327	claudin 1	3.18	2,37
	440704		Hs.162	insulin-like growth factor binding prote hypothetical protein MGC2408	2.89 2.02	2.09 1.41
	440943 440994	AW082298 Al160011	Hs.146161 Hs.272068	ESTs	1.29	1.14
~ -	441020	AA401369	Hs.190721	ESTs	142.99	17.00
85	441031	Al110684	· Hs.7645	fibrinogen, B beta polypeptide	1.41	99.00

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	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	4.13 1.00	3.50 1.00
	441290 441362	W27501 BE614410	Hs.89605 Hs.23044	cholinergic receptor, nicotinic, alpha p RAD51 (S. cerevisiae) homolog (E coli Re	130.23	43.00
	441377	BE218239	Hs.202656	ESTs	22.03	1.00
5	441390	Al692560	Hs.131175	ESTs	3.65	7.70
	441497 441525	R51064 AW241867	Hs.23172 Hs.127728	ESTs ESTs	1.00 1.53	1.00 1.42
,	441553	AA281219	Hs.121296	ESTs	1.89	1.57
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	1.47	2.11
10	441633	AW958544	Hs.112242 Hs.7921	normal mucosa of esophagus specific 1 Homo sapiens mRNA; cDNA DKFZp566E183 (fr	216.22 2.31	363.00 2.05
	441636 441737	AA081846 X79449	Hs.7957	adenosine deaminase, RNA-specific	1.30	1.49
	441790	AA401369	Hs.190721	ESTs	44.15	17.00
15	441801	AW242799	Hs.86366	ESTs	1.00 1.00	1.00 122.00
15	441919 441937	Al553802 R41782	Hs.128121 Hs.22279	ESTs ESTs	0.86	1.37
	441954	Al744935	Hs.8047	Fanconi anemia, complementation group G	1.48	1.39
	442025	AW887434	Hs.11810	CDA11 protein	1.00 9.92	46.00 45.00
20	442029 442072	AW956698 AJ740832	Hs.14456 Hs.12311	neural precursor cell expressed, develop Homo sapiens clone 23570 mRNA sequence	25.05	77.00
20	442108	AW452649	Hs.166314	ESTs	3,61	3.14
	442117	AW664964	Hs.128899	ESTS	3.00	5.49
	442137	AA977235	Hs.128830 Hs.278554	ESTs, Weakly similar to Z192_HUMAN ZINC heterochromatin-like protein 1	1.00 1.92	1.00 1.66
25	442159 442179	AW163390 AA983842	Hs.333555	chromosome 2 open reading frame 2	27.22	50.00
	442328	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.00	3.42
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468 Homo sapiens cDNA FLJ14712 fis, clone NT	181.59 10.59	76.00 144.00
	442530 442547	Al580830 AA306997	Hs.176508 Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU S	109.23	98.00
30	442556	AL137761	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	1.00	53.00
	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	29.02 1.00	50.00 19.00
	442710 442717	A)015631 R88362	Hs.23210 Hs.180591	ESTs ESTs, Weakly similar to T23976 hypotheti	1.00	5.00
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	22.85	50.00
35	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	25.33	82.00 4.41
	442932 442942	AA457211 AW167087	Hs.8858 Hs.131562	bromodomain adjacent to zinc finger doma ESTs	3.18 8.45	64.00
	443068	Al188710	15.101002	ESTs	1.00	27.00
40	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	1.00	24.00 2.00
40	443211	Al128388	Hs.143655 Hs.333893	ESTs c-Myc target JPO1	12.42 128.84	96.00
	443247 443324	8E614387 R44013	Hs.164225	ESTs	0.02	4.59
	443383	A1792453	Hs.166507	ESTs	1.00	47.00
45	443400	R28424	Hs.250648 Hs.9329	ESTs chromosome 20 open reading frame 1	18.52 4.02	61.00 1.75
40	443426 443572	AF098158 AA025610	Hs.9605	cleavage and polyadenylation specific fa	2.98	2.57
	443575	A1078022	Hs.269636	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00	29.00
	443614	AV655386	Hs.7645 Hs.9654	fibrinogen, B beta polypeptide simitar to pregnancy-associated plasma p	1.00 1.00	16.00 39.00
50	443633 443648	AL031290 Al085377	Hs.143610	ESTs	39.81	70.00
-	443715	AI583187	Hs.9700	cyclin E1	48.74	7.00
	443723	A1144442	Hs.157144	syntaxin 6 KIAA1291 protein	1.29 1.75	1.30 1.61
	443802 443859	AW504924 NM_013409	Hs.9805 Hs.9914	follistatin	1.35	1.13
55	443892	AA401369	Hs.190721	ESTs	1.00	17.00
	443947	W24187	11- 40002	gb:zb47f09.r1 Soares_fetat_lung_NbHL19W potassium intermediate/small conductance	1.33 5.71	1.64 6.87
	443991 444006	NM_002250 BE395085	Hs.10082 Hs.10086	type I transmembrane protein Fn14	1.47	1.92
	444009	Al380792	Hs.135104	ESTs	1.00	77.00
60	444017	U04840	Hs.214	neuro-oncological ventral antigen 1	1.00 1.00	1.00 29.00
	444127 444129	N63620 AW294292	Hs.13281 Hs.256212	ESTS ESTS	1.00	1.00
	444279	U62432	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.60	7.80
65	444371	BE540274	Hs.239	forkhead box M1 ESTs	2.91 1.00	1.14 1.00
05	444378 444381	R41339 BE387335	Hs.12569 Hs.283713	ESTs, Weakly similar to S64054 hypotheti	469.00	556.00
	444461	R53734	Hs.25978	ESTs, Wealdy similar to 2109260A B cell	12.88	105.00
	444471	AB020684	Hs.11217	KIAA0877 protein	24.91 1.00	90.00 111.00
70	444489 444619		Hs.157774 Hs.8172	ESTs ESTs, Moderately similar to A46010 X-lin	1.00	70.00
70	444665		Hs.47783	B aggressive lymphoma gene	30.56	139.00
	444707		Hs.41690	desmocollin 3	1.00	1.00 90.00
	444735 444781		Hs.243122 Hs.11950	hypothetical protein FLJ 13057 similar to GPI-anchored metastasis-associated prote	77.02 1.57	1.31
75	444783		Hs.62180	aniilin (Drosophila Scraps homolog), act	77.55	2.00
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	1.00	27.00
	445258		Hs.147613	ESTs CGI-147 protein	1.00 28.14	73.00 50.00
	445413 445417		Hs.12677 Hs.12680	Homo saplens cDNA FLJ10196 fis, clone HE	1.81	2.62
80	445443	AV653838	Hs.322971	ESTs	1.00	1.00
	445462		Hs.288649	hypothetical protein MGC3077	2.09 1.87	1.70 70.00
	445517 445537		Hs.12830 Hs.12844	hypothetical protein EGF-like-domain, multiple 6	1.71	2.72
	445580	AF167572	Hs.12912	skb1 (S. pombe) homolog	1.52	1.34
85	445654	X91247	Hs.13046	thioredoxin reductase 1	1.51	1.52

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	445669	AI570830	Hs.174870	ESTs	10.95	11.45 1.00
	445818 445873	BE045321 AA250970	Hs.136017 Hs.251946	ESTs poty(A)-binding protein, cytoplasmic 1-4	1.00 49.42	54.QO
	445885	A1734009	Hs.127699	KIAA1603 protein	1.00	132.00
5	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	1.00	1.00
	445903	Al347487	Hs.132781	class I cytokine receptor	1.00	36.00
	445932	BE046441	Hs.333555	Homo sapiens clone 24859 mRNA sequence pescadillo (zebrafish) homolog 1, contai	2,41 1,60	2.88 1.35
	445982 446078	8E410233 Al339982	Hs.13501 Hs.156061	ESTs	1.00	42.00
10	446102	AW168067	Hs.317694	ESTs	1.00	1.00
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	1.70	1.53
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	73.01 1.55	48.00 1.26
	446292 446293	AF081497 Al420213	Hs.279682 Hs.149722	Rh type C glycoprotein ESTs	1.00	2.00
15	446423	AW139655	Hs.150120	ESTs	1.10	4.19
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	0.53	3.26
	446432	Al377320	Hs.150058 Hs.15243	ESTS	1,00 1,36	5.00 1,31
	446528 446574	AU076640 Al310135	Hs.335933	nucleolar protein 1 (120kD) ESTs	3.89	72.00
20	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	32.03	20.23
	446636	AC002563	Hs.15767	citron (rho-Interacting, serine/threonin	4.19	5.07
	446783	AW138343	Hs.141867	ESTs	2.82 110.28	9.47 28.00
	446839 446849	8E091926 AU076617	Hs.16244 Hs.16251	mitotic spindle coiled-coil related prot cleavage and polyadenylation specific fa	3.26	2.94
25	446856	AI814373	Hs.164175	ESTs	6.38	11.30
	446872	X97058	Hs.16362	pyrimidinergic receptor P2Y, G-protein c	1.98	2.03
	446880	AI811807	Hs.108646	Homo saptens cDNA FLJ14934 fis, clone PL small inducible cytokine subfamily A (Cy	94.90 1.67	113.00 3.90
	446921 446989	AB012113 AK001898	Hs.16530 Hs.16740	hypothetical protein FLJ11036	2.82	3.12
30	447022	AW291223	Hs.157573	ESTs	1.00	170.00
	447033	Al357412	Hs.157601	ESTs	7.15	107.00
	447078	AW885727	Hs.9914	ESTs potassium inwardly-rectifying channel, s	47.24 0.12	24.00 17.88
	447081 447131	Y13896 NM_004585	Hs.17287 Hs.17466	retinoic acid receptor responder (tazaro	0.97	1.48
35	447149	BE299857	Hs.326	TAR (HIV) RNA-binding protein 2	1.24	1.26
	447153	AA805202	Hs.315562	ESTS	1.00	54.00
	447164	AF026941	Hs.17518	Homo sapiens clg5 mRNA, partial sequence	1.00 3.42	67.00 50.00
	447178 447250	AW594641 Al878909	Hs.192417 Hs.17883	ESTs protein phosphatase 1G (formerly 2C), ma	1.60	1.52
40	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00	1.00
	447342	Al199268	Hs.19322	Homo saplens, Similar to RIKEN cDNA 2010	28.63	1.00
	447343 447350	AA256641 Al375572	Hs.236894 Hs.172634	ESTs, Highly similar to S02392 alpha-2-m ESTs	146,62 1.00	51.00 12.00
	447377	N27687	Hs.334334	transcription factor AP-2 alpha (activat	2.55	63.00
45	447415	AW937335	Hs.28149	ESTs, Weakly similar to KF3B_HUMAN KINES	0.91	1.13
	447425	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)	1.00 59.89	35.00 49.00
	447519 447532	U46258 AK000614	Hs.339665 Hs.18791	ESTs hypothetical protein FLJ20607	1.23	1.63
	447534	AA401369	Hs.190721	ESTs	1,00	17.00
50	447636	Y10043		high-mobility group (nonhistone chromoso	1.41	1.11
	447688	N87079 AF157482	Hs.19236 Hs.19400	Target CAT MAD2 (milotic arrest deficient, yeast, h	1.00 1.17	39,00 1,12
	447733 447769	AW873704	Hs.320831	Homo saplens cDNA FLJ14597 fis, clone NT	6.47	5.95
	447802	AW593432	Hs.161455	ESTs	0.73	2.34
55	447850	AB018298	Hs.19822	SEC24 (S. cerevisiae) related gene famil	86.45	116.00 1.00
	447924 447973	Al817226 AB011169	Hs.313413 Hs.20141	ESTs, Weakly similar to T23110 hypotheti similar to S. cerevisiae SSM4	1.00 3.50	4.27
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.13	142.00
~ 0	448105	AI538613	Hs.298241	Transmembrane protease, serine 3	1.15	2.24
60	448243	AW369771	Hs.52620	integrin, beta 8 ESTs	15.84 0.97	1.00 1.90
	448278 448290	W07369 AK002107	Hs.11782 Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	1.00	1.00
	448296	BE622756	Hs.10949	Homo saplens cDNA FLJ14162 fis, clone NT	2.42	2.17
CE	448357	BE274396	Hs.108923	RAB38, member RAS oncogene family	1.44	1.08
65	448390 448469	AL035414 AW504732	Hs.21068 Hs.21275	hypothetical protein hypothetical protein FLJ11011	1.00 2.63	43.00 2.49
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.84	2,53
	448663	BE614599	Hs.106823	hypothetical protein MGC14797	3.29	46.00
70	448672	Al955511	Hs.225106	ESTs	1.00 1.82	21.00 1.08
70	448733 448741	NM_005629 BE614567	Hs.187958 Hs.19574	solute carrier family 6 (neurotransmilte hypothetical protein MGC5469	2,48	1.92
	448757	Al366784	Hs.48820	TATA box binding protein (TBP)-associate	23,53	20.00
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moi	2.34	1.97
75	448826	Al580252	Hs.293246	ESTs, Weakly similar to putative p150 [H hypothetical protein dJ310013.3	74.07 1.37	62.67 1.31
13	448830 448844	AL031658 Al581519	Hs.22181 Hs.177164	ESTs	1.00	31.00
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.84	1.95
	448993	Al471630		KIAA0144 gene product	1.63	1.49
80	449003	X76342	Hs.389 Hs.22891	alcohol denydrogenase 7 (class IV), mu o solute carrier family 7 (cationic amino	. 1.00 1.97	1.00 2.26
50	449029 449040	N28989 AF040704	Hs.149443	putative tumor suppressor	0.97	1.56
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	27.13	90.00
	449053	A1625777	Hs.344766	ESTs	8.33 73.85	44.00 104.00
85	449054 449101	AF148848 AA205847	Hs.22934 Hs.23016	myoneurin G protein-coupled receptor	73.85 2.58	27.00
	. 10101		, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,			

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	449167	T05095	Hs.19597	KIAA1694 protein	1.61	2.36
	449207 · 449228	AL044222 AJ403107	Hs.23255	nucleoporin 155kD	2.36 1.15	1.56 1.15
	449228	BE613348	Hs.148590 Hs.211579	protein related with psoriasis melanoma cell adhesion molecule	206.65	151.00
5	449305	Al638293	110.01	gb:tt09b07.x1 NCI_CGAP_GC6 Homo saplens	17.28	45.00
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	26.39	35.00
	449448	D60730	Hs.57471	ESTs	1.00 1.00	1.00 1.00
	449467 449523	AW205006 NM_000579	Hs.197042 Hs.54443	ESTs chemokine (C-C motif) receptor 5	56.80	216.86
10	449722	BE280074	Hs.23960	cyclin B1	150.03	1.00
	449976	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	2.16	2.85
	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitte	1.17	1.45
	450098 450101	W27249 AV649989	Hs.8109 Hs.24385	hypothetical protein FLJ21080 Human hbc647 mRNA sequence	1.79 1.00	2.38 69.00
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	1.00	1.00
	450193	AI916071	Hs.15607	Homo sapiens Fanconi anemia complementat	29.85	34.00
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1.00	1.00
	450372	BE218107	Hs.202436	ESTs a disintegrin and metalloproteinase doma	1.00 51.26	1.00 93.00
20	450375 450447	AA009647 AF212223	Hs.8850 Hs.25010	hypothetical protein P15-2	123.20	181.00
20	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	19.00
	450589	AJ701505	Hs.202526	ESTs	1.00	23.00
	450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	1.00	100.00
25	450701 450705	H39960 U90304	Hs.288467 Hs.25351	Homo sapiens cDNA FLJ12280 fis, ctone MA troquots homeobox protein 2A (IRX-2A) (1.89 1.00	1.55 45.00
23	450832	AA401369	Hs.190721	ESTs	25.17	17.00
	450937	R49131	Hs.26267	ATP-dependant interferon response protel	90.92	90.00
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.33	1.70
30	451105 451110	A1761324 A1955040	Hs.265398	gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens ESTs, Weakly similar to transformation-r	15.02 1.00	124.00 143.00
30	451253	H48299	Hs.26126	claudin 10	3.02	2.29
	451291	R39288	Hs.6702	ESTs	1.00	1.00
	451320	AW498974		diacytglycerol kinase, zeta (104kD)	2.92	18.00
35	451380	H09280 AB029006	Hs.13234	ESTs spastic paraplegia 4 (autosomat dominant	6,90 35.75	6.67 72.00
33	451386 451437	H24143	Hs.26334 Hs.31945	hypothetical protein FLI11071	1.00	69.00
	451462	AK000367	Hs.26434	hypothetical protein FLJ20360	1.83	2.10
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.13	1.07
40	451541	BE279383	Hs.26557	plakophilin 3	1.88 1.00	1.33 1.00
40	451592 451635	AI805416 AA018899	Hs.213897 Hs.127179	ESTs cryptic gene	1.52	1.92
	451743	AA401369	Hs.190721	ESTs	4.95	17.00
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	13.55	31.00
45	451807	W52854	Un 110500	hypothetical protein FLJ23293 similar to	1.55 1.81	35.00 2.53
45	451871 451952	AI821005 AL120173	Hs.118599 Hs.301663	ESTs ESTs	1.00	22.00
	452012	AA307703	Hs.279766	kinesin family member 4A	3.43	2.26
•	452046	AB018345	Hs.27657	KIAA0802 protein	56.59	19,00
50	452194	A1694413	Hs.332649	offactory receptor, family 2, subfamily	1.67 9.31	4.09 53.00
20	452206 452240	AW340281 AA401369	Hs.33074 Hs.190721	Homo sapiens, clone IMAGE:3606519, mRNA, ESTs	13.42	17.00
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	39.03	94.00
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fls, clone PL	153.01	340.00
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi programmed cell death 10	1.95 42.33	23.00 61.00
33	452295 452304	BE379936 AA025386	Hs.28866 Hs.61311	ESTs, Weakly similar to \$10590 cysteine	1.17	2.14
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.00	13.00
	452349	AB028944	Hs.29189	ATPase, Class VI, type 11A	1.09	1.42
60	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	54.49 1.00	53.00 32.00
oo	452401 452410	NM_007115 AL133619	Hs.29352	tumor necrosis factor, alpha-induced pro Homo saptens mRNA; cDNA DKFZp434E2321 (f	1.26	1.99
	452461	N78223	Hs.108106	transcription factor	24.47	35.00
	452571	W31518	Hs.34665	ESTs	54.61	102.00
65	452613	AA461599	Hs.23459	ESTS	1.39 1.00	1.32 26.00
05	452699 452705	AW295390 H49805	Hs.213062 Hs.246005	ESTS ESTS	1.00	1.00
	452747	AF160477	Hs.61460	Ig superfamily receptor LNIR	112.87	1.29
	452787	AW294022	Hs.222707	KIAA1718 protein	1.00	1.00
70	452795	AW392555	Hs.18878	hypothetical protein FLJ21620 transcription factor-like 5 (basic helix	1.00 7.91	1.00 75.00
70	452823 452833	AB012124 BE559681	Hs.30696 Hs.30736	KIAA0124 protein	3.16	1.92
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	174.35	1.00
	452862	AA401369	Hs.190721	ESTs	98.26	17.00
75	452865	AW173720	Hs.345805	ESTs, Weakly similar to A47582 B-cell gr	1.55	1.00
75	452934 452946	AA581322 X95425	Hs.4213 Hs.31092	hypothetical protein MGC16207 EphA5	1.73 1.00	1.19 1.00
	452976	R44214	Hs.101189	ESTs	1.58	1.98
	453028	AB006532	Hs.31442	RecQ protein-like 4	1.80	1.60
90	453095	AW295660	Hs.252756	ESTs	0.77 4.00	1.50
80	453102 453103	NM_007197 Al301052	Hs.31664 Hs.153444	frizzled (Drosophila) homolog 10 ESTs	1.00 1.00	1.00 1.00
	453103 453120	AA292891	Hs.31773	pregnancy-induced growth inhibitor	1.23	1.20
	453153	N53893	Hs.24360	ESTs	1.00	83.00
05	453160	AI263307	Hs.239884	H2B histone family, member L	1.00 1.00	30.00 134.00
85	453197	Al916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU 8	1.00	134.00

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	453210	AL133161	Hs.32360	hypothetical protein FLJ10867	1.69	1.93		
		A1969564	Hs.166254	hypothetical prolein DKFZp566I133	1.00	1.00		
	453317	NM_002277 AF034102	Hs.41696 Hs.32951	keratin, hair, acidic, 1 solute carrier family 29 (nucleoside tra	1.19 4.90	1,27 4.11		
5		AI240665	Hs.8850	ESTs	199.42	340.00		
~	453392		Hs.32964	SRY (sex determining region Y)-box 11	1.00	16.00		
	453431		Hs.32973	glycine receptor, beta	1.00	1.00		
		AI572438	Hs.32976	guanine nucleotide binding protein 4	3.44 2.84	5.17 5.58		
10	453459 453563	BE047032 AW608906.com	Hs.257789	ESTs Hs.181163		I protein MGC5629	4.58	90.00
10	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.74	1.60		*****
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	19.49	1.00		
	453830	AA534296	Hs.20953	ESTs	24.92	25.00		
15	453857	AL080235 Al929383	Hs.35861 Hs.33032	DKFZP586E1621 protein hypothetical protein DKFZp434N185	167.59 1.00	66.00 39.00		
13	453883	Al638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.97	1.58		
	453884	AA355925	Hs.36232	KIAA0186 gene product	63.89	20.00		
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALUS_HUMAN ALU S	20.41	16.00		
20	453922	AF053306	Hs.36708 Hs.36820	budding uninhibited by benzimidazoles 1	7.09 29.75	22.00 19.00		
20	453941 453964	U39817 Al961486	Hs.12744	Bloom syndrome ESTs	1.00	1.00		
	453968	AA847843	Hs.62711	Homo saplens, clone IMAGE:3351295, mRNA	2.06	1.81		
	453976	BE463830	Hs.163714	ESTs	3.02	131.00		
25	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	1.00 1.23	131.00 1.02		
23	454034 454042	NM_000691 T19228	Hs.575 Hs.172572	aklehyde dehydrogenase 3 family, member hypothetical protein FLJ20093	30.63	171.00		
	454059	NM_003154	Hs.37048	statherin	1.00	1.00		
	454066	X00356	Hs.37058	calcitonIn/calcitonin-related polypeptid	1.01	1.45		
20	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.26 6.33	1.11 5.04		
30	454241 454417	BE144666 A)244459	Hs.110826	gb:CM2-HT0176-041099-017-c02 HT0176 Homo trinucleotide repeat containing 9	4.30	7.82		
	454439	AW819152	Hs.154320	DKFZP566O1646 protein	1.00	1.00		
	455175	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	13.75	103.00		
25	455601	Al368680	Hs.816	SRY (sex determining region Y)-box 2	206.11	1.00		
35	456237 456321	AA203682 NM_001327	Hs.87225	gb:zx52e07.r1 Soares_fetal_liver_spleen_ cancer/testis antigen	1.00 1.14	1.00 1.10		
	456475	NM_000144	Hs.95998	Friedreich ataxia	1.00	48.00		
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	162.25	189.00		
40	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	2.12	1.80 1.94		
40	456736 456759	AW248217 BE259150	Hs.1619 Hs.127792	achaete-scute complex (Drosophila) homol delta (Drosophila)-like 3	1.15 1.00	1.00		
	456990	NM_004504	Hs.171545	HIV-1 Rev binding protein	16.42	84.00		
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.57	1.76		
AS	457234		Hs.14355	Homo saplens cDNA FLJ13207 fis, clone NT	2.71 46.37	4.15 47.00		·
45	457465 457489	AW301344 Al693815	Hs.122908 Hs.127179	DNA replication factor cryptic gene	1.12	1.35		
	457646		Hs.112948	ESTs	1.55	2.51		
	457733	AW974812	Hs.291971	ESTs	1.00	55.00		
50	457819		Hs.35406	ESTs, Highly similar to unnamed protein	4.36 1.00	3.18 1.32		
30	458092 458098	BE545684 BE550224	Hs.343566	KIAA0251 protein metallothionein 1E (functional)	1.00	22.00		
	458207	T28472	Hs.7655	U2 small nuclear ribonucleoprotein auxil	2.06	1.88		
	458242	8E299588	Hs.28465	Homo sapiens cDNA: FLI21869 fis, clone H	1.00	1.00		
55	458247	R14439	Hs.209194	ESTs	7.00 1.00	9.85 3.00		
55	458679 458778	AW975460 AW451034	Hs.142913 Hs.326525	ESTs arylsulfatase D	1.31	2.01		
	458933	Al638429	Hs.24763	RAN binding protein 1	1.98	1,71		
	459352	AW810383	Hs.206828	ESTs	12.60	63.00		
60	459670	F01020	Hs.172004	fitin gb:an03c03.x1 Stratagene schizo brain S1	1.00 1.00	1.00 237.00		
00	439702	A1204995		gu,anococx i oranagene someo tram o i	1.00	207.00		
	TABLE 9	18						
65	Pkev:	Delgue Fo	r amhacatida	anlifier number				
05		nber: Gene clust		numer introct	•			
	Accessio		ccession nun	nbers				
	C1	CATALogic		-1				
70	Pkey 407746	CAT Numbe 10125_1	r Acces	sion 1962 R69415 BE464605 AA418699 AA053293 AA149	075 AA058396 AW	338226 AW272659 AA4	154607 AI139535	5 AW469852 AI275461
10	701170	10120_1	AW27	1982 AA730033 AA576507 AA991217 AA782067 AI9	35851 AA805864 A	A505598 AW469857 R6	39546 AA988279	9 AW001647 N63320
			D8266	61 T27343 AA306950 AA360989 R58778				
	408070	1036688_1		8852 BE350895				
75	408660 409522	107294_1 113735_1		5775 AA056342 A1538978 AW975281 AA664986 5382 AA075431				
15	409866	1156522_1		2152 H41202 H29772				
	410032	1170435_1	BE06	5985 RE065944 RE066008 BE066083 BE066093				
	411089	123172_1	AA456	5454 AA713730 AA091294 AA584921 N86077 AW836	781 AA601031 AA	579876 AA551106 AA6	33188 AW90557	7 A1955808 A1679386
80	444450	1224020 4	Al679	895 AA514764 AA454562 A1082382 AA595822 AA55 9199 AW936012 AW877466 AW819782 AW935798 A	NR35546 AWQ360.	000304 AA 100934 AAb 12 REARMA 12102014 AB	5 AW877536 AV	V935885 BE069202
30	411152	1234028_1	AW82	0019 AW935937 BE160180 AW935946 BE069101 BE	069125 AW877527	7 BE160316 BE160398 .	AW935794 AW8	335701 AW935784
	412537	1304_1	A) (131	778 Y59711 NIM 002505 M59079 AIR70439 AI49425	AW664010 AA40	5063 AA436132 BE174!	516 AA412691 A	V400314 AA436024
			T2940)3 BE079412 BE079428 N90322 Al631202 Al141758 3918 AA927051 AA889823 BE003094 AW390155 AV	967566 EVIOLE EVIOLENTS	5 A1862075 A1375230 A1 3 AW380810 AAA35473	205445 AW2357 AI694292 AI 04	103 ALU441 13 AA382556 IA114 A1684577 A1809865
			CEVVA	PI 501 INCERES HEROCOGO CONTRACTOR (22 WA			. AUG PEUE PIEUP	

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	***	02/000443	AI478773 AI160445 AI674630 N69088 AW665529 N49278 AI129239 AI457890 AI621264 AW297152 AI268215 AA907787 AI286170 AI017982
-	412811	132943_1	AI963541 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AW292026 H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240
5	413690 414883	1383256_1 15024_1	AA121202 R17734 BE157489 BE157560 AA926960 AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245
10			AA082436 H72525 H77575 N49786 W80565 H78746 BE569085 W04339 R98127 T55938 BE279271 AW960304 T29812 AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955 AI204630 W25243 AI935150 AA872039 W72395 T99630 AI422691 H98460 N31428 BE255916 H03265 AI857576 AA776920 AA910644 AA459522 AA293140 AW514667
			R75953 AW662396 AA662522 Al865147 Al423153 AW262230 AA584410 AA583187 AW024595 AW069734 Al828996 AA282997 AA876046 AW613002 AA527373 AW972459 Al831360 AA621337 AA100926 AA772418 AA594628 Al033892 W95096 Al034317 AA398727 Al085031 N95210 Al459432 Al041437 AA932124 AA627684 AA935829 Al004827 Al423513 Al094597 H42079 R54703 Al630359 AA617681 AA978045
15			AA643280 W44661 AI991988 AI537692 AI090262 AA740817 AI312104 AI911822 AA416871 AI185409 AA129784 AA701623 AI075239 AI139549 AA633648 AI339996 AI336880 AA399239 AI078708 AI085351 AI362835 AI346618 AI146955 AI989380 AI348243 N92892 AA765850 AI494230 AI278887 AA982596 AI492600 W80435 AA001979 R97424 AI129015 N24127 AA157451 AA235549 AAA59292 AA037114 AA129785 AI494231 AW0559601 AW866710 R92790 N59755 AI361128 AW589407 H47725 H97534 H48076 H48450 T99531 AW300758 H03431 R76789 AA954344 H77576 R96823 AI457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AA701624 N74173 R54704 H79520 H72923
20			H03266 BE261919 AA769633 AA480310 AA507454 AA910586 Al203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
20	415989	156454_1	W95095 R97470 AA702275 T77551 AA911952 H82956 N83673 AA283672 Al267700 Al720344 AA191424 Al023543 Al469633 AA172056 AW958465 AA172236 AW953397 AA355086
	417324	166714_1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
	418574	17690_1	N28754 N28747 AI568146 AI979339 AA322671 AA322672 AW955043 AI990326 AA776406 AI016250 AA843678 AW451882 N23137 N23129
25	440740	4704405 4	W70051 Al038748 AA831327 Al925845 AW945895
23	418712 419443	1784125_1 184788_1	Z42183 T31621 T97478 D62703 AA242966 D79798
	419502	18535_1	AU076704 174854 174850 172098 173265 173873 169180 174658 158786 160385 173410 168781 167845 167593 173952 167864 160630
		_	T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T74645 T72037 T68688 T72063 T73258 T72826 T64242
30			T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60631 T73277 T73203 T70498 T61409 T58925 NM_000508 M64982 T68301 T73729 T69445 T60424 T60422 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T61109 T68329 T58850 T71857 T73425 T53736 T68607 T58898 T64309 T72031 T72079 T64306 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T71958 T69440 T61875 R06796 H48353 T71914 T53939 T64121 A4693996 T72525 T67779 T68078 AA011465 AA345378 AV654847 AV654272 AV656001 A1064740 T82897
35			N33594 AA344542 AW805054 AI207457 T61743 AA026737 H94389 AA382695 AA918409 T68044 S82092 T39959 AI017721 AA312395 AA312919 T40156 H66239 AV652989 H38728 R98521 AV655200 R95790 W03250 W00913 AA344136 AV660126 R97923 AA343596
			AW470774 AV651256 N54417 AA812862 AW182929 Al111192 H61463 H72060 AA344503 H38639 Al277511 AV661108 Al207625 T47810
			AA235252 T27853 T47778 R95746 H70620 AA701463 AW827166 R98475 C20925 AV657287 T71959 T71313 T73920 T73333 T61618 T69293
			T69283 T73931 T72178 T72456 AV645639 AV653476 T72957 T72300 T58906 T71457 T70494 T72956 T70495 T68267 T74407 T85778 AA344726 T27854 T74485 T74101 T73868 T71518 T72304 AA343853 T73909 T68070 T72065 H72149 T73493 T73495 AV645993 R02293
40			T70475 T64751 AA344441 AA343657 AA345732 AA344328 A1110639 AA344603 AF083513 T64696 T68516 T72223 T60507 T67633 R29500
••			T72517 R02292 T60599 T69206 T70452 T74677 R29366 T61277 T74914 T60352 R29675 T74843 AV645792 AA344408 T69197 T72057
			T69368 T69358 T68258 AV650429 T73341 T61702 T74598 T40095 K02272 T40106 AA343045 AA341908 AA341907 AA342807 AA341964
			T53747 T72042 T62764 Al064899 AA343060 T67832 T72440 T71770 T68091 T69108 T72449 T69167 T71289 T68251 AV654844 T64375
45			AA345234 T67598 AA011414 T68036 H48262 A1207557 T68219 W86031 T6923 R93196 T62136 AV650539 H67459 T72978 AA345234 T67598 A2011414 T68036 H48262 A1207557 T68219 W86031 T692081 T6423 R93196 T62136 AV650539 H67459 T72978 AA345234 T67598 A2011414 T68036 H48262 A1207557 T68219 W86031 T692081 T6423 R93196 T62136 AV650539 H67459 T72978 T6781 T6782
73			AA344583 T60362 H58121 T95711 T72803 T68055 T71715 R29036 T72793 T69122 T64595 T62888 T69139 T68291 T64652 T67971 T46862 AA693592 AI248502 R29454 T64764 T57001 T73052 T71429 T51176 T58866 AV655414 H90426 AA342489 T73666 T67848 T72512 T53835
			T67837 T73317 T74273 T69420 T68245 T74380 T67862 T74474 T56068
	419936	189181_1	AI792788 BE142230 AA252019
50	421582	2041_1	AI910275 X00474 X52003 X05030 NM_003225 AA314326 AA308400 AA506787 AA314825 AI571948 AA507595 AA614579 AA587613 R83818 AA568312 AA614409 AA307578 AI925552 AW950155 AI910083 M12075 BE074052 AW004668 AA578674 AA582084 BE074053 BE074126
-			BE074140 AA514776 AA588034 BE074051 BE074068 AW009769 AW050690 AA858276 R55389 Al001051 AW050700 AW750216 AA614539
			BE074045 Al307407 AW602303 BE073575 Al202532 AA524242 Al970839 Al909751 BE076078 Al909749 R55292
	422128	211994_1	AW881145 AA490718 M85637 AA304575 T06067 AA331991
55	423034 423816	224122_1 23234_1	AL119930 AA320696 AW752565 AL031985 AL137241 Al792386 Al733664 Al857654 Al049911
55	424200	236595_1	AL337221 AA336756 AW966196
	424999	245835_1	AW953120 R56325 AA349562
	426966	273896_1	Al493134 Al498691 AW771508 Al498457 Al768408 Al783624 Al383985 Al580267 D79813 AA393768
60	426991	27415_1	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
00	427260 428023	276598_1 28589_2	AA663848 AA400100 AA401424 AL038843 AA161338 BE268213 AA425597 N87306 AA092969 BE566038 AA247451 N47392 AI928802 AW182584 AW027872 AI819831
			AI936994 W56258 AI653448 AI278611 AI283557 AI824306 AW338658 AW150899 AA687514 N47393 N29885 AA973469 AI038904 AI292064
			Al034339 AW674593 N72156 Al079733 Al038683 Al291616 AA491599 AA993675 AA837380 BE006554 BE006473 Al087090 T33044
65			AA652043 Al203503 AA583959 W35283 Al129926 Z41844 AW020925 AW575848 Al684603 AA493297 Al140689 Al277175 AA425444 Al932767 W02632 BE396786 R37261
05	429220	301384_1	AW207206 AW341473 AA448195 Al951341
	429978	31150_1	AA249027 AL038984 AK001993 AL080066 AV652725 BE566226 AA345557 AA315222 AA090585 AA375688 AA301092 AA298454 W05762
			AW607939 H51658 D83880 N84323 BE296821 AW947007 D61461 AW079261 AA329482 AW901780 Al354442 AA772275 R31663 Al354441
70			AJ767525 H92431 AJ916735 H93575 AJ394255 AW014741 AJ573090 C06195 AW612857 AW255195 AJ339558 AJ377532 AJ308821 AJ919424
70			AI589705 AW055215 AI336532 AI338051 AA806547 C75509 C00618 AW071172 AW769904 AA630381 AI678018 AI863985 D79662 BE221049 AW265018 AI589700 AW196655 N76573 AI370908 BE042393 N75017 AI698870 AW960115
	430439	31808_1	AL133561 AL041090 AL117481 AL122069 AW439292 AI968826
	430935	325772_1	AW072916 A1184913 AA489195 AW466994 AW469044 N59350 A1819642 A1280239 A1220572 AA789302 A1473611 AW841126 D60937
75	431089	327825_1	BE041395 AA491826 AA621946 AA715980 AA666102 AM8736629 AA623090 AA623090 AA623090 AA62306 TOOLIGO
15	431322 432407	331543_1 34624_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188 AA221036 R87170 BE537068 BE544757 C18935 AW812058 T92565 AA227415 AA233942 AA223237 AA668403 AA601627 AW869639
	.02701		BE091833 BE000620 AW961170 AW847519 AA308542 AW821833 AW945588 C04699 AA205504 AA377241 AW821667 AA055720
			AW817981 AW856468 AA155719 AA179928 T03007 AW754298 AA227407 AA113928 AA307904 C16859
90	434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
80			AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 AA149776 AA699829 AW879188 AW813567 AW813538 Al267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
			AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
			AI829309 AW991957 N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662
85	400000	40004 0	AW817705 AW817703 AW817659 BE081531 H59570
رن	436608	42361_3	AA628980 Al126603 BE504035

	W	02/086	443	PCT/US02/12476
	438091	44964_1	,	AW373062 T55662 Al299190 BE174210 AW579001 H01811 W40186 R67100 Al923886 AW952164 AA628440 AW898607 AW898616 AA709126 AW898628 AW998544 AA947932 AW898625 AW898622 Al276125 Al185720 AW510698 AA987230 T52522 BE467708 AW243400 AW043642 Al288245 Al186932 D52654 D55017 D52715 D52477 D53933 D54679 Al298739 Al146984 Al922204 N98343 BE174213 AA845571 AIB13854 Al214518 Al635262 Al139455 Al707807 Al698085 AW884528 Al024768 Al004723 AW087420 Al565133 N94964 Al268939
5			,	AWS13280 AID61126 AIA35818 AI859106 AI360506 AI024767 AAS13019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI866295 AA780994 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096
	439000 439285	467716_1 47065_1	4	AW979121 AAB47986 AAB29098 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AIB67454 N54784 AIG55270 AI421279 AW014882
10		_		AA775552 N62351 N59253 AA626243 Al341407 BE175639 AA456968 Al358918 AA457077
	439780 441128	47673_1 51021_2	4	AL109688 R23665 R26578 AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171 AI359627 AI005068 AI366567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923
15	443068	558874_1		AI188710 AI032142 AW078833 N30308 AW675632 AI219028 AI341201 N22181 H95390 W24187 W24194 R17789
	443947 447636	586160_1 7301_1	,	Y10043 NM_005342 L05085 AL034450 BE614226 AW749053 AA379173 AA248230 BE514634 AA334622 R70656 AA367593 AA214649 AA369318 AW957081 R05760 AA039903 AI886597 AW630122 AA906264 AA041527 R01145 AI088688 BE463637 AA398795 AI354883 AI768938 AI569996 AI452952 AI168582 AI189869 AI086670 AW262560 AW613854 AA862839 AAA35840 AA670197 AI024032 AI990659 AI990089 NB1095 AA847919 AW960150 AA211075 AA044704 AA367594 AW582587 AW858854 AW818630 AW818281 AW818433 AW582595
20	440000	70005 4		AA096002 N83992 AI471630 BE540637 BE265481 AW407710 BE513882 BE546739 AA053597 BE140503 BE218514 AW956702 AI656234 AI636283 AI567265
	448993	79225_1		ANY340858 BE207794 AA053085 R69173 AA292343 AA454908 AA293504 AI659741 AI927478 AA399460 AI760441 AA346416 BE047245 AA730380 AA394063 AA454833 AI982791 AI667270 AI813332 AI767858 AA427705 D20284 AI221458 BE048537 AI263048 AA346417 AA911497 BE537702
25	449305	804424_1		Al638293 AW813561 Al761324 AW880941 AW880937
	451105 451320	859083_1 86576_1		AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AAB30570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI884316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612
30	451807 .	8865_1		W52854 AL117600 BE208116 BE208432 BE206239 BE082291 AW953423 AA351619 BE180648 BE140560 W60080 AA865478 N90291 AW450652 AW449519 AA993634 AI806539 AA351618 AW449522 AI827626 AA904788 AA380381 AA886045 AA774409 BE003229 Z41756 AL133619 AA468118 AA383064 AI476447 T09430 AI673758 AA524895 AI581345 AI300820 AW498812 AA256162 AI559724 AI685732
2.5	452410	9163_1		AA602400 AA905453 AI204595 AW166541 AA157456 AA156269 AA383652 AA431072 AW592707 AI435410 AW272464 AI215594 AA622747
35				AI269603 AI565082 AI807095 AI476629 AA505909 AI368449 AI686077 AI582930 AW085038 AA757863 AA730154 AI767072 AA468316 AI734130 AI734138 AA426284 AA433997 AI741241 AW043563 AI732741 AI732734 AA437369 AA425820 AA664048 R74130
	454241	1067807_1		BE144666 BE184942 AW238414 BE184946
	455175 456237	1257335_1 168730_1		AW993247 AW861464 AA203682 R11958
40	458098	47395_1		ACCIDED N. 1386 N. 138
45				
	TABLE 90	;		
	Pkey: Ref:	Unique n	umber o	orresponding to an Eos probeset 5. The 7 digit numbers in this collumn are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
50	rus.	sequence	of hum	an chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand: Nt_position			rand from which exons were predicted. Ide positions of predicted exons.
	M_posia.	KI. UIUICAICS		
55	Pkey 400512	Ref 9796593	Strand	
55	400517	9796686	Minus	49996-50346
	400560 400664	9843598 8118496	Plus Plus	94182-94323,97056-97243,101095-101236,102824-103005 13558-13721,13942-14090,14554-14679
	400665	8118496	Plus	16879-17023
60	400566	8118496	Plus Minus	17982-18115,20297-20456 9162-9293
	400749 400763	7331445 8131616	Minus	35537-35784
	401027	7230983	Minus	
65	401093 401203	8516137 9743387	Minus Minus	
-	401212	9858408	Plus	87839-88028
	401411 401435	7799787 8217934	Minus Minus	
	401464	6682291	Minus	
70	401714	6715702	Plus	96484-96681 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-
	401747	9789672	Minus	131932,132451-132575,133580-134011
	401760 401780	9929699 7249190	Plus Minus	83126-83250,85320-85540,94719-95287 28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
75	401781	7249190	Minus	83215-83435 83531-83656 83740-83901.84237-84393.84955-85037,86290-86814
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401797 401961	6730720 4581193	Plus Minus	6973-7118 124054-124209
	401985	2580474	Ptus	61542-61750
80	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402075 402260	8117407 3399665	Plus Minus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076 113765-113910,115653-115765,116808-116940
	402265	3287673	Plus	21059-21168
05	402297	6598824	Plus	35279-35405,35573-35659
85	402408	9796239	Minus	5 110326-110491

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	**	0 02/00	0443	
	402420	9796339	Pius	129750-129919
	402674	8077108	Minus	39290-39502
	402802	3287156	Minus	53242-53432
_	402994	2996643	Minus	4727-4969
5	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403306	8099945	Plus	127100-127251
	403329	8516120	Ptus	96450-96598
	403381	9438267	Minus	26009-26178
	403478	9958258	Plus	116458-116564
10	403485	9966528	Plus .	2888-3001,3198-3532,3655-4117
	403627	8569879	Minus	23868-24342
	403715	7239669	Plus	85128-85292
	404044	9558573	Minus	225757-225939
	404076	9931752	Minus	3848-3967
15	404101	8076925	Minus	125742-125997
	404140	9843520	Ptus	37761-38147
	404165	9926489	Minus	69025-69128
	404185	4572584	Minus	129171-129327
~~	404210	5006246	Plus	169926-170121
20	404253	9367202	Minus	55675-56055
	404287	2326514	Plus	53134-53281
	404298	9944263	Minus	73591-73723
	404347	9838195	Plus	74493-74829
0.0	404440	7528051	Plus	80430-81581
25	404721	9856648	Minus	173763-174294
	404794	4826439	Plus	101619-101898
	404854	7143420	Plus	14260-14537
	404877	1519284	Plus	1095-2107
20	404927	7342002	Plus	68690-69563
30	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405449	7622497	Plus	42236-42570
	405568	6006906	Plus	35912-36065 95339 95339
	405572	3800891	Plus	85230-85938
35	405646	4914350	Pius	741-969 73195-73917
33	405676	4557087	Plus Plus	61057-62075
	405770 405932	2735037 7767812	Minus	123525-123713
		9166422	Minus	30487-31058
	405137 405360	9256107	Minus	7513-7673
40	406399	9256288	Minus	63448-63554
70	406467	9795551	Plus	182212-182958
	400407	ar 3333 I	1 143	(APP.15-1APRA)

- TABLE 10A: Potential Therapeutic, Diagnostic and Prognostic targets for Therapy of Lung Cancer and Non-mailgnant Lung Disease
 Table 2A shows about 307 genes up-regulated in non-mailgnant lung disease relative to lung tumors and normal body tissues and/or down-regulated in lung tumors relative to
 normal lung and non-mailgnant lung disease. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. 45
- Table 108 show the accession numbers for those Pkey's lacking UnigenelD's for table 10A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the 50 "Accession" column.
 - Table 10C show the genomic positioning for those Pikey's lacking Unigene ID's and accession numbers in table 10A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number Pkey: ; ExAccn:

UnigenelD: Unigene number 60 Unigene Title:

55

Unigene gene title
Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinold tumors) divided by the
'average of normal lung samples R1:

Average of non-matignant lung disease samples (Including bronchitis, emphysema, fibrosis, atelectasis, asihma) divided by the average of normal lung samples R2:

65	Pkey	ExAcon	UnigenelD	Unigene Title	R1	R2
	404394		-	ENSP00000241075:TRRAP PROTEIN.	0.79	3.10
	404916			Target Exon	1.00	159.00
	405257			Target Exon	1.00	422.00
	407228	M25079	Hs.155376	hemoglobin, beta	0.47	2.33
70	407568	AA740964	Hs.62699	ESTs	1.00	123.00
, ,	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
	409031	AA376836	Hs.76728	ESTs	1.00	128.00
	410434	AF051152	Hs.63668	tofi-like receptor 2	39.65	149.00
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	1.00	109.00
75	410808	T40326	Hs.167793	ESTs	1.14	13.14
	412351	AL135960	Hs.73828	T-cell acute lymphocytic teukemia 1	0.37	2,27
	412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
	413795	AL040178	Hs.142003	ESTs	0.10	11.90
	414154	AW205314	Hs.323060	ESTs	0.62	2.09
80	414214	D49958	Hs.75819	glycopratein M6A	0.03	4.55
00	414998	NM 002543	Hs.77729	oxidised low density lipoprotein (lectin	0.64	2.97
	415122	D60708	Hs.22245	ESTs	0.07	8.97
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	0.67	1.65
	415775	H00747	Hs.29792	ESTs, Weakly similar to 138022 hypotheti	0.29	2.64
85	415773	U20350	Hs.78913	chemokina (C-X3-C) receptor 1	1.00	145.00
O.J	410010	U2003U	113.10310	minimization of sochor i		, , , , , ,

	w	O 02/086				007.40
	416319	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i complement component 4-binding protein,	15.32 0.64	237,00 4.00
	416402 417355	NM_000715 D13168	Hs.1012 Hs.82002	endothelin receptor type B	0.01	3.90
_	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	36.30	357.00
5	417511	AL049176	Hs.82223	chordin-like adenosine deaminase, RNA-specific, B1 (h	1.00 0.02	179.00 6.00
	418489 418726	U76421 BE241812	Hs.85302 Hs.87860	protein tyrosine phosphalase, non-recept	1.00	113.00
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	0.44	1.90
10	418883	BE387036	Hs.1211	acid phosphatase 5, tartrale resistant	0.96 0.62	2.04 2.74
10	419086 419150	NM_000216 T29618	Hs.89591 Hs.89640	Kallmann syndrome 1 sequence TEK tyrosine kinase, endothelial (venous	0.02	6.90
	419235	AW470411	Hs.288433	neurotrimin	1.48	5.13
	419407	- AW410377	Hs.41502	hypothetical protein FLJ21276	37.55	336.00 3.65
15	420556 420656	AA278300 AA279098	Hs.124292 Hs.187636	Homo saplens cDNA: FLJ23123 fis, clone L ESTs	0.80 1.65	8.07
15	420729	AW964897	Hs.290825	ESTs	2.99	25.82
	421177	AW070211	Hs.102415	Homo saplens mRNA; cDNA DKFZp586N0121 (f	0.46 1.00	1.95 156.00
	422060 422426	R20893 W79117	Hs.325823 Hs.58559	ESTs, Moderately similar to ALU5_HUMAN A ESTs	0.03	7.44
20	422652	AW967969	Hs.118958	syntaxin 11	0.14	3.62
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	0.01 0.75	3.16 141,75
	424433 424585	H04607 AA464840	Hs.9218 Hs.131987	ESTs ESTs	1.00	167.00
	424711	NM_005795	Hs.152175	calcitonin receptor-like	0.43	3.01
25	424973	X92521	Hs.154057	matrix metalloproteinase 19	0.37 0.14	19.45 3.35
	425023 425664	AW956889 AJ006276	Hs.154210 Hs.159003	endothelial differentiation, sphingolipi transient receptor potential channel 6	1.00	94.00
	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	0.68	1.42
20	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.03	3.74 141.00
30	426753 427558	T89832 D49493	Hs.170278 Hs.2171	ESTs growth differentiation factor 10	1.00 1.00	117.00
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	0.75	2.20
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	0.76	2.25
35	428927 429496	AA441837 AA453800	Hs.90250 Hs.192793	ESTs ESTs	0.01 1.00	3.62 138.00
33	430468	NM_004673	Hs.241519	anglopoietin-like 1	1.00	132.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00 157.00
	431728 431848	NM_007351 Al378857	Hs.268107 Hs.126758	multimentn ESTs, Highly similar to AF175283 1 zinc	1.00 0.34	2.24
40	432128	AA127221	Hs.117037	ESTs	0.00	1,15
	432519	Al221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	0.01 1.00	2,06 267.00
	433043 433803	W57554 AI823593	Hs.125019 Hs.27688	lymphoid nuclear protein (LAF-4) mRNA ESTs	1.00	105.00
	434730	AA644669	Hs.193042	ESTs	1.05	3.15
45	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	0.83 1.00	1.94 218.00
	436532 437119	AA721522 Al379921	Hs.177043	gb:nv54h12.r1 NCI_CGAP_Ew1 Homo saplens ESTs	1.00	133.00
	437140	AA312799	Hs.283689	activator of CREM in testis	0.67	122.67
50	437211	AA382207	Hs.5509 Hs.222194	ecotropic viral integration site 2B ESTs	1.00 1.00	142.00 147.00
30	437960 438202	Al669586 AW169287	Hs.22588	ESTs	1.00	141.00
	438873	A1302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	0.71	3.66
	438875 441048	AA827640 AA913488	Hs.189059 Hs.192102	ESTs ESTs	23.32 0.77	370.00 8.50
55	441188	AW292830	Hs.255609	ESTs	3.43	16.36
	441499	AW298235	Hs.101689	ESTs	1.00	167.00
	444513 444527	AL120214 NM_005408	Hs.7117 Hs.11383	glutamate receptor, ionotropic, AMPA 1 small inducible cytokine subfamily A (Cy	1.00 46.47	151.00 153.00
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	0.01	3.08
60	445279	R41900	Hs.22245	ESTs	0.60	141.00 2.39
	446017 446984	N98238 AB020722	Hs.55185 Hs.16714	ESTs Rho guanine exchange factor (GEF) 15	0.18 0.10	2.16
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.01	2.53
65	447357	A1375922	Hs.159367	ESTs	0.46 18.05	2.64 296.00
UJ	448106 448253	A1800470 H25899	Hs.171941 Hs.201591	ESTs ESTs	1.00	141.00
	449275	AW450848	Hs.205457	periaxin	0.56	1.38
	450400	A1694722	Hs.279744	ESTs hypothetical protein FLJ23191	0.88 0.52	4.33 2.08
70	450698 450726	AI654223 AW204600	Hs.16026 Hs.250505	retinoic acid receptor, alpha	0.79	2.01
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	0.35	2.03
	451533	NM_004657	Hs.26530 Hs.169872	serum deprivation response (phosphalidy) ESTs	0.13 1.00	2.25 116.00
	453636 458332		Hs.220491	ESTs	1.00	192.00
75	459580	AA022888	Hs.176065	ESTs	0.20	2.98
	400269			Eos Control NM_016369*:Homo sapiens claudin 18 (CLDN	0.40 0.53	2.40 1.77
	403421 407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	0.01	3.18
90	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.56	1.74
80	414517		Hs.76305 Hs.1074	surfactant, pulmonary-associated protein surfactant, pulmonary-associated protein	0.64 0.33	1.50 1.16
	417204 418307		Hs.83974	solute carrier family 21 (prostaglandin	0.53	1.55
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.20	1.28
85	421502 421798		Hs.105039 Hs.29877	solute carrier family 34 (sodium phospha N-acylsphingosine amidohydrolase (acid c	0.78 0.59	1.90 1.54
05	721130	147-4000	1 10.23011	sa control de como antenante de como en como e		•••

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	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	0.59	1.55
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	0.35	1.62
_	425438	T62216	Hs.270840	ESTs	0.23	9.45
5	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	0.03	1.71
	427019	AA001732 T92248	Hs.173233	hypothetical protein FLJ10970	0.01 0.42	1.49 1.26
	428043 430280	AA361258	Hs.2240 Hs.237868	uteroglobin Interleukin 7 receptor	0.46	2.43
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	0.57	1.59
10	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	0.29	1.80
	432985	T92363	Hs.178703	ESTs	0.32	2.27
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	0.31	1.51
•	442275	AW449467	Hs.54795	ESTs ESTs	0.55 0.00	1.78 3.02
15	443709 444325	A1082692 AW152618	Hs.134662 Hs.16757	ESTs	0.32	2.49
13	450954	AJ904740	Hs.25691	receptor (calcitonin) activity modifying	0.46	1.74
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	0.52	1.87
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	0.00	3.30
20	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.01	2.31
20	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	0.66 1.00	2.20 297.00
	400754 401045			Target Exon C11001883*:gi[6753278[ref[NP_033938.1] c	1.00	109.00
	401043			NM_016582*:Homo sapiens peptide transpor	0.89	1.39
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.45	4.47
25	402808			ENSP00000235229:SEMB.	1.00	1.87
	403021			C21000030:gij9955960[ref]NP_063957.1] AT	1.00	149.00
	403438			NM_031419*:Homo sapiens molecule possess	1.06 0.04	2.96 4.89
	403687 403764			NM_007037*:Homo saplens a disintegrin-li NM_005463:Homo saplens heterogeneous nuc	1.00	225.00
30	404277			NM_019111*:Homo sapiens major histocompa	0.97	1.93
	404288			NM_002944*:Homo sapiens v-ros avian UR2	1.00	68.00
	404518	Al815601		CD83 antigen (activated B lymphocytes, i	0.02	1.83
	405106			C11001637*:gi 5032241 ref NP_005732.1 z	1.00	235.00
25	405381			Target Exon	1.00 1.37	93.00 6.02
35	406387 406646	M33600		Target Exon major histocompatibility complex, class	0.86	2.46
	406714	Al219304	Hs.266959	hemoglobin, gamma G	0.01	3.19
	406753	AA505665	Hs.217493	annexin A2	1.00	147.00
40	406973	M34996	Hs.198253	major histocompatibility complex, class	1.03	2.04
40	407248	U82275	Hs.94498	teukocyte immunoglobulin-like receptor,	1.00	64.00
	407510	U96191	U- 200C0	gb:Human trophoblast hypoxia-regulated f	1.00 1.00	90.00 67.00
	407731 407830	NM_000066 NM_001086	Hs.38069 Hs.587	complement component 8, beta polypeptide arylacetamide deacetylase (esterase)	1.00	102.00
	408045	AW138959	Hs.245123	ESTs	1.00	70.00
45	408074	R20723		ESTs	1.00	112.00
_	408374	AW025430	Hs.155591	forkhead box F1	0.07	10.17
	409064	AA062954	Hs.141883	ESTs	0.39	2.31
	409083	AF050083	Hs.673	interleukin 12A (natural killer cell sti	1.00 0.01	95.00 4.55
50	409153 409203	W03754 AA780473	Hs.50813 Hs.687	hypothetical protein FLJ20022 cytochrome P450, subfamily IVB, polypept	0.01	3.72
50	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.00	79.00
	409389	AB007979	Hs.301281	Homo saplens mRNA, chromosome 1 specific	0.14	27.35
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.00	113.00
55	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	0.64 0.55	2.47 2.40
23	411020 411687	NM_006770 BE160198	Hs.67726	macrophage receptor with collagenous str gb:QV1-HT0413-010200-059-h03 HT0413 Homo	1.00	111.00
	412000	AW576555	Hs.15780	ATP-binding cassette, sub-family A (ABC1	1.00	95.00
	412358	BE047490	Hs.24172	ESTs	1.00	87.00
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.43	8.07
60	412564	X83703	Hs.31432	cardiac ankyrin repeat protein	0.02	3.07
	412869	AA290712	Hs.82407 Hs.82407	CXC chemokine ligand 16 CXC chemokine ligand 16	0.93 0.97	1.72 1.51
	412870 413529	N22788 U11874	Hs.846	interteukin 8 receptor, beta	0.02	2.42
	413533	BE146973	14.040	gb:QV4-HT0222-011199-019-e05 HT0222 Homo	0.65	1.50
65	413689	BE157286	Hs.20631	zinc finger protein, subfamily 1A, 5 (Pe	20.87	232.00
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	1.00	80.00
	413800	Al129238	Hs.192235	ESTS	1.00	85.00 213.00
	413802	AW964490	Hs.32241 Hs.75572	ESTs, Weakly similar to \$65657 alpha-1C- carboxypeptidase B2 (plasma)	1.00 0.02	3.93
70	413829 414376	NM_001872 BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [1.00	115.00
,,	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	0.49	1.94
	414700	H63202	Hs.38163	ESTs	0.03	3.75
	415078	AA311223	Hs.283091	found in Inflammatory zone 3	0.86	1.95
76	415120	N64464	Hs.34950	ESTs	1.00	120.00
75	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	0.60 1.00	2.48 95.00
	415335	AA847758 W92445	Hs.111030 Hs.165195	ESTs Homo saplens cDNA FLJ14237 fis, clone NT	1.00	136.00
	415582 416030	W92445 H15261	Hs.21948	ESTs	0.02	8.07
	416427	BE244050	Hs.79307	Rac/Cdc42 guanine exchange factor (GEF)	1.00	73.00
80	416464	NM_000132	Hs.79345	coagulation factor VIII, procoagulant co	0.70	3.36
	416585		Hs.79386	leiomodin 1 (smooth muscle)	0.06	6.56
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do hypothetical protein FLJ14902	0.70 1.00	3.66 114.00
	417148 417370	AA359896 T28651	Hs.293885 Hs.82030	tryptophanyl-tRNA synthetase	0.85	1.30
85	417673	T87281	Hs.16355	ESTs	0.15	15.54

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	418067	Al127958	Hs.83393	cystatin E/M	0.81 1.00	1.74 99.00
	418296 418643	C01566 J03798	Hs.86671 Hs.86948	ESTs small nuclear ribonucleoprotein D1 polyp	1.00	60.00
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	2.40	14.74
5	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	0.67	3.16
	419261 419564	X07876 U08989	Hs.89791 Hs.91139	wingless-type MMTV integration site fami solute carrier family 1 (neuronal/epithe	1.00 1.00	73.00 192.00
	419574	AK001989	Hs.91165	hypothetical protein	1.00	94.00
10	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	61.16	500.00
10	420256	U84722	Hs.76206 Hs.293878	cadherin 5, type 2, VE-cadherin (vascula ESTs, Moderately similar to ZN91_HUMAN Z	0.52 1.00	1.70 172.00
•	420285 420577	AA258124 AA278436	Hs.186649	ESTs. Wilder acting surmar to 21431_1014F41 2	1.00	97.00
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	1.00	64.00
15	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	0.88 0.05	1.51 11.26
13	421470 421478	R27496 Al683243	Hs.1378 Hs.97258	annexin A3 ESTs, Moderately similar to \$29539 ribos	1.00	73.00
	421563	NM_006433	Hs.105806	granulysin	0.82	2.42
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	5.50 1.00	31.57 129.00
20	421855 421913	F06504 A1934365	Hs.27384 Hs.109439	ESTs, Moderately similar to ALU4_HUMAN A osteoglycin (osteoinductive factor, mime	1.00	101.00
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	0.60	63.60
	422232	D43945	Hs.113274	transcription factor EC	1.00 1.40	148.00 3.98
	422386 423168	AF105374 R34385	Hs.115830 Hs.124940	heparan sulfale (glucosamine) 3-O-sulfot GTP-binding protein	0.34	3.59
25	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	0.55	2.00
	423387	AJ012074	11- 400400	vasoactive intestinal peptide receptor 1	0.09 1.00	2.13 141.00
	423424 423456	AF150241 AL110151	Hs.128433 Hs.128797	prostaglandin D2 synthase, hematopoletic DKFZP586D0824 protein	1.00	66.00
	423696	Z92546		Sushi domain (SCR repeat) containing	0.73	1.27
30	424027	AW337575	Hs.201591	ESTs	0.54	2.58 2.47
	424212 425087	NM_005814 R62424	Hs.143131 Hs.126059	glycoprotein A33 (transmembrane) ESTs	0.77 1.00	74.00
	425175	AF020202	Hs.155001	UNC13 (C. elegans)-like	0.85	1.96
25	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.18	2.56 76.00
35	426486 427507	BE178285 AF240467	Hs.170056 Hs.179152	Homo sapiens mRNA; cDNA DKFZp586B0220 (f toll-like receptor 7	1.00 1.00	63.00
	427618	NM_000760	Hs.2175	colony stimulating factor 3 receptor (gr	0.60	2.19
	427732	NM_002980	Hs.2199	secretin receptor	0.97	1.42 105.00
40	427952 428709	AA765368 BE268717	Hs.293941 Hs.104916	ESTs, Moderately similar to A53959 throm hypothetical protein FLJ21940	1.00 1.00	80.00
70	428769	AW207175	Hs.106771	ESTs	0.09	2,55
	428780	Al478578	Hs.50636	ESTs	1.00	98.00 113.00
	428833 429657	Ai928355 D13626	Hs.185805 Hs.2465	ESTs KIAA0001 gene product; putative G-protei	1.00 1.00	52.00
45	430212	AA469153	1 10.2700	gb:nc67f04.s1 NCI_CGAP_Pr1 Homo saplens	1.00	132.00
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	0.11 1.00	15.60 103.00
	430376 430414	AW292053 AW365665	Hs.12532 Hs.120388	chromosome 1 open reading frame 21 ESTs	0.50	6.96
~ 0	430656	AA482900	Hs.162080	ESTs	1.00	70.00
50	430843	AI734149	Hs.119514 Hs.204038	ESTs indolethylamine N-methyltransferase	1.00 0.29	90.00 1.84
	430998 431217	AF128847 NM_013427	Hs.250830	Rho GTPase activating protein 6	1.00	79.00
	431921	N46466	Hs.58879	ESTs	0.91	1.67
55	432176 432203	AW090386	Hs,112278 Hs.49	arrestin, beta 1 macrophage scavenger receptor 1	0.66 1.00	2.63 76.00
33	432231	AA305746 AA339977	Hs.274127	CLST 11240 protein	0.46	1.46
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	0.79	2.25 4.83
	432522 432596	D11466 AJ224741	Hs.51 Hs.278461	phosphatidylinositol glycan, class A (pa matrilin 3	1.93 0.04	5.79
60	432850	X87723	Hs.3110	angiotensin receptor 2	1.00	167.00
	433138	AB029496	Hs.59729	semaphorin sem2	0.04 1.00	9.16 91.00
	433563 433588	A1732637 A1056872	Hs.277901 Hs.133386	ESTs ESTs	120.16	315.00
	434445	AJ349306	Hs.11782	ESTs	0.60	1.84
65	435496	AW840171	Hs.265398	ESTs, Wealdy similar to transformation-r	1.00 1.00	128.00 108.00
	435974 436061	U29690 A1248584	Hs.37744 Hs.190745	Homo sapiens beta-1 adrenergic receptor Homo sapiens cDNA: FLJ21326 fis, clone C	1.00	91.00
	437157	BE048860	Hs.120655	ESTs	1.00	87.00
70	437207	T27503	Hs.15929	hypothetical protein FLJ12910 SWI/SNF related, matrix associated, acti	1.00 1.00	105.00 71.00
70	437311 437439	AA370041 H29796	Hs.9456 Hs.269622		1.00	115.00
	438199	AW016531	Hs.122147	ESTs	1.00	80.00
	439551	W72062	Hs.11112 Hs.7239	ESTs SEC24 (S. cerevisiae) related gene famil	0.30 1.00	3.10 77.00
75	440515 440887	AJ131245 AI799488	Hs.135905	ESTs	1.00	85.00
	441025	AA913880	Hs.176379	ESTs	1.00	82.00
	441384		Hs.288660 Hs.127346	Homo sapiens cDNA: FLJ22182 fis, clone H ESTs	0.7 9 1.00	1.89 75.00
	441735 442200		Hs.235768	ESTS	0.78	5.83
80	442832	AW206560	Hs.253569	ESTs	0.03	10.88
	442957		Hs.49397 Hs.132917	ESTs ESTs	1.00 1.00	70.00 197.00
	443282 443547		Hs.23767	hypothetical protein FLJ12666	1.00	253.00
05	443951	F13272	Hs.111334	ferritin, light polypeptide	0.55	2.09
85	444330	AI597655	Hs.49265	ESTs	1.00	90.00

PCT/US02/12476 WO 02/086443 Hs.169979 1.00 84.00 444515 AW204908 **ESTs** 4.38 97.00 445769 AI741471 Hs.23666 0.02 445908 R13580 Hs.13436 Homo saplens clone 24425 mRNA sequence 1.00 0.93 1.69 446291 446917 BE397753 Hs.14623 Interferon, gamma-inducible protein 30 5 Hs.156672 1.00 106.00 AI347863 **ESTs** extracellular link domain-containing 1 0.40 47.20 447261 NM_006691 Hs.17917 1.00 100.00 447432 AW958473 Hs.301957 nudix (nucleoside diphosphate linked moi 8.21 KIAA1233 orolein 0.05 447482 AB033059 Hs.18705 ESTs, Weakly similar to 138022 hypotheti 0.02 5.42 447997 H00656 Hs.29792 10 Hs.20887 hypothetical protein FLJ10392 1.00 79.00 448299 AA497044 0.42 1.56 448782 AL050295 Hs.22039 KIAA0758 protein purine-rich element binding protein A ESTs 0.17 NM_005859 AA040403 450575 Hs.29117 1.00 94.00 Hs.60371 450584 1.00 91.00 450693 AW450461 Hs.203965 **ESTs** 152.00 ESTs, Weakly similar to KIAA1324 protein DKFZP564D206 protein 15 450715 Al266484 Hs.31570 1.00 86.00 451103 R52804 Hs 25956 AF124251 Hs.26054 novel SH2-containing protein 3 0.60 1.30 451220 451668 0.54 1.00 191 Z43948 Hs.326444 cartilage acidic protein 1 67.00 AW023595 Hs.232048 452197 purine-rich eternent binding protein A 4.53 11.07 20 452331 AA598509 Hs.29117 epithelial membrane protein 2 0.72 2.24 C18825 452353 Hs.29191 1.00 68.00 BE537217 Hs.30343 **ESTs** 453049 vanillold receptor-like protein 1 Homo sapiens cDNA FLJ11422 fis, clone HE 1.70 0.83 453107 NM_016113 Hs.279746 1.00 132.00 453355 AW295374 Hs.31412 1.00 72.00 25 453390 AA862496 Hs.28482 **ESTs** ESTs, Wealdy similar to JC5795 CDEP prot gb:CM2-HT0342-091299-050-b05 HT0342 Homo 453531 1.00 68.00 AA417940 2.89 0.57 454741 BE154396 up-regulated by BCG-CWS 1.00 82.00 Hs.284205 456579 AA287827 Homo saplens, clone MGC:16327, mRNA, com 0.79 1.96 3.25 Hs.114727 456672 AK002016 30 Hs.252549 cathepsin Z 1.03 457400 AF032906 ESTs, Weakly similar to ALU4_HUMAN ALU S gb:HSC1KA072 normalized infant brain cDN 113.00 1.00 457718 F18572 Hs.22978 544.00 459696 F03027 TABLE 10B 35 Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Genbank accession numbers Accession: 40 Pkey 408074 CAT Number R20723 AA263003 AA333976 AA334725 AA334151 AW965490 AA310513 AIB10530 D31302 AW134897 AAB30127 AA046953 AI668930 103684_1 C06094 AW104534 BE160198 AW935898 T11520 AW935930 AW856073 AW861034 411667 1253334 1 BE146973 BE146972 BE147042 BE147018 BE145783 BE147020 BE146781 BE147019 BE146766 BE147021 BE146952 BE146767 BE147044 BE146773 BE146776 BE146985 BE146793 BE146778 BE146784 BE146771 BE146985 BE146793 BE146789 BE146771 BE146984 BE146760 BE147048 BE147025 BE147030 AJ012074 U11087 L13288 X75299 L20295 AW630780 H14880 T28037 AJ872991 R72136 AW449839 T81622 T79697 T29519 R94105 T83923 1375344_1 413533 45 423387 22779_1 AUD12074 U1 1U87 L13288 X79299 L20259 AWG030780 H14500 126037 ABO 22591 R72130 AWG48035 H1622 173037 122515 R54105 163525 R73300 A1797007 R73390 AA961010 H74168 A1668932 BE045543 AI808418 A1608912 A1806573 AW884084 AW872978 AW872985 AA565655 A1022915 R50647 R73210 H45098 R46451 AW166269 T71132 A1264547 R52146 A1304920 R73391 AW884085 W884085 H73241 T50038 T73612 R73145 R50549 A1094557 A1668793 R72302 A1564366 W01956 AA418962 W32571 R72840 H45409 R72085 R46356 R46758 AA508805 AA418798 T83751 R94072 T16182 AA928785 AA903896 A2576 A257678 A1672488 AW341487 A1827050 AW298668 A1792189 A1015693 A1733599 A1572251 A1672488 AW193262 A1244716 50 23112_1 423698 Al864375 Al206100 AA912444 Al269365 Al640254 AW772466 Al867336 AA627604 H16914 AA358477 AA338009 AA469153 AI718503 AA469225 314437_1 430212 AA721522 AW975443 T93070 436532 421802_1 AA417940 AA036735 T07025 55 453531 97026 1 1232559_1 BE154396 AW817959 BE154393 454741 TABLE 10C 60 Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA Pkey: Ref sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495. Indicates DNA strand from which exons were predicted. Strand: 65 Indicates nucleotide positions of predicted exons. Nt_position: Nt_position 144559-144684 Strand Pkey 400754 7331445 Plus 90044-90184,91111-91345 401045 401083 8117619 Plus 70 3242744 Plus 33192-33360 53526-53628,55755-55920,57530-57757 114964-115136,115461-115585,115931-116047,117666-117771,118004-118102 402474 7547175 Minus 402808 6456148 Minus 403021 120799-120966 7547270 Plus 126609-126773,139986-140205 9665041 Minus 75 403438 90792-90938 9719679 Plus 403687 7387384 9009-9534 118692-118853 403764 7717105 1834458 Minus 91665-91946 Minus 2769644 404288 Plus 3512-3691 37121-37205,37491-37762,41053-41140,41322-41593,41773-41919 84494-84603 80 404394 3135305 Minus 404518 8151988 Plus 91057-91188 7341826 404916 Plus

80877-81418

73121-73273

7636-8054

405106

405381

85

8079395

7329310

6006920

Minus

Minus

 $\begin{tabular}{ll} WO & 02/086443 \\ TABLE 11A: Genes Distinguishing Adenocarchoma from Other Lung Diseases and Normal Lung\\ \end{tabular}$

Table 11A shows about 84 genes upregulated in lung adenocarcinomas relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechlp array.

Table 118 show the accession numbers for those Pkey's lacking UnigenetD's for table 11A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the

Table 11C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 11A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Unique Eos probeset Identifier number Exemplar Accession number, Genbank accession number Unigene number 15

ExAccn: UnigenelD:

5

10

Unigene Title: Unigene gene title

R1:

Average of fung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinold tumors) divided by the average of normal lung samples

Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples 20 R2:

	10.	7110108	o or non many	in the same of the	.,	
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
	403329		J	Target Exon	1.00	61.00
	406399			NM_003122*:Homo saplens serine protease	1.00	39.00
25	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	226.37	350.00
	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	0.77	1.18
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	1.00	10.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	7.76	1.00
	409103	AF251237	Hs.112208	XAGE-1 protein	80.44	40.00
30	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00	1.00
-	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	1.00	1.00
	410076	T05387	Hs.7991	ESTs	1.12	1.50
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	9.89	1.00
	410399	BE068889		synuclein, gamma (breast cancer-specific	0.92	1.06
35	411908	L27943	Hs.72924	cytidine deaminase	1.00	1.00
-	412612	NM_000047	Hs.74131	arylsulfatase E (chondrodysplasia puncta	1.02	1.03
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	0.84	1.07
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.67	1.00
	417542	J04129	Hs.82269	progestagen-associated endometrial prote	1.28	1.35
40	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	1.00	1.00
	419502	AU076704		fibrinogen, A alpha polypeptide	13.05	115.00
	419631	AW188117	Hs.303154	popeye protein 3	1.00	13.00
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	1.00	8.00
	421155	H87879	Hs.102267	lysyl oxidase	1.00	15.00
45	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	1.17	1.55
10	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	1.46	1.76
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialytransferase 1, 1	1.00	3.00
	421582	Al910275	1.5	trefoll factor 1 (breast cancer, estroge	1.23	1.00
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	1.00	52.00
50	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	4.37	2.34
50	422311	AF073515	Hs.114948	cytokine receptor-like factor 1	1.15	1.78
	422867	L32137	Hs.1584	cartilage digomeric matrix protein (pse	1,69	3.17
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	48.13	72.00
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	1.00	50.00
55	424502	AF242388	Hs.149585	lengsin	1.00	1.00
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.00	59.00
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	21.35	1.00
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	1.00	1.00
	425523	AB007948	Hs.158244	KIAA0479 protein	1.00	35.00
60	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.00	83.00
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	7.41	34.00
	428585	AB007863	Hs.185140	KIAA0403 protein	1.00	6.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	1.06	1.13
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	16.18	105.00
65	429263	AA019004	Hs.198396	ATP-binding cassette, sub-family A (ABC1	1.07	1.00
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.59	1.69
	430508	AI015435	Hs.104637	ESTs	4.75	7.27
	430985	AA490232	Hs.27323	ESTs, Wealdy similar to 178885 serine/th	0.94	1.28
	431548	AJ834273	Hs.9711	novel protein	5.66	15.00
70	431566	AF176012	Hs.260720	J domain containing protein 1	49.76	37.00
	431986	AA536130	Hs.149018	Novel human gene mapping to chomosome 20	1.19	1.47
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.65	1.06
	432677	NM_004482	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.00	48.00
	433556	W56321	Hs.111460	calcium/catmodulin-dependent protein kin	1.00	19.00
75	433819	AW511097	Hs.112765	ESTs	3.71	8.00
• -	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	29.31	72.00
	434424	Al811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L.	1.00	64.00
	434792	AA649253	Hs.132458	ESTs	8.52	44.00
	436217	T53925	Hs.107	fibrinogen-like 1	57.97	31.00
80	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.10	1.41
	436972	AA284679	Hs.25640	claudin 3	1.59	1.46
	437866	AA156781	· -	metallothionein 1E (functional)	3.62	101.00
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	1.60	1.39
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00	1.00
85	439451	AF086270	Hs.278554	heterochromatin-like protein 1	23.28	52.00

	w	O 02/086	443				PCT/US02/12476	
5	439759 441031 441377 443614 443813 443991 444670 444931	AL359055 AI110684 BE218239 AV655386 AA876372 NM_002250 H58373 AV652066	Hs.67709 Hs.7645 Hs.202656 Hs.7645 Hs.93961 Hs.10082 Hs.332938 Hs.75113	Homo saplens mRNA full length insert cDN fibrinogen, B beta polypeptide ESTs fibrinogen, B beta polypeptide Homo saplens mRNA; cDNA DKFZp667D095 (fr potassium intermediate/small conductance hypothetical protein MGC5370 general transcription factor IIIA	1.00 1.41 22.03 1.00 1.20 5.71 1.98 1.00	21.00 99.00 1.00 16.00 1.99 6.87 38.00 54.00		
10	446102 446163 446469 447388 447532	AW168067 AA026880 BE094848 AW630534 AK000614	Hs.317694 Hs.25252 Hs.15113 Hs.76277 Hs.18791	ESTs Homo sapiens cDNA FLJ13603 fis, clone PL homogentisate 1,2-dioxygenase (homogenti Homo sapiens, clone MGC:9381, mRNA, comp hypothetical protein FLJ20607	1.00 1.00 1.00 1.24 1.23	1,00 36,00 11,00 1,16 1,63		
15	448243 448844 449444 451807 452689	AW369771 AI581519 AW818436 W52854 F33868	Hs.52620 Hs.177164 Hs.23590 Hs.284176	integrin, beta 8 ESTs solute carrier family 16 (monocarboxylic hypothetical protein FLJ23293 similar to transferrin	15.84 1.00 1.00 1.55 1.54	1,00 31.00 83.00 35.00 1,44		
20	453392 453464 453735	U23762 AI884911 AI066629	Hs.32964 Hs.32989 Hs.125073	SRY (sex determining region Y)-box 11 receptor (catcitonin) activity modifying ESTs	1.00 1.55 1.01	16.00 2.45 1.30		
	TABLE 1	1B						
25	Pkey: CAT num Accessio	ber: Gene clus		nlifier number abers				
30	Pkey 410399	CAT Numbe 11995_1	BE068 Al9365	889 BE068882 AF044311 AF017256 NM_003087 A 527 AA804675 AA394097 A1139933 AA946606 BE1	71313 AA722407	7 AA293803 A146848	0 AA056035 AA055968 AW796957 Al637713	
35	419502	AA410737 H49348 AA486472 AA411094 AA235594 AA402624 AA443638 AW462137 AA421708 AW266211 Al4932266 AA365132 AW966044 A19502 18535_1 AU076704 T74854 T74860 T72098 T73265 T73873 T69180 T74658 T58786 T60385 T73410 T68781 T67845 T67593 T73952 T67864 T60630 T68367 T68401 T53959 T72360 T72099 T60377 T58961 T71712 T72821 T64738 T73465 T72037 T68688 T72063 T73258 T72826 T64242 T68220 T74673 T71800 T68355 T61227 T62738 T69317 T53850 T64692 T73768 T73962 T73382 T68914 T70975 T73400 T60531 T73277 T73203 T70498 T61409 T58925 NM, 000508 M64982 T68301 T73729 T69443 T60424 T67922 T67736 T68716 T67755 T74765 T73819 T58719 T74756 T60477 T74863 T81109 T68329 T58850 T71857 T73425 T53736 T68698 T64309 T72031 T72079 T64305 T71908 T68107 T71916 T73787 T56035 T64425 T71870 T60476 T61376 T67820 T71895 T41006 T69441 T68170 T74617 T7198 T69440 T61875 R06796						
40			N3359 AA312 AW476 AA235	3 T71914 T53939 T64121 AA693996 T72525 T677; 4 AA344542 AW805054 A120745T T61743 AA0267; 919 T40156 H66239 AV852989 H38728 R98521 A\ 9774 AV651256 N54417 AA812882 AW182292 A11; 252 T27853 T47778 R95746 H70620 AA701463 AV	07 H94389 AA38 7655200 R95790 11192 H61463 H 7827166 R98479	12695 AA918409 T68 1 W03250 W00913 A 72060 AA344503 H3 5 C20925 AV657287	044 S82092 T39959 A1017721 AA312395 A344136 AV660126 R97923 AA343596 8639 A1277511 AV661108 A1207625 T47810 T71959 T71313 T73920 T73333 T61618 T69293	
45	-		AA344 T7047: T7251 T6936	3 T73931 T72178 T72456 AV645639 AV653476 T7: 772754 T74485 T74101 T73668 T71518 T7236 6 T64751 AA344441 AA343657 AA345732 AA34437 7 R02292 T60599 T69206 T70452 T74677 R29366 8 T69358 T68258 AV650429 T73341 T61702 T7455	4 AA343853 T7: 28 Al110639 AA: 161277 T74914 28 T40095 K022	3909 T68070 T72065 344603 AF063513 T6 T60352 R29675 T74 72 T40106 AA343045	5 H72149 T73493 T73495 AV645993 R02293 W696 T68516 T72223 T60507 T67633 R29500 843 AV645792 AA344408 T69197 T72057 5 AA341908 AA341907 AA342807 AA341964	
50			AA345 AA344 AA693 T6783	7 T72042 T62764 A1064899 AA343080 T67832 T72 234 T67598 AA011414 T68036 H48262 A1207557 T 583 T60362 H58121 T95711 T72803 T68055 T717 592 A1248502 R29454 T64764 T67001 T73052 T71 7 T73317 T74273 T69420 T68245 T74380 T67862	68219 W86031 IS R29036 T727 429 T51176 T58 174474 T56068	T69081 T64232 R93 93 T69122 T64595 T 8666 AV655414 H904	196 T62136 AV650539 H67459 T72978 62888 T69139 T68291 T64652 T67971 T46862 126 AA342489 T73666 T67848 T72512 T53835	
55	421582	2041_1	AA568 BE074	275 X00474 X52003 X05030 NM_003225 AA314326 1312 AA614409 AA307578 A1925652 AW950155 A1 1140 AA514776 AA588034 BE074051 BE074068 AV 1045 A1307407 AW602303 BE073575 A1202532 AA3	10083 M12075 7009769 AW050	BE074052 AW00466 1690 AA858276 R553	8 AA578674 AA582084 BE074053 BE074126 189 Al001051 AW050700 AW750216 AA614539	
60	437866	44433_2	AA156 AA837 AA812	1781 AW293839 U52054 AA024963 AA778446 BEO 1481 AW468444 BE185091 AW468002 AA687333 A 1489 AW874142 A1471883 W84421 AA156850	73977 AW44490 AB1 1630 AA581	4 AW602574 BE1640 806 Al866686 Al572	040 BE164012 BE163972 BE163974 BE163992 124 AA043777 AA040926 D20160 Al536733	
	451807	8865_1	W5285 AW45	54 AL117600 BE208116 BE208432 BE206239 BE06 0652 AW449519 AA993634 AI806539 AA351618 AN	V449522 Al8276	3 AA331019 BE 1806 126 AA904788 AA380	1381 AA886045 AA774409 BE003229 Z41756	
65	TABLE 1	1C					1	
5 0	Pkey: Ref:	Sequence sequence	source. The	onding to an Eos probeset 7 digit numbers in this column are Genbank Identifie prosome 22.° Dunham I. et al., Nature (1999) 402:4	r (GI) numbers. 189-495.	"Dunham I. et al." ref	ers to the publication entitled "The DNA	
70	Strand: Ni_positi	Indicates I	DNA strand fro	em which exons were predicted. itions of predicted exons.				

Strand Plus Minus Nt_position 96450-96598 63448-63554

Ref 8516120 9256288

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PCT/US02/12476 WO 02/086443

TABLE 12A: Genes Distinguishing Squamous Cell Carcinoma from Other Lung Diseases and Normal Lung

Table 12A shows about 72 genes upregulated in squamous cell carcinomas of the lung relative to other lung tumors, non-malignant lung disease, and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. 5

Table 12B show the accession numbers for those Pkey's lacking UnigenelD's for table 12A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oaldand California). The Genbank accession numbers for sequences comprising each cluster are listed in the

Table 12C show the genomic positioning for those Pikey's lacking Unigene ID's and accession numbers in table 12A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

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Pkey: ExAccn:

Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unique gene title

Verage of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the Unigene Title: 20 R1:

lung samples

	average of normal lung samples R2: Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average								
	6 1			Unigene Title	R1	R2			
25	Pkey	ExAccn	UnigenelD	matrix metalloproteinase 10 (stromelysin	132.45	4.00			
23	400289	X07820	Hs.2258	NM_002425:Homo sapiens matrix metallopro	3.26	3.22			
	400666				26.47	10.50			
	401780			NM_005557*:Homo saplens keratin 16 (foca	10.33	4.61			
	401781			Target Exon		2.70			
20	401785			NM_002275*:Homo saplens keratin 15 (KRT1	4.13				
30	401994			Target Exon	61.84	47.00			
	402075			ENSP00000251056*:Plasma membrane calcium	1.00	1.00		•	
	404996			Target Exon	1.00	1.00			
	407839	AA045144	Hs.161566	ESTs	173.91	108.00			
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	151.17	8.00			
35	408522	Al541214	Hs.46320	Small proline-rich protein SPRK [human,	1.98	1.24			
	410561	BE540255	Hs.6994	Homo saplens cDNA: FLJ22044 fis, clone H	10.04	1.00			
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.00	30.00			
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	24.30	1,00			
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	53.29	51.00			
40	417034	NM_006183	Hs.80962	neurotensin	1.00	1.00			
	417366	BE185289	Hs.1076	small proline-rich protein 18 (cornifin)	8.97	3.27			
	418663	AK001100	Hs.41690	desmocollin 3	112.17	19.00			
	418678	NM_001327	Hs.87225	cancer/testis antigen	1.18	1.10			
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1.00	1.00			
45	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	3.04	1.25			
	421773	W69233	Hs.112457	ESTs	1.12	1.14			
	421948	L42583	Hs.334309	keratin 6A	51.83	20.25			
	421978	AJ243662	Hs.110196	NICE-1 protein	1.01	0.91			
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	2.37	1.10			
50	422440	NM_004812	Hs.116724	aldo-kelo reductase family 1, member B10	47.53	32.00			
50	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	76.02	1.00			
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.20	1.00			
	423738	AB002134	Hs.132195	airway trypsin-like protease	10.14	51.00	•		
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	233.42	68.00			
55	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	1.00	1.00			
55	424098	AF077374	Hs.139322	small proline-rich protein 3	137.82	54.00			
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	56.19	12.00			
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	33.45	1.00			
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.24	17.00			
60	427335	AA448542	Hs.251677	Gantigen 7B	51.83	4.00			
00	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.00			
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00	16.00			
	428748	AW593206	Hs.98785	Ksp37 protein	1.00	87.00			
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.01	1.18			
65	429538	BE182592	Hs.11261	small proline-rich protein 2A	4.43	2.90			
05	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	11.80	1.00			
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	12.28	41.00			
	430890	X54232	Hs.2699	glypican 1	1.58	1.40			
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	60.25	28.00			
70	431846	BE019924	Hs.271580	uroplakin 18	4.49	2.51			
70	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, tocus D	1.20	1.09			
	434360	AW015415	Hs.127780	ESTs	40.98	27.00			
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.00	1.00			
		AF200492	Hs.211238	interleukin-1 homolog 1	1.00	38.00			
75	435505		Hs.4993	KIAA1313 protein	23.68	42.00			
13	435793	AB037734	Hs.291502		16.76	14.00			
	436511	AA721252	Hs.292206	ESTs	1.00	1.00			
	438403	AA806607	MS.Z9ZZU0	hypothelical protein FLJ20093	46.23	139.00			
	439285	AL133916	11- 50564		33.61	1.00			
80	439606	W79123	Hs.58561	G protein-coupled receptor 87 ESTs, Weakly similar to AC004858 3 U1 sm	1.00	1.00			
οU	439670	AF088076	Hs.59507	ESTS, Weakly similar to DAP1_HUMAN DEATH	86.55	11.00			
	439706	AW872527	Hs.59761	a disintegrin and metalloproteinase doma	62.88	147.00			
	440325	NM_003812	Hs.7164	•	1.53	1.42			
	441525	AW241867	Hs.127728	ESTs DKFZP434G032 protein	31.11	38.00			
85	443162	T49951	Hs.9029 Hs.12569	ESTs	1.00	1.00			
0,5	444378	R41339	113, 12303	Cora					

	W	O 02/086	443				PCT/US02/12476			
5	446292 447078 447342 449003 449101 450832 452240 453317 453830	AF081497 AW885727 A1199268 X76342 AA205847 AW970602 A1591147 NM_002277 AA534296	Hs.279682 Hs.9914 Hs.19322 Hs.389 Hs.23016 Hs.105421 Hs.61232 Hs.41696 Hs.20953	Rh type C glycoprotein ESTs Homo saptens, Similar to RIKEN cDNA 2010 alcohol dehydrogenase 7 (class IV), mu o G protein-coupled receptor ESTs ESTs keratin, hair, acidic, 1 ESTs	1.55 47.24 28.63 1.00 2.58 25.17 13.42 1.19 24.92 1.26	1.26 24.00 1.00 1.00 27.00 36.00 1.00 1.27 25.00 1.11				
10	454098 455601 TABLE 12	W27953 AI368680 B	Hs.292911 Hs.816	ESTs, Highly similar to S60712 band-6-pr SRY (sex determining region Y)-box 2	206.11	1.00				
15	Pkey: CAT numb Accession:	er: Gene cluste	probeset iden er number ecession numb							
20	Pkey 439285	CAT Number 47065_1	AL1339	on 16 N79113 AF086101 N76721 AW950828 AA36401: 52 N62351 N59253 AA626243 Al341407 BE175639	3 AW955684 Al34 AA456968 Al358	6341 A1867454 N5478 918 AA457077	14 A1655270 A1421279 AW014882			
25	TABLE 12	TABLE 12C .								
25	Pkey: Ref:									
30	Strand: Nt_position	Indicates D	NA strand from	n which exons were predicted. ons of predicted exons.						
35	Pkey 400666 401780 401781 401785 401994 402075	Ref 8118496 7249190 7249190 7249190 4153858 8117407	Strand Plus Minus Minus Minus Minus Plus	Nt_position 17982-18115,20297-20456 28397-28617,28920-29045,29135-29296,29411-2 83215-83435,83531-83656,83740-83901,84237-8 165776-165996,166189-166314,166408-166569, 42904-43124,43211-43336,44607-44763,45199-4 121907-122035,122804-122921,124019-124161,	14393,84955-8503 167112-167268,1 15281,46337-4673 124455-124610,1	17,86290-86814 67387-167469,168634 12 25672-126076	-168942 ·			
40	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-4	lub/4,42351-424	DU .				

TABLE 13A: Genes Distinguishing Non-Malignant Lung Disease from Lung Tumors and Normal lung

Table 13A shows about 23 genes upregulated in non-malignant lung disease relative to lung tumors and normal lung. These genes were selected from about 59680 probesets on the Eos/Affymetrix Hu03 Genechip array.

Table 13B show the accession numbers for those Pkey's lacking UnigenelD's for table 13A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the

Table 13C show the genomic positioning for those Pkey's tacking Unigene ID's and accession numbers in table 13A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

15 Pkey: Unique Eos probeset identifier number ExAcon: Exemplar Accession number, Genbank accession number UnigeneiD: Unigene number

Unigene Title: Unigene gene title R1: Average of lung tumors (including squamous cell carcinomas, adenocarcinomas, small cell carcinomas, granulomatous and carcinoid tumors) divided by the

average of normal lung samples

Average of non-malignant lung disease samples (including bronchitis, emphysema, fibrosis, atelectasis, asthma) divided by the average of normal lung samples R2:

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
408562	Al436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	1.00	230.00
409031	AA376836	Hs.76728	ESTs	1.00	128.00
412372	R65998	Hs.285243	hypothetical protein FLJ22029	1.00	173.00
415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	1.00	145.00
417511	AL049176	Hs.82223	chordin-like	1.00	179.00
418819	AA228776	Hs.191721	ESTs	1.00	140.00
422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.00	156.00
424585	AA464840	Hs.131987	ESTs	1.00	167.00
426753	T89832	Hs.170278	ESTs	1.00	141.00
429496	AA453800	Hs.192793	ESTs	1.00	138.00
430719	AA488988	Hs.293796	ESTs	1.00	133.00
431089	BE041395		ESTs, Weakly similar to unknown protein	23.32	941.00
431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.00	157.00
431728	NM_007351	Hs.268107	multimerin		157.00
436532	AA721522		gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens		218.00
437960	AI669586	Hs.222194	ESTs		147.00
438202	AW169287	Hs.22588	ESTs		141.00
441499	AW298235	Hs.101689			167.00
444513	AL120214	Hs.7117	glutamate receptor, fonotropic, AMPA 1		151.00
448253	H25899	Hs.201591	ESTs		141.00
453636	R67837	Hs.169872	ESTs		116.00
458332	Al000341	Hs.220491	ESTs		192.00
459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	1.00	154.00
	408562 409031 412372 415910 417511 418819 422060 424585 426753 429496 431728 431728 436532 43760 438202 441499 444513 448253 458332	408562 Al436323 409031 AA376836 412372 R65998 415910 U20350 417511 AL049176 418819 AA228776 422060 R20893 424585 AA464840 426753 T89832 429496 AA453800 430719 AA488988 431089 BE041395 431385 BE178536 431385 BE178536 4316532 AA721522 437960 Al669586 438202 AW169287 444499 AW296235 444513 AL120214 448253 H25899 453636 R67837 458332 AK000341	408562 Al436323 Hs.31141 409031 AA376836 Hs.76728 412372 R65998 Hs.285243 415910 U20350 Hs.78913 417511 AL049176 Hs.82223 418819 AA228776 Hs.191721 422060 R20893 Hs.325823 424585 AA464840 Hs.131987 426753 T89832 Hs.170278 429496 AA453800 Hs.192793 A30719 AA488988 Hs.293796 431089 BE041395 431089 BE041395 431385 BE178536 Hs.11090 431728 NM_007351 Hs.268107 436532 AA721522 437960 Al699586 Hs.22194 438202 AW169287 Hs.22194 438202 AW169287 Hs.22588 441499 AW298235 Hs.101689 444513 AL120214 Hs.7117 448253 H258899 Hs.201591 453636 R67837 Hs.169872 458332 Al000341 Hs.220491	408562	408562 Al436323 Hs.31141 Homo saplens mRNA for KIAA1568 protein, 1.00 409031 AA376836 Hs.76728 ESTs 1.00 412372 R65998 Hs.285243 hypothetical protein FLJ22029 1.00 415910 U20350 Hs.78913 hypothetical protein FLJ22029 1.00 417511 AL049176 Hs.82223 chernokine (C-X3-C) receptor 1 1.00 418819 AA228776 Hs.191721 Hs.191721 1.00 422060 R20893 Hs.191721 ESTs 1.00 424585 AA464840 Hs.131987 ESTs 1.00 424585 AA468800 Hs.19279 ESTs 1.00 430719 AA488988 Hs.293796 ESTs 1.00 431089 BE0178536 Hs.11090 Hs.268107 mmbrane-spanning 4-domains, subfamily A 1.00 436532 AA721522 ESTs 1.00 43728 NM_007351 Hs.268107 multimerin 1.00 438202 AW169287 Hs.2228

TABLE 13B

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50 Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey 431089 55

CAT Number Accession 327825_1 BE041395 AA491826 AA621946 AA715980 AA666102 436532

AA721522 AW975443 T93070 421802_1

TABLE 13C 60

Pkey: Unique number corresponding to an Eos probeset Ref:

Offique fighter carriesponding to all 20s process.

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Indicates DNA strand from which exons were predicted.

Strand: 65

Nt_position: Indicates nucleotide positions of predicted exons.

Pkey Strand Nt position Ref

121907-122035,122804-122921,124019-124161,124455-124610,125672-126076 402075 8117407 Plus 70

Table 14A shows the subcellular localization and preferred utility for the genes appearing in Tables 9A and 10A. mAb symbolizes monoclonal antibody, diag symbolizes diagnostic, s.m. symbolizes small molecule, and CTL symbolizes cytotoxic lymphocytic ligand. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. 5

Table 14B show the accession numbers for those Pkey's lacking UnigenelD's for table 14A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubteTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the

Table 14C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 14A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: ExAccn:

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
Unigene number

Unigene Title: Unigene gene title
Pref. Utility: Preferred Utility
Pred.Loc: Predicted subcellular localization

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	Pred.Loc	Predicted :	subceima iocai	ization		
	Pkey	ExAccn	UnigenelD	Unigene Title	Pref Utility	Pred. Loc
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (strometysin	mAb & diag & s.m.	extracellular
25	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	mAb	plasma membrane
	402075			ENSP00000251056*:Plasma membrane calcium	mAb & diag	secreted
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	diag	secreted
	408243	Y00787	Hs.624	interleukin 8	diag	secreted
	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	mAb & s.m.	plasma membrane
30	408908	BE296227	Hs.250822	serine/threonine kinase 15	s.m.	cytoplasm
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	CTL & diag	secreted
	409103	AF251237	Hs.112208	XAGE-1 protein	CTL	nuclear
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	diag	secreted
~ ~	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	diag	secreted
35	409757	NM_001898	Hs.123114	cystatin SN	diag	extracellular
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	CTL ·	nuclear
	409956	AW103364	Hs.727	inhibin, bela A (activin A, activin AB a	diag	extracellular
	410001	AB041036	Hs.57771	kallikrein 11	diag	extracellular
40	410407	X66839	Hs.63287	carbonic anhydrase IX	mAb & s.m.	plasma membrane
40	410418	D31382	Hs.63325	transmembrane protease, serine 4	mAb & diag & s.m.	plasma membrane
	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	s.m.	
	412719	AW016610	Hs.816	ESTs	s.m.	nuclear
	414774	X02419	Hs.77274	plasminogen activator, urokinase	diag	extracellular
45	414883	AA926960		CDC28 protein kinase 1	S.M.	extracellular
45	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	CTL & diag mAb & diag & s.m.	secreted
	415669	NM_005025	Hs.78589 Hs.78867	serine (or cysteine) proteinase inhibito protein tyrosine phosphatase, receptor-t	mAb & s.m.	plasma membrane
	415817	U88967	Hs.79432	fibrillin 2 (congenital contractural ara	diag	extracellular
	416658 417034	U03272 NM_006183	Hs.80962	neurotensin	diag	extracellular
50	417079	U65590	Hs.81134	Interleukin 1 receptor antagonist	diag	extracellular
J 0	417308	H60720	Hs.81892	KIAA0101 gene product	s.m.	mitochondrial
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	mAb & diag	secreted
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	mAb	plasma membrane
	417933	X02308	Hs.82962	thymidylate synthetase	s.m.	endoplasmic reticulum
55	418478	U38945	Hs.1174	cyclin-dependent kinase Inhibitor 2A (me	s.m.	cytoplasm
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	mAb & s.m.	plasma membrane
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	CTL	cytoplasmic
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	diag	secreted
	419171	NM_002846	Hs.89655	protein tyrosine phosphatase, receptor t	mAb & s.m.	plasma membrane
60	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	CTL & s.m.	mitochondrial
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	diag	secreted
	419235	AW470411	Hs.288433	nimintonuen	mAb & diag	plasma membrane
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	mAb & s.m.	plasma membrane
15	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	mAb & diag	extracellular*
65	420610	AI683183	Hs.99348	distal-less homeo box 5	CTL	nuclear
	421110	AJ250717	Hs.1355	cathepsin E	sm & diag	extracellular
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	diag mAb & s.m.	secreted plasma membrane
	421474	U76362	Hs.104637	solute carrier family 1 (glutamate trans	diag	secreted
70	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	mAb & s.m.	plasma membrane
70	421753	BE314828	Hs.107911 Hs.108660	ATP-binding cassette, sub-family B (MDR/ ATP-binding cassette, sub-family C (CFTR	mAb & s.m.	plasma membrane
	421817	AF146074	Hs.1473	gastrin-releasing peptide	diag	secreted
	422109 422158	S73265 L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	diag	secreted
	422282	AF019225	Hs.114309	apolipoprolein L	điag	secreted
75	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	s.m.	nuclear
13	422424	A1186431	Hs.296638	prostate differentiation factor	dian	extracellular
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	s.m.	cyloplasm
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	s.m.	nuclear
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	diag	extracellular
80	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	CTL & s.m.	
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	diag	
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	mAb & diag & s.m.	secreted
	423961	D13666	Hs.136348	periostin (OSF-2os)	mAb & diag	extracellular
	424046		Hs.138202	serine (or cysteine) proteinase inhibito	diag	secreted
85	424381	AA285249	Hs.146329	protein kinase Chk2	s.m.	nuclear

	w	O 02/086	443			
	424502	AF242388	Hs.149585	lengsin	s.m.	cytoplasmic
	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	mAb & s.m.	plasma membrane
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	diag	extracellular
_	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	mAb & diag & s.m.	secreted
5	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	s.m. mAb	cytoplasmic plasma membrane
	425650 425734	NM_001944 AF056209	Hs.1925 Hs.159396	desmoglein 3 (pemphigus vulgaris antigen peptidylglycine alpha-amidating monooxyg	S.M.	plasma membrane
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	mAb & diag	plasma membrane
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	mAb & s.m.	plasma membrane
10	426215	AW963419	Hs.155223	stanniocalcin 2	mAb & diag	secreted
	426427	M86699	Hs.169840	TTK protein kinase	CTL & s.m.	nuclear secreted
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic G antigen 78	mAb & diag CTL	cytoplasmic
	427335 427747	AA448542 AW411425	Hs.251677 Hs.180655	serine/threonine kinase 12	s.m.	cytoplasmic
15	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	diag	
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	mAb & diag & s.m.	extracellular
	428450	NM_014791	Hs.184339	KIAA0175 gene product	s.m.	nuclear
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	s.m. mAb & s.m.	nuclear plasma membrane
20	428484 428664	AF104032 AK001666	Hs.184601 Hs.189095	solute carrier family 7 (cationic amino similar to SALL1 (sal (Drosophila)-like	CTL & s.m.	nuclear
20	428698	AA852773	Hs.334838	KIAA1866 protein	mAb	
	428748	AW593206	Hs.98785	Ksp37 protein	diag	extracellular
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	diag	mitochodria*
~~	428969	AF120274	Hs.194689	artemin	diag	extracellular
25	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	mAb & s.m. mAb & s.m.	plasma membrane plasma membrane
	429263	AA019004	Hs.198396 Hs.99376	ATP-binding cassette, sub-family A (ABC1 ESTs	diag at s.m.	secreted
	429547 429610	AW009166 AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	mAb & diag	secreted
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	s.m.	
30	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	mAb & s.m.	plasma membrane
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	diag	extracellular
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	mAb & s.m. mAb & diag	plasma membrane plasma membrane
	431846	BE019924 X63629	Hs.271580 Hs.2877	uroplakin 18 cadherin 3, type 1, P-cadherin (placenta	mAb & diag	plasma membrane
35	431958 432201	A1538613 ·	Hs.298241	Transmembrane protease, serine 3	mAb & diag & s.m.	plasma membrane
55	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	s.m.	nuclear
	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	diag	secreted
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	s.m.	autoplacm
40	437016	AU076916	Hs.5398	guanine monphosphate synthetase	s.m. CTL	cytoplasm ER
40	437044 437789	AL035864 Al581344	Hs.69517 Hs.127812	differentially expressed in Fanconi's an ESTs, Weakly similar to T17330 hypotheti	CTL	nuclear
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	mAb & s.m.	plasma membrane
	439223	AW238299	Hs.250618	UL16 binding protein 2	mAb	plasma membrane
45	439477	W69813	Hs.58042	ESTs, Moderately similar to GFR3_HUMAN G	mAb & s.m.	plasma membrane
45	439606	W79123	Hs.58561	G protein-coupled receptor 87	mAb & s.m. mAb & s.m.	plasma membrane
	439738 440006	BE246502 AK000517	Hs.9598 Hs.6844	sema domain, immunoglobulin domain (Ig), NALP2 protein; PYRIN-Containing APAF1-li	s.m.	nuclear
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	s.m.	
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	mAb & s.m.	plasma membrane
50	443247	BE614387	Hs.333893	c-Myc target JPO1	CTL	extracellular*
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	CTL	extracellular
	443859	NM_013409	Hs.9914 Hs.10086	follistatin type I transmembrane protein Fn14	diag mAb	plasma membrane
	444006 444371	BE395085 BE540274	Hs.239	forkhead box M1	s.m.	nuclear
55	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	diag	secreted
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	mAb & diag	plasma membrane
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	mAb & diag	secreted
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	diag diag	secreted extracellular
	446921	AB012113	Hs.16530	small Inducible cytokine subfamily A (Cy		
60			Up 157601		CH. A diad	secreted
60	447033	Al357412	Hs.157601 He 19322	ESTs Home sapiens, Similar to RIKEN cDNA 2010	CTL & diag CTL	secreted
60	447033 447342	Al357412 Al199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	CTL & diag CTL mAb & s.m	plasma membrane
60	447033	Al357412		Homo saplens, Similar to RIKEN cDNA 2010 integrin, beta 8 ESTs	CTL mAb & s.m mAb & s.m.	plasma membrane
	447033 447342 448243 448844 449048	Al357412 Al199268 AW369771 Al581519 Z45051	Hs.19322 Hs.52620 Hs.177164 Hs.22920	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc	CTL mAb & s.m mAb & s.m. mAb	plasma membrane
60 65	447033 447342 448243 448844 449048 449722	Al357412 Al199268 AW369771 Al581519 Z45051 BE280074	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960	Homo sapiens, Similar to RIKEN cDNA 2010 integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1	CTL mAb & s.m mAb & s.m. mAb s.m.	plasma membrane plasma membrane cytoplasm
	447033 447342 448243 448844 449048 449722 450001	Al357412 Al199268 AW369771 Al581519 Z45051 BE280074 NM_001044	Hs.19322 Hs.52620 Hs.177164 Hs.22920	Homo sapiens, Similar to RIKEN cDNA 2010 integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmitte	CTL mAb & s.m mAb & s.m. mAb s.m. mAb s.m.	plasma membrane plasma membrane cytoplasm plasma membrane
	447033 447342 448243 448844 449048 449722 450001 450375	Al357412 Al199268 AW369771 Al581519 Z45051 BE280074 NM_001044 AA009647	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960 Hs.406	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmitte a disintegrin and metalloproteinase doma	CTL mAb & s.m mAb & s.m. mAb s.m. mAb & s.m. mAb & s.m.	plasma membrane plasma membrane cytoplasm
	447033 447342 448243 448844 449048 449722 450001 450375 450701	Al357412 Al199268 AW369771 Al581519 Z45051 BE280074 NM_001044 AA009647 H39960	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960 Hs.406	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmitte a disintegrin and metalloproteinase doma hypothetical protein XP_098151 (teucine-	CTL mAb & s.m mAb & s.m. mAb s.m. mAb s.m.	plasma membrane plasma membrane cytoplasm plasma membrane plasma membrane plasma membrane secreted
	447033 447342 448243 448844 449048 449722 450001 450375	Al357412 Al199268 AW369771 Al581519 Z45051 BE280074 NM_001044 AA009647	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960 Hs.406	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmitte a disintegrin and metalloproteinase doma hypothetical protein XP_098151 (leucine- ERO1 (S. cerevislae)-like cartilage acidic protein 1	CTL mAb & s.m mAb & s.m. mAb s.m. mAb & s.m. mAb & diag & s.m. mAb & diag diag mAb & diag	plasma membrane plasma membrane cytoplasm plasma membrane plasma membrane plasma membrane
65	447033 447342 448243 448844 449048 449722 450001 450375 450701 450983 451668 452281	A1357412 A199268 AW369771 A1581519 Z45051 BE280074 NM_001044 AA009547 H39960 AA305384 Z43948 T93500	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960 Hs.406 Hs.288467 Hs.25740 Hs.326444 Hs.28792	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmitte a disintegrin and metalloproteinase doma hypothetical protein XP_098151 (leucine-ERO1 (S. cerevislae)-like cartilage acidic protein 1 Homo sapiens cDNA FLJ11041 fis, clone PL	CTL mAb & s.m mAb & s.m. mAb s.m. mAb s.m. mAb & diag & s.m. mAb & diag diag mAb & diag diag diag diag	plasma membrane plasma membrane cytoplasm plasma membrane plasma membrane plasma membrane secreted plasma membrane
65	447033 447342 448243 448844 449048 449722 450001 450375 450701 450983 451668 452281 452401	A1357412 A1199268 AW369771 A1581519 Z45051 BE280074 NM_001044 AA009547 H39960 AA305384 Z43948 T93500 NM_007115	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960 Hs.406 Hs.288467 Hs.26740 Hs.326444 Hs.28792 Hs.29352	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmitte a disintegrin and metalloproteinase doma hypothetical protein XP_098151 (leucine-ERO1 (S. cerevislae)-like cartilage acidic protein 1 Homo sapiens cDNA FLJ11041 fis, clone PL tumor necrosis factor, alpha-induced pro	CTL MAB & s.m MAB & s.m. mAb & s.m. mAb & s.m. mAb & diag & s.m. mAb & diag diag mAb & diag diag diag diag diag diag diag diag	plasma membrane plasma membrane cytoplasm plasma membrane plasma membrane plasma membrane secreted plasma membrane extracellular
65	447033 447342 448243 448844 449722 450001 450375 450701 450983 451686 452281 452401 452747	A1357412 A1199268 AW369771 A1581519 Z45051 BE280074 NM_001044 AA009647 H39960 AA305384 Z43948 T93500 NM_007115 BE153855	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960 Hs.406 Hs.268467 Hs.25740 Hs.326444 Hs.28792 Hs.29352 Hs.61460	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmitte a disintegrin and metalloproteinase doma hypothetical protein XP_098151 (leucine-ERO1 (S. cerevislae)-like cardiage acidic protein 11041 fis, clone PL tumor necrosis factor, alpha-induced protig superfamily receptor LNIR	CTL mAb & s.m mAb & s.m. mAb & s.m. mAb & s.m. mAb & diag & s.m. mAb & diag diag mAb & diag diag diag mAb	plasma membrane plasma membrane cytoplasm plasma membrane plasma membrane plasma membrane secreted plasma membrane extracellular plasma membrane
65 70	447033 447342 448243 448844 449048 449722 450001 450375 450701 450983 451668 452281 452747 452747	A1357412 A1199268 AW369771 A1581519 Z45051 BE280074 NM_001044 AA009647 H39960 AA305384 Z43948 T93500 NM_007115 BE153855 U65011	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960 Hs.406 Hs.288467 Hs.25740 Hs.257444 Hs.28792 Hs.29352 Hs.61460 Hs.30743	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmittle a disintegrin and metalloproteinase doma hypothetical protein XP_098151 (leucine-ERO1 (S. cerevislae)-like cartilage acidic protein 1 Homo sapiens cDNA FLJ11041 fis, clone PL turnor necrosis factor, alpha-induced pro tg superfamily receptor LNIR preferentially expressed antigen in meta	CTL mAb & s.m mAb & s.m. mAb & s.m. mAb & s.m. mAb & diag & s.m. mAb & diag diag mAb & diag diag diag mAb CTL	plasma membrane plasma membrane cytoplasm plasma membrane plasma membrane plasma membrane secreted plasma membrane extracellular
65	447033 447342 448243 448844 449722 450001 450375 450701 450983 451686 452281 452401 452747	A1357412 A1199268 AW369771 A1581519 Z45051 BE280074 NM_001044 AA009547 H39960 AA305384 Z43948 T93500 NM_007115 BE153855 U65011 AAB47843	Hs.19322 Hs.52620 Hs.177164 Hs.22920 Hs.23960 Hs.406 Hs.268467 Hs.25740 Hs.326444 Hs.28792 Hs.29352 Hs.61460	Homo sapiens, Similar to RIKEN cDNA 2010 Integrin, beta 8 ESTs similar to S68401 (cattle) glucose induc cyclin B1 solute carrier family 6 (neurotransmitte a disintegrin and metalloproteinase doma hypothetical protein XP_098151 (leucine-ERO1 (S. cerevislae)-like cardiage acidic protein 11041 fis, clone PL tumor necrosis factor, alpha-induced protig superfamily receptor LNIR	CTL mAb & s.m mAb & s.m. mAb & s.m. mAb & s.m. mAb & diag & s.m. mAb & diag diag mAb & diag diag diag mAb	plasma membrane plasma membrane cytoptasm plasma membrane plasma membrane plasma membrane secreted plasma membrane extracellular plasma membrane nuclear

TABLE 14B

80

Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers

Pkey CAT Number

	wo	02/08644		PCT/US02/12476
5	414883	15024_1	AA082436 AA292753 AA872033 R75953 A AW61300 N95210 A	AA926959 W76521 W24270 W21526 AA037172 BE267636 H83186 AA469909 N86396 AA001348 BE535736 AA081745 BE566245 H75255 H77575 N49786 W80565 H78746 BE559638 W04339 R89127 T55938 BE2779271 AW960304 T29812 AA476873 BE297387 AA177048 NM_001826 X54941 BE314366 AA908783 A1719075 BE270172 BE269819 AA889955 A1204630 W25243 A1935150 W72395 T99630 A1422691 H98460 N31428 BE255916 H03265 A1657576 AA776920 AA910844 AA459522 AA293140 AW514667 W662396 AA662522 A1865147 A1423153 AW262230 AA584410 AA583187 AW024595 AW069734 A1828995 AA22997 AA876046 22 AA527373 AW972459 A1831360 AA621337 AA100926 AA772418 AA594626 A1033892 W95096 A1034317 AA398727 A1085031 A1459432 A1041437 AA932124 AA627684 AA935829 A1004827 A1423513 A1094597 H24079 R54703 A1630359 AA617681 AA978045 W44561 A1991988 A1537692 A1090262 AA740817 A1312104 A1911822 AA416671 A185409 AA129784 AA701623 A1075239
10			A1139549 A1494230 A1494211 AA95434 H03266 B	AA633648 AJ339996 AJ336880 AA399239 AJ078708 AJ085351 AJ362835 AJ346618 AJ146955 AJ99380 AJ348243 N92882 AA765850 AJ278887 AA962596 AJ492600 W80435 AA001979 R97424 AJ129015 N24127 AA157451 AA235549 AA459292 AA037114 AA129785 AW059601 AW886710 R92790 N59755 AJ361128 AW589407 H47725 H97534 H48076 H48450 T99631 AW300758 H03431 R76789 I H77576 R96823 AJ457100 N92845 N49682 H42038 BE220698 BE220715 H99552 AJ701624 N74173 R54704 H79520 H72923 E261919 AA769633 AA480310 AA507454 AA910586 AJ203723 AW104725 W25611 W25071 T88980 H03513 T77589 R99156
15	450375	83327_1	AA00964	R97470 AA702275 T77551 AA911962 H82956 N83673 AA283672 P AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 I H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 Al161014 AA099554 R69067
20	TABLE 14C			
20	Pkey: Ref:	Sequence sou	irce. The 7 d	ing to an Eos probeset git numbers in this column are Genbank Identiñer (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA Isome 22." Dunham I. et al., Nature (1999) 402:489-495.
25	Strand: Nt_position:	Indicates DNA	strand from	which exons were predicted. ns of predicted exons.
	Pkey	Ref	Strand	Nt_position
30	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076

TABLE 15A: Information for all sequences in Table 16

Table 15A shows the Seq ID No, Pkey, ExAcon, UnigeneID, and Unigene Title for all of the sequences in Table 16.

Table 15B show the accession numbers for those Pkey's lacking UnigenelD's for table 15A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column. 5

Table 15C show the genomic positioning for those Pkey's lacking Unigene ID's and accession numbers in table 15A. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed. 10

15

Seq ID No: Sequence ID number
Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank

r.kg. Orique Eus proposed container number
Exaccn: Exemplar Accession number, Genbank accession number
Unigenel Title: Unigene gene title

20	Seq ID No:	Pkey	ExAcon	UnigeneiD	Unigene Title
	Seq ID No: 1 & 2	410407	X66839	Hs.63287	carbonic anhydrase IX
	Seq ID No: 3 & 4	412719	AW016610	Hs.816	ESTs
~ ~	Seq ID No: 5 & 6	417034	NM_006183	Hs.80962	neurotensin
25	Seq ID No: 7 & 8	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam
	Seq ID No: 9 & 10	407788	BE514982	Hs.38991	S100 calcium-binding protein A2 S100 calcium-binding protein A2
	Seq ID No: 11 & 12	407788	BE514982	Hs.38991	S100 calcium-binding protein A2
	Seq ID No: 13 & 14	407788	BE514982 BE514982	Hs.38991 Hs.38991	S100 calcium-binding protein A2
30	Seq ID No: 15 & 16	407788 439285	AL133916	1 13,5055 1	hypothetical protein FLJ20093
30	Seq ID No: 17 & 18 Seq ID No: 19 & 20	413753	U17760	Hs.75517	taminin, beta 3 (niceln (125kD), kalinin
	Seq ID No: 21 & 22	120486	AW368377	Hs.137569	turnor protein 63 kDa with strong homolog
	Seg ID No: 23 & 24		NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 25 & 26	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
35	Seq ID No: 27 & 28	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	Seq ID No: 29 & 30	452838	U65011	Hs.30743	preferentially expressed antigen in mela
	Seq ID No: 31 & 32	418663	AK001100	Hs.41690	desmocollin 3
	Seq ID No: 33 & 34	418663	AK001100	Hs.41690	desmocollin 3
40	Seq ID No: 35 & 36	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito LUNX protein; PLUNC (palate lung and nas
40	Seq ID No: 37 & 38	429610	AB024937 M29540	Hs.211092 Hs.220529	carcinoembryonic antigen-related cell ad
	Seq ID No: 39 & 40	406690 431846	BE019924	Hs.271580	uroplakin 1B
	Seq ID No: 41 & 42 Seq ID No: 43 & 44	418830	BE513731	Hs.88959	hypothetical protein MGC4816
	Seq ID No: 45 & 46	424098	AF077374	Hs.139322	small proline-rich protein 3
45	Seq ID No: 47 & 48	443648	Al085377	Hs.143610	ESTs
•••	Seq ID No: 49	311034	BE567130	Hs.311389	ESTs, Highly similar to NKGD_HUMAN NKG2-
	Seq ID No: 50 & 51	408522	Al541214	Hs.46320	Small proline-rich protein SPRK [human,
	Seq ID No: 52 & 53	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
50	Seq ID No: 54 & 55	435505	AF200492	Hs.211238	interlaukin-1 homolog 1
50	Seq ID No: 56 & 57	417366	BE185289	Hs.1076 Hs.2877	small proline-rich protein 1B (comifin) cadherin 3, type 1, P-cadherin (placenta
	Seq ID No: 58 & 59	431958 441020	X63629 W79283	Hs.35962	ESTs
	Seq ID No: 60 & 61 Seq ID No: 62 & 63	423217	NM_000094	Hs.1640	collagen, type Vil, alpha 1 (epidermolys
	Seq ID No: 64 & 65	429538	BE182592	Hs.11261	small proline-rich protein 2A
55	Seq ID No: 66 & 67	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte
	Seq ID No: 68 & 69	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 70 & 71	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 72 & 73	444371	BE540274	Hs.239	forkhead box M1
	Seq ID No: 74 & 75	422168	AA586894	Hs.112408	\$100 calcium-binding protein A7 (psorias
60	Seq ID No: 76 & 77	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias Plakophilin
	Seq ID No: 78 & 79	429259	AA420450	Hs.292911 Hs.169902	solute carrier family 2 (facilitated glu
	Seq ID No: 80 & 81	426440 437044	BE382756 AL035864	Hs.69517	differentially expressed in Fanconi's an
	Seq ID No: 82 & 83 Seq ID No: 84 & 85	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro
65	Seq ID No: 86 & 87	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino
Ų,	Seg ID No: 88 & 89	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3
	Seq ID No: 90 & 91	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
	Seq ID No: 92 & 93	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr
- -	Seq ID No: 94 & 95	417515	L24203	Hs.82237	ataxia-telanglectasia group D-associated
70	Seq ID No: 96 & 97	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
	Seq ID No: 98 & 99	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
	Seq ID No: 100 & 101	449003	X76342	Hs.389 Hs.48956	alcohol dehydrogenase 7 (class IV), mu o gap junction protein, beta 6 (connexin 3
	Seq ID No: 102 & 103	431009	BE149762 AF251237	Hs.112208	XAGE-1 protein
75	Seq ID No: 104 & 105	409103 417542	J04129	Hs.82269	progestagen-associated endometrial prote
13	Seq ID No: 106 & 107 Seq ID No: 108 & 109	428471	X57348	Hs.184510	stratifin
	Seq ID No: 110 & 111	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member
	Seq ID No: 112 & 113	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
	Seq ID No: 114 & 115	418203	X54942	Hs.83758	CDC28 protein kinase 2
80	Seq ID No: 116	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m
	Seq ID No: 117 & 118	437016	AU076916	Hs.5398	guanine monphosphate synthetase
	Seq ID No: 119 & 120	449230	BE613348	Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 121 & 122	446989	AK001898	Hs.16740 Hs.35406	hypothetical protein FLJ11036 ESTs, Highly similar to unnamed protein
85	Seq ID No: 123 & 124	457819	AA057484 J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B
0,5	Seq ID No: 125 & 126	424687	400010	10,101100	

	WO 02/086	443			
	Seq ID No: 127 & 128	414430	Al346201	Hs.76118	ubiquifin carboxyl-terminal esterase L1
	Seq ID No: 129 & 130	418462 100668	BE001596 L05424	Hs.85266 Hs.169610	integrin, beta 4 CD44 antigen (horning function and Indian
	Seq ID No: 131 & 132 Seq ID No: 133 & 134	458933	Al638429	Hs.24763	RAN binding protein 1
5	Seq ID No: 135 & 136	418478	U38945	Hs.1174	cyclin-dependent kinase Inhibitor 2A (me
	Seq ID No: 137 & 138	418478 418478	U38945 U38945	Hs.1174 Hs.1174	cyclin-dependent kinase Inhibitor 2A (me cyclin-dependent kinase Inhibitor 2A (me
	Seq ID No: 139 & 140 Seq ID No: 141 & 142	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
10	Seq ID No: 143 & 144	446269	AW263155	Hs.14559	hypothetical protein FLJ 10540
10	Seq ID No: 145 & 146	422765 436481	AW409701 AA379597	Hs.1578 Hs.5199	baculoviral IAP repeat-containing 5 (sur HSPC150 protein similar to ubiquitin-con
	Seq ID No: 147 & 148 Seq ID No: 149 & 150	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma
	Seq ID No: 151 & 152	439606	W79123	Hs.58561	G protein-coupled receptor 87
15	Seq ID No: 153 & 154	453884 453884	AA355925 AA355925	Hs.36232 Hs.36232	KIAA0186 gene product KIAA0186 gene product
13	Seq ID No: 155 & 156 Seq ID No: 157 & 158	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 159 & 160	453884	AA355925	Hs.36232	KIAA0186 gene product
	Seq ID No: 161 & 162	404877 413129	AF292100	Hs.104613	NM_005365:Homo sapiens melanoma antigen, RP42 homolog
20	Seq ID No: 163 & 164 Seq ID No: 165 & 166	413281	AA861271	Hs.222024	transcription factor BMAL2
	Seq ID No: 167 & 168	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
	Seq ID No: 169 & 170	416819 451320	U77735 AW118072	Hs.80205	pim-2 oncogene diacylglycerol kinase, zeta (104kD)
	Seq ID No: 171 & 172 Seq ID No: 173 & 174	418543	NM_005329	Hs.85962	hyaluronan synthase 3
25	Seq ID No: 175 & 176	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member
	Seq ID No: 177 & 178	425397 415817	J04088 U88967	Hs.156346 Hs.78867	topoisomerase (DNA) II alpha (170kD) protein tyrosine phosphatase, receptor-t
	Seq ID No: 179 & 180 Seq ID No: 181 & 182	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
20	Seq ID No: 183 & 184	415817	U88967	Hs.78867	protein tyrosine phosphalase, receptor-t
30	Seq ID No: 185 & 186 Seq ID No: 187 & 188	415817 415817	U88967 U88967	Hs.78867 Hs.78867	protein tyrosine phosphalase, receptor-t protein tyrosine phosphalase, receptor-t
•	Seq ID No: 189 & 190	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 191 & 192	448993	AI471630	Hs.8127	KIAA0144 gene product
35	Seq ID No: 193 & 194 Seq ID No: 195 & 196	421817 430393	AF146074 BE185030	Hs.108660 Hs.241305	ATP-binding cassette, sub-family C (CFTR estrogen-responsive B box protein
33	Seq ID No: 197 & 198	425057	AA826434	Hs.1619	achaete-scute complex (Orosophila) homol
	Seq ID No: 199 & 200	420462	AF050147	Hs.97932	chondromodulin i precursor calcitonin-related polypeptide, beta
	Seq ID No: 201 & 202 Seq ID No: 203 & 204	102963 100576	X02404 X00356	Hs.274534 Hs.37058	calcitonin/calcitonin-related polypeptid
40	Seq ID No. 205 & 206	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	Seq ID No: 207 & 208	429038	AL023513	Hs.194766 Hs.167379	seizure related gene 6 (mouse)-like cancer/testis antigen (NY-ESO-1)
	Seq ID No: 209 & 210 Seq ID No: 211 & 212	418678 418678	NM_001327 NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
4~	Seq ID No: 213 & 214	131927	AJ003112	Hs.34780	doublecortex; lissencephaly, X-linked (d
45	Seq ID No: 215 & 216	428182 427335	BE386042 AA448542	Hs.293317 Hs.251677	ESTs, Weakly similar to GGC1_HUMAN G ANT G antigen 7B
	Seq ID No: 217 & 218 Seq ID No: 219 & 220	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini
	Seq ID No: 221 & 222	114346	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II Human DNA sequence from clone RP5-850E9
50	Seq ID No: 223 & 224 Seq ID No: 225 & 226	438956 404440	W00847	Hs.135056	NM_021048:Homo sapiens melanoma antigen,
30	Seq ID No: 227 & 228	415669	NM_005025	Hs.78589	serine (or cystelne) proteinase inhibito
	Seq ID No: 229 & 230	103312	Y12642	Hs.3185	lysosomał Homo sapiens mRNA; cDNA DKFZp547C136 (fr
	Seq ID No: 231 & 232 Seq ID No: 233	320843 429065	BE069288 AI753247	Hs.34744 Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT
55	Seq ID No: 234 & 235	446102	AW168067	Hs.317694	ESTs
	Seq ID No: 236 & 237	330495 413573	U47924 A1733859	Hs.71642 Hs.149089	guanine nucleolide binding prolein (G pr ESTs
	Seq ID No: 238 Seq ID No: 239 & 240	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 241 & 242	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to
60	Seq ID No: 243 & 244 Seq ID No: 245	332180 437915	AF134160 Al637993	Hs.7327 Hs.202312	claudin 1 Homo sapiens clone N11 NTera2D1 teratoca
	Seq ID No: 246 & 247	441553	AA281219	Hs.121296	ESTs
	Seq ID No: 248 & 249	331692	Al683487 NM_014058	Hs.152213 Hs.201877	wingless-type MMTV integration site fami DESC1 protein
65	Seq ID No: 250 & 251 Sea ID No: 252 & 253	429413 422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis
	Seq ID No: 254 & 255	448357	N20169	Hs.108923	RAB38, member RAS oncogene family
	Seq ID No: 256 & 257 Sea ID No: 258 & 259	446292 416209	AF081497 AA236776	Hs.279682 Hs.79078	Rh type C glycoprotein MAD2 (mitotic arrest deficient, yeast, h
	Seq ID No: 250 & 261	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
70	Seq ID No: 262 & 263	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito
	Seq ID No: 264 & 265 Seq ID No: 266 & 267	439223 429228	AW238299 Al553633	Hs.250618 Hs.326447	UL16 binding protein 2 ESTs
•	Seq ID No: 268 & 269	409757	NM_001898	Hs.123114	cystatin SN
76	Seq ID No: 270 & 271	411089	AA456454	Hs.214291	cell division cycle 2-like 1 (PITSLRE pr ESTs
75	Seq ID No: 272 & 273 Seq ID No: 274 & 275	436511 428969	AA721252 AF120274	Hs.291502 Hs.194689	artemin
	Seq ID No: 276 & 277	428969	AF120274	Hs.194689	artemin
	Seq ID No: 278 & 279	428969	AF120274	Hs.194689	artemin artemin
80	Seq ID No: 280 & 281 Seq ID No: 282	428969 407137	AF120274 T97307	Hs.194689	gb:ye53h05.s1 Soares fetal liver spieen
50	Seq 1D No: 283 & 284	412723	AA648459	Hs.335951	hypothetical protein AF301222
	Seq ID No: 285 & 286	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine- NM_002362:Homo sapiens melanoma antigen,
	Seq ID No: 287 & 288 Seq ID No: 289 & 290	405770 439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13
85	Seq ID No: 291 & 292	414774	X02419	Hs.77274	plasminogen activator, urokinase

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	Seq 1D No: 293 & 294	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub
	Seq ID No: 295 & 296	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 297 & 298	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheli
_	Seq ID No: 299 & 300	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
5	Seq ID No: 301 & 302	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 303 & 304	437789	Al581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti
	Seq ID No: 305 & 306	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso
	Seq ID No: 307 & 308	403478			NM_022342:Homo sapiens kinesin protein 9
• •	Seq ID No: 309	441525	AW241867	Hs.127728	ESTs
10	Seq ID No: 310 & 311	434105	AW952124	Hs.13094	presentlins associated rhombold-like pro
	Seq ID No: 312 & 313	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep
	Seq ID No: 314 & 315	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B
	Seq ID No: 316 & 317	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f
1.5	Seq ID No: 318 & 319	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell
15	Seq ID No: 320 & 321	425734	AF056209	Hs.159396	peptidylglycine alpha-amidaling monooxyg
	Seq ID No: 322 & 323	413582	AW295647	Hs.71331	hypothetical protein MGC5350
	Seq ID No: 324 & 325	438403	AA806607	Hs.292206	ESTS
	Seq ID No: 326 & 327	403329	AW247090	Un 67404	unnamed protein product [Homo sapiens] minichromosome maintenance deficient (S.
20	Seq ID No: 328 & 329	409893		Hs.57101 Hs.279477	v-ets erythroblastosis virus E26 oncogen
20	Seq ID No: 330 & 331	119073	BE245360 H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	Seq ID No: 332 & 333	113195 102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	Seq ID No: 334 & 335 Seq ID No: 336 & 337	101345	NM_005795	Hs.152175	calcitonin receptor-like
	Seq ID No: 338 & 339	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
25	Seq ID No: 340 & 341	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
20	Seq ID No: 342 & 343	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	Seq ID No: 344 & 345	134299	AW580939	Hs.97199	complement component C1q receptor
	Seq ID No: 346 & 347	412719	AW016610	Hs.816	ESTs
	Seq ID No: 348 & 349	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
30	Seq ID No: 350 & 351	128924	BE279383	Hs.26557	plakophilin 3
	Seq ID No: 352 & 353	100486	T19006	Hs.10842	RAN, member RAS oncogene family
	Seq ID No: 354 & 355	419121	AA374372	Hs.89626	parathyroid hormone-like hormone
	Seq ID No: 356 & 357	409459	D86407	Hs.54481	low density lipoprotein receptor-related
25	Seq ID No: 358 & 359	330493	M27826		endogenous retroviral protease
35	Seq ID No: 360 & 361	417866	AW067903	Hs.82772	collagen, type XI, alpha 1
	Seq ID No: 362 & 363	418113	Al272141	Hs.83484	SRY (sex determining region Y)-box 4
	Seq ID No: 364 & 365	437016	AU076916	Hs.5398	guanine monphosphate synthetase
	Seq ID No: 366 & 367	429612	AF062649	Hs.252587	pituitary tumor-transforming 1
40	Seq ID No: 368 & 369	440704	M69241	Hs.162	insulin-like growth factor binding prote
40	Seq ID No: 370 & 371	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye
	Seq ID No: 372 & 373	431565	AF161470 AF161470	Hs.260622 Hs.260622	butyrate-induced transcript 1 butyrate-induced transcript 1
	Seq ID No: 374 & 375	431565 132354	BE185289	Hs.1076	small proline-rich protein 18 (comitin)
	Seq ID No: 376 & 377 Seq ID No: 378 & 379	424441	X14850	Hs.147097	H2A histone family, member X
45	Seq ID No: 380 & 381	103768	AF086009	Hs.296398	gb:Homo sapiens full length insert cDNA
	Seq ID No: 382 & 383	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb
	Seq ID No: 384 & 385	425266	J00077	Hs.155421	alpha-fetoprotein
	Seq ID No: 386 & 387	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,
	Seq ID No: 388 & 389	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
50	Seq ID No: 390 & 391	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	Seq ID No: 392 & 393	418007	M13509	Hs.83169	matrix metalloprotelnase 1 (interstitlal
	Seq ID No: 394 & 395	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	Seq ID No: 396 & 397	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2
<i>5 6</i>	Seq ID No: 398 & 399	418506	AA084248	Hs.85339	G protein-coupled receptor 39
55	Seq ID No: 400 & 401	423961	D13666	Hs.136348	periostin (OSF-2os) monokine induced by gamma interferon
	Seq ID No: 402 & 403	414812	X72755 BE270266	Hs.77367 Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 404 & 405	417433 417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein
	Seq ID No: 406 & 407 Seq ID No: 408 & 409	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
60	Seq ID No: 410 & 411	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
00	Seq ID No: 412 & 413	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	Seq ID No: 414 & 415	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated
	Seq ID No: 416 & 417	411789	AF245505	Hs.72157	Adlican
	Seq ID No: 418 & 419	428698	AA852773	Hs.334838	KIAA1866 protein
65	Seq ID No: 420 & 421	450098	W27249	Hs.8109	hypothetical protein FLJ21080
	Seq ID No: 422 & 423	421552	AF026692	Hs.105700	secreted frizzled-related protein 4
	Seq ID No: 424 & 425	452747	BE153855	Hs.61460	lg superfamily receptor LNIR
	Seq ID No: 426 & 427	450375	AA009647		a disintegrin and metalloproteinase doma
	Seq ID No: 428 & 429	426215	AW963419	Hs.155223	stanniocalcin 2
70	Seq ID No: 430 & 431	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
	Seq ID No: 432 & 433	432201	AI538613	Hs.298241	Transmembrane protease, serine 3
	Seq ID No: 434 & 435	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph
	Seq ID No: 436 & 437	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447
75	Seq ID No: 438 & 439	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn
75	Seq ID No: 440 & 441	447033	Al357412	Hs.157601	ESTs EST-
	Seq ID No: 442 & 443	447033	Al357412	Hs.157601	ESTs ESTo
	Seq ID No: 444 & 445	447033	Al357412	Hs.157601	ESTs c.Mvc tamet IPO1
	Seq ID No: 446 & 447	115522	BE614387 D31382	Hs.333893 Hs.63325	c-Myc target JPO1 transmembrane protease, serine 4
80	Seq ID No: 448 & 449 Seq ID No: 450 & 451	410418 409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
50	Seq ID No: 450 & 451 Seq ID No: 452 & 453	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119
	Seq 10 No: 454 & 455	452461	N78223	Hs.108106	transcription factor
	Seq ID No: 456 & 457	412420	AL035668	Hs.73853	bone morphogenetic protein 2
	Seq ID No: 458 & 459	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
85	Seq ID No: 460 & 461	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon

	WO 02/086	6443			
	Seq ID No: 462 & 463	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa
	Seq ID No: 464 & 465	402075	A 1000747	Hs.1355	ENSP00000251056*:Plasma membrane calcium cathepsin E
	Seq ID No: 466 & 467 Seq ID No: 468 & 469	421110 451668	AJ250717 Z43948	Hs.326444	cartilage acidic protein 1
5	Seq ID No: 470 & 471	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 472 & 473	451668	Z43948	Hs.326444	cartilage acidic protein 1
	Seq ID No: 474 & 475 Seq ID No: 476 & 477	422282 425852	AF019225 AK001504	Hs.114309 Hs.159651	apolipoprotein L. death receptor 6, TNF superfamily member
	Seq ID No: 478 & 479	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),
10	Seq ID No: 480 & 481	427747	AW411425	Hs.180655	serine/threonine kinase 12
	Seq ID No: 482 & 483	420281 405932	Al623693	Hs.323494	Predicted cation efflux pump C15000305:gij3806122[gb]AAC69198.1] (AF0
	Seq ID No: 484 & 485 Seq ID No: 486 & 487	405932			C15000305:glj3806122[gb]AAC69198.1] (AF0
	Seq ID No: 488 & 489	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane
15	Seq JD No: 490 & 491	421379	Y15221	Hs.103982 Hs.81134	small inducible cytokine subfamily B (Cy Interleukin 1 receptor antagonist
	Seq ID No: 492 & 493 Seq ID No: 494 & 495	417079 430890	U65590 X54232	Hs.2699	glypican 1
	Seq ID No: 496 & 497	419721	NM_001650	Hs.288650	aquaporin 4
20	Seq ID No: 498 & 499	444471	AB020684	Hs.11217	KIAA0877 protein chitinase 3-like 1 (cartilage glycoprote
20	Seq ID No: 500 & 501 Seq ID No: 502 & 503	413063 433800	AL035737 Al034361	Hs.75184 Hs.135150	tung type-i cell membrane-associated gly
	Seq ID No: 504 & 505	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro
	Seq ID No: 506 & 507	452401	NM_007115	Hs.29352	turnor necrosis factor, alpha-induced pro
25	Seq ID No: 508 & 509	450001 410407	NM_001044 X66839	Hs.406 Hs.63287	solute carrier family 6 (neurotransmitte carbonic anhydrase IX
23	Seq ID No: 510 & 511 Seq ID No: 512 & 513	309931	AW341683	1.5.00207	gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s
	Seq ID No: 514 & 515	412719	AW016610	Hs.816	ESTs
	Seq ID No: 516 & 517	417034	NM_006183 BE062109	Hs.80962 Hs.241551	neurotensin chloride channel, calcium activated, fam
30	Seq ID No: 518 & 519 Seq ID No: 520 & 521	430486 413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin
50	Seq ID No: 522 & 523	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen
	Seq ID No: 524 & 525	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage desmocollin 3
	Seq ID No: 526 & 527 Seq ID No: 528 & 529	418663 418663	AK001100 AK001100	Hs.41690 Hs.41690	desmocollin 3
35	Seq ID No: 530 & 531	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas
	Seq ID No: 532 & 533	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad uroplakin 1B
	Seq ID No: 534 & 535 Seq ID No: 536 & 537	431846 422158	BE019924 L10343	Hs.271580 Hs.112341	protease inhibitor 3, skin-derived (SKAL
	Seq ID No: 538 & 539	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta
40	Seq ID No: 540 & 541	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an solute carrier family 7 (cationic amino
	Seq ID No: 542 & 543 Seq ID No: 544 & 545	428484 429211	AF104032 AF052693	Hs.184601 Hs.198249	gap junction protein, bela 5 (connexin 3
	Seq ID No: 546 & 547	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor
15	Seq ID No: 548 & 549	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connextn 3 progestagen-associated endometrial prote
45	Seq ID No: 550 & 551 Seq ID No: 552 & 553	417542 449230	J04129 BE613348	Hs.82269 Hs.211579	melanoma cell adhesion molecule
	Seq ID No: 554 & 555	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	Seq ID No: 556 & 557	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma matrix metalloproteinase 9 (gelatinase B
50	Seq ID No: 558 & 559 Seq ID No: 560 & 561	424687 418462	J05070 BE001596	Hs.151738 Hs.85266	integrin, beta 4
50	Seq ID No: 562 & 563	410274	AA381807	Hs.61762	hypoxia-inducible protein 2 ·
	Seq ID No: 564 & 565	439606	W79123	Hs.58561	G protein-coupled receptor 87 NM_005365:Homo saptens melanoma antigen,
	Seq ID No: 566 & 567 Seq ID No: 568 & 569	404877 444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote
55	Seq ID No: 570 & 571	418543	NM_005329	Hs.85962	hyaluronan synthase 3
-	Seq ID No: 572 & 573	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 574 & 575	415817 415817	U88967 U88967	Hs.78867 Hs.78867	protein tyrosine phosphatase, receptor-t protein tyrosine phosphatase, receptor-t
	Seq ID No: 576 & 577 Seq ID No: 578 & 579	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
60	Seq ID No: 580 & 581	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	Seq ID No: 582 & 583 Seq ID No: 584 & 585	41581 <i>7</i> 421817	U88967 AF146074	Hs.78867 Hs.108660	protein tyrosine phosphalase, receptor-t ATP-binding cassette, sub-family C (CFTR
	Seg ID No: 586 & 587	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
نور	Seq ID No: 588 & 589	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
65	Seq ID No: 590 & 591	409420 332180	Z15008 AF134160	Hs.54451 Hs.7327	łaminin, gamma 2 (nicein (100kD), kalini claudin 1
	Seq ID No: 592 & 593 Seq ID No: 594 & 595	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
	Seq ID No: 596 & 597	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,
70	Seq ID No: 598 & 599	439223 409757	AW238299 NM_001898	Hs.250618 Hs.123114	UL16 binding protein 2 cystatin SN
70	Seq ID No: 600 & 601 Seq ID No: 602 & 603	428969	AF120274	Hs.194689	artemin
	Seq ID No: 604 & 605	428969	AF120274	Hs.194689	artemin
	Seq ID No: 606 & 607	428969	AF120274 AF120274	Hs.194689 Hs.194689	artemin artemin
75	Seq ID No: 608 & 609 Sea ID No: 610 & 611	428969 450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
,,,	Seq ID No: 612 & 613	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-
	Seq ID No: 614 & 615	414774	X02419	Hs.77274 Hs.239727	plasminogen activator, urokinase desmocollin 2
	Seq ID No: 616 & 617 Seq ID No: 618 & 619	407944 407944	R34008 R34008	Hs.239727	desmocolin 2
80	Seq ID No: 620 & 621	457489	Al693815	Hs.127179	cryptic gene
-	Seq ID No: 622 & 623	429547	AW009166	Hs.99376	ESTs gb:Human nonspecific crossreacting antig
	Seq ID No: 624 & 625 Seq ID No: 626 & 627	407242 407242	M18728 M18728	•	gb:Human nonspecific crossreacting antig
	Seq ID No: 628 & 629	407242	M18728		gb:Human nonspecific crossreacting antig
85	Seq ID No: 630 & 631	444006	BE395085	Hs.10086	type I transmembrane protein Fn14

	wo	02/0864	443			PCT/US02/12476
-	Seq ID No: 6	32 & 633	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma
	Seq ID No: 6		422109	S73265	Hs.1473	gastrin-releasing peptide
	Seq ID No: 6		419235	AW470411	Hs.288433	neurotrimin
5	Seq ID No: 6		449048 419216	Z45051 AU076718	Hs.22920 Hs.164021	similar to S68401 (catile) glucose Induc small inducible cytokine subfamily B (Cy
,	Seq ID No: 6 Seq ID No: 6		431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu
	Seq ID No: 6		448243	AW369771	Hs.52620	integrin, beta 8
	Seg ID No: 6		426427	M86699	Hs.169840	TTK protein kinase
• •	Seq ID No: 6		445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6
10	Seq ID No: 6		422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
	Seq ID No: 6		428450	NM_014791	Hs.184339	KIAA0175 gene product secreted phosphoprotein 1 (osteopontin,
•	Seq ID No: 6 Seq ID No: 6		446619 453392	AU076643 U23752	Hs.313 Hs.32964	SRY (sex determining region Y)-box 11
	Seq ID No: 6		426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic
15	Seq ID No: 6		425776	U25128	Hs.159499	parathyroid hormone receptor 2
	Seq ID No: 6	62 & 663	425776	U25128	Hs.159499	parathyroid hormone receptor 2
	Seq ID No: 6		431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha
	Seq ID No: 6		419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7 ESTs, Weakty similar to JC7328 amlno aci
20	Seq ID No: 6 Seq ID No: 6		432653 432653	N62096 N62096	Hs.293185 Hs.293185	ESTs, Wealdy similar to JC7328 amino aci
20	Seq ID No. 6		432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino acl
	Seq ID No: (432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci
	Seq ID No: 6		410001	AB041036	Hs.57771	kallikrein 11
25	Seq ID No: 6		426501	AW043782	Hs.293616	ESTs
25	Seq ID No: 6		408369	R38438 AA151342	Hs.182575 Hs.12677	solute carrier family 15 (H??? transport CGI-147 protein
	Seq ID No: 6 Sea ID No: 6		445413 422424	AI186431	Hs.296638	prostate differentiation factor
	Seq ID No: (428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
	Seq ID No: (420610	AI683183	Hs.99348	distal-less homeo box 5
30	•					
	TABLE 158					
	Pkey:	I Inique Se	e erebesel i	dentifier number		
	CAT number			dennier mander		
35	Accession:		accession nu	ımbers		
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40	439285	47065_1	AL 13	33916 N79113 AF	086101 N76721	AW950828 AA364013 AW955684 Al346341 Al867454 N54784 Al655270 Al421279 AW014882
	100200	47.000	AA7	75552 N62351 N	59253 AA626243 .	Al341407 BE175639 AA456968 Al358918 AA457077
	450375	83327_1	AAO	09647 AA131254	AA374293 AW95	4405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532
		4	AA1	90993 H03231 H	59605 H01642 AA	852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067
45	451320	86576_1	AWI	18072 AI631962 4099 AA224269	115/34 AA22419 MINEASSA MISEARS	5 A1701458 W20198 F26326 AA890570 N90552 AW071907 A1671352 A1375892 T03517 R88265 36 T33652 A1140719 A1720211 T03490 A1372637 T15415 AW205836 AA630384 T03515 T33230
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50	Pkey:	Unique nu	mber corres	ponding to an Eo	s probeset	
	Ref:	Sequence	source. Th	e 7 digit numbers	in this column are	Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
		sequence	of human cl	romosome 22."	Dunham I. et al., f	Nature (1999) 402:489-495.
55	Strand:			from which exons		
55	Nt_position:	indicates r	incieorae b	ositions of predict	ea exons.	
	Pkey	Ref	Strand	Nt_position	1	
	402075	8117407	Plus			921,124019-124161,124455-124610,125672-126076
	403329	8516120	Plus	96450-965	98 `	
60	403478	9958258	Plus	116458-11		
	404440	7528051	Plus	80430-815		
	404877 405770	1519284 2735037	Plus Plus	1095-2107 61057-620		
	405770	7767812	Minus	123525-12		
65	100006	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	**********	0020*12	••	

Table 16

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM 001216 5 Coding sequence: 43..1422 31 GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 10 AGCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120 CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT 180 TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300 GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC 360 15 TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCCAG AATAATGCCC ACAGGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480 CCGCCCTGGC CCCGGGTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC 540 CGCCCCAGC TOGCCGCCTT CTGCCCGGCC CTGCGCCCCC TGGAACTCCT GGGCTTCCAG 600 CTCCCGCCGC TCCCAGAACT GCGCCTGCGC AACAATGGCC ACAGTGTGCA ACTGACCCTG 20 CCTCCTGGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT 720 CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAGG CCACCGTTTC CCTGCCGAGA TCCACGTGGT TCACCTCAGC ACCGCCTTTG CCAGAGTTGA CGAGGCCTTG 780 GGGCGCCCGG GAGGCCTGGC CGTGTTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900 AGTGCCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960 25 CAGGTCCCAG GACTGGACAT ATCTGCACTC CTGCCCTCTG ACTTCAGCCG CTACTTCCAA 1020 CAGACAGTGA TGCTGAGTAC ACCGCCCTGT GCCCAGGGTG TCATCTGGAC TGTGTTTAAC CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCTCT CTGACACCCT GTGGGGACCT 1080 1140 GGTGACTCTC GGCTACAGCT GAACTTCCGA GCGACGCAGC CTTTGAATGG GCGAGTGATT 1200 GAGGCCTCCT TCCCTGCTGG AGTGGACAGC AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG 1260 30 AATTCCTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC 1320 ACCAGCGTCG CGTTCCTTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380 GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT AGAGGCTGAC TCTTGGAGAA
TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGGTA ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTTAACTG CCAAGAAATT TTTTAAAATA AATATTTATA AT 35 Seg ID NO: 2 Protein seguence: Protein Accession #: NP_001207 51 31 40 MAPLCPSPWL PLLIPAPAPG LTVOLLLSLL LLMPVHPQRL PRMQEDSPLG GGSSGEDDPL 60 GEEDLPSEED SPREEDPPGE EDLPGEEDLP GEEDLPEVKP KSEEEGSLKL EDLPTVEAPG DPQEPQNNAH RDKEGDDQSH WRYGGDPPWP RVSPACAGRF QSFVDIRPQL AAFCPALRPL 180 ELIGFOLPPL PELRLRINGH SVOLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT VEGHRFPAEI HVVHLSTAFA RVDEALGRPG GLAVLAAFLE EGPEENSAYE QLLSRLEEIA 240 45 EEGSETQVPG LDISALLPSD FSRYFQYEGS LTTPPCAQGV IWTVFNQTVM LSAKQLHTLS 360 DTLWGPGDSR LQLNFRATQP LNGRVIEASF PAGVDSSPRA AEPVQLNSCL AAGDILALVF 420 GLLFAVTSVA FLVOMRROHR RGTKGGVSYR PAEVAETGA 50 Seq ID NO: 3 DNA sequence Nucleic Acid Accession #: BC013923 Coding sequence: 438-1391 51 41 55 60 GTGTTTGCAA AAGGGGGAAA GTAGTTTGCT GCCTCTTTAA GACTAGGACT GAGAGAAAGA 120 AGAGGAGAG GAAAGAAAG GAGAGAAGTT TGAGCCCCAG GCTTAAGCCT TTCCAAAAAA TAATAATAAC AATCATCGGC GGCGGCAGGA TCGGCCAGAG GAGGAGGGAA GCGCTTTTTT 240 60 TGATCCTGAT TCCAGTTTGC CTCTCTTT TTTTCCCCCA AATTATCTT CGCCTGATTT TCCTCGCGGA GCCCTGCGCT CCCGACACCC CCGCCCGCCT CCCCTCCTCC TCTCCCCCCG 300 420 CCGCGCACAG CGCCCGCATG TACAACATGA TGGAGACGGA GCTGAAGCCG CCGGGCCCGC 480 AGCAAACTTC GGGGGGCGGC GGCGCAACT CCACCGCGC GGCGCCCGC GGCAACCAGA AAAACAGCCC GGACCGCGTC AAGCGGCCCA TGAATGCCTT CATGGTGTGG TCCCGCGGGC 540 65 600 AGCGGCGCAA GATGGCCCAG GAGAACCCCA AGATGCACAA CTCGGAGATC AGCAAGCGCC 660 TEGGCGCCCA GTGGAAACTT TTGTCGGAGA CGGAGAAGCG GCCGTTCATC GACGAGGCTA AGCGGCTGCA ATGAAGGAGC ACCCGGATTA TAAATACCGG CCCCGGCGGA 720 AAACCAAGAC GCTCATGAAG AAGGATAAGT ACACGCTGCC CGGCGGGCTG CTGGCCCCCG 840 70 GCGGCAATAG CATGGCGAGC GGGGTCGGGG TGGGCGCCGG CCTGGGCGCG GGCGTGAACC AGCGCATGGA CAGTTACGCG CACATGAACG GCTGGAGCAA CGGCAGCTAC AGCATGATGC 900 AGGACCAGCT GGGCTACCCG CAGCACCCGG GCCTCAATGC GCACGGCGCA GCGCAGATGC 1020 AGCCCATGCA CCGCTACGAC GTGAGCGCCC TGCAGTACAA CTCCATGACC AGCTCGCAGA 1080 CCTACATGAA CGGCTCGCCC ACCTACAGCA TGTCCTACTC GCAGCAGGG ACCCCTGGCA
TGGCTCTTGG CTCCATGGGT TCGGTGGTCA AGTCCGAGGC CAGCTCCAGC CCCCCTGTGG 1140 75 1200 TTACCTCTTC CTCCCACTCC AGGGCGCCCT GCCAGGCCGG GGACCTCCGG GACATGATCA 1260 GCATGTATCT CCCCGGCGCC GAGGTGCCGG AACCCGCCGC CCCCAGCAGA CTTCACATGT CCCAGCACTA CCAGAGCGGC CCGGTGCCCG GCACGGCCAT TAACGGCACA CTGCCCCTCT CACACATGTG AGGGCCGGAC AGCGAACTGG AGGGGGGAGA AATTTTCAAA GAAAAACGAG 1320 1380 1440 80 GGAAATGGGA GGGGTGCAAA AGAGGAGAGT AAGAAACAGC ATGGAGAAAA CCCGGTACGC 1500 1560 1620 GAGAGATCCT GGACTTCTTT TKGGGGGACT ATTTTTGTAC AGAGAAAACC TGGGGAGGGT 1680 GGGGAGGGCG GGGGAATGGA CCTTGTATAG ATCTGGAGGA AAGAAAGCTA CGAAAAACTT 1740 85 TTTAAAAGTT CTAGTGGTAC GGTAGGAGCT TTGCAGGAAG TTTGCAAAAG TCTTTACCAA 1800 TAATATTTAG AGCTAGTCTC CAAGCGACGA AAAAAATGTT TTAATATTTG CAAGCAACTT 1860 TTGTACAGTA TTTATCGAGA TAAACATGGC AATCAAAATG TCCATTGTTT ATAAGCTGAG 1920

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_	AATTTGCCAA TTAGGACAGT TAAAAATTGT GTTTAAAAAG	TATTTTCAA TGCAAACGTG ACAAAAGGAA GGCAAAAGTT	AAAAGAAGAA AAAATTAGAA TTAGACTGTA	AATTATTCAA TAAGTACTGG CTAAATTTTA	ATTTGGACAT CGAACCATCT TAACTTACTG	TTTAATTGTT CTGTGGTCTT TTAAAAGCAA	1980 2040 2100 2160
5	AAATGGCCAT TTCCATTTTG GTTTGTAATA GTAGTTGTAT	TTCAGATAAA TTTCTGTAAA TTTAAAAGAT	AAAAACCATG TTTATTGTGA TCGGCTCTGT	AAATTACTGT TATTTTAAGG ATTATTTGAA	GTTTGAAATA TTTTCCCCCC TCAGTCTGCC	TTTTCTTATG TTTATTTTCC GAGAATCCAT	2220 2280 2340 2400 2460
10	CCATTATGCA AAAAAAACAA CACAACACAA	CAGTTTGAGA AACAAAAAAA	TAAATAAATT CAAAAAAACAA AAAAAAAAAGA	TTTGAAATAT AAACAGAAAA	GGACACTGAA AACAAAAAAA	AAAAAAAAAC AAAACAAAAAC CAACACAAAA	2520 2580 2640
15		4 Protein a cession #:CA					
	1	11	21	31	41	51	
20	QENPKMHNSE KKDKYTLPGG POHPGLNAHG	LLAPGGNSMA AAOMOPMHRY	LLSETEKRPF SGVGVGAGLG DVSALOYNSM	IDEAKRLRAL AGVNQRMDSY TSSOTYMNGS	HMKEHPDYKY AHMNGWSNGS PTYSMSYSQQ	WSRGQRRKMA RPRRKTKTLM YSMMQDQLGY GTPGMALGSM RLHMSQHYQS	60 120 180 240 300
25	GPVPGTAING						
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	1	11	21	31	41	51 !	
	CGGACTTGGC	TTGTTAGAAG	GCTGAAAGAT	[GATGGCAGGA	ATGAAAATCC	AGCTTGTATG	60
35	CATGCTACTC	CTGGCTTTCA GCAGATTTCT	GCTCCTGGAG	TCTGTGCTCA	GATTCAGAAG	AGGAAATGAA	120 180
55	TO CONTRACTOR OF THE PARTY OF T	AAGATGACTC	TGCTAAATGT	TTGCAGTCTT	GTAAATAATT	TGAACAGCCC	240
	AGCTGAGGAA	ACAGGAGAAG	TTCATGAAGA	GGAGCTTGTT	GCAAGAAGGA TACCAGCTCC	ACAAAATCTG	300 360
40	TCACAGCAGG	GCTTTTCAAC	ACTGGGAGTT	AATCCAGGAA	GATATTCTTG	ATACTGGAAA	420
40	COTOTATGAG	AATAAACCCA	GAAGACCCTA	CATACTCAAA	AGAGATTCTT	TGAAACGGCA ACTATTACTG	480 540
	ACACAATAAA	ብሊ የ ብላተው የ ለኅብሔ	ACATGTGATT	GTGATTCATC	ATCCCTTAAT	TAAATATCAA	600
•	ATTATATTTG	TTTTTCTGCA	TGACAAACAC	TTAGACTAAG	TGTTTTCAAA	ATTGTGGTTT TAAATCTAAA	660 720
45	TCTTCAAAAA	AAAAAAAA	AAATGGGGCC	GCAATT			
50		6 Protein : cession #: 2					
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55	VCSLVNNLNS	CMLLLAFSSW PAEETGEVHE NDKNGKEEVI	EELVARRKLP	TALDGFSLEA	MLTIYQLHKI	VPSWKMTLLN CHSRAFQHWE	60 120
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65	ATGTATGCAG	CAGGGTCAGT	GTGAGTGAAC	TGGAGGCTTC	TCTACAACAT	ACCTGACACA GACCCAAAGG	60 120
05	እርር እጥተር ር አ ር	GTCCTATTTG	CAACCTGAAG	TTTGTGACTC	TCCTGGTTGC	CTTAAGTTCA	180
	ልምምረር ስ አ ምምል	ATCCTCAGGT	ACCTGAGAAT	CAGAACCTCA	TCTCAAACAT	TGGATTGCTC TAAGGAAATG	300
70	ATAACTCAAG	ርጥተ ሮል ጥተ ጥል	CCTATTTAAT	GCTACCAAGA	GAAGAGTATT	TTTCAGAAAT	360
70	ምርአጥአጥር ልልል	እርርር	CATAGTGACT	GACTGGTATG	GGGCACATGG	AAAACAAGAA AGATGATCCA	480
	ምአርአርርር ቸልር	AATACAGAGG	GTGTGGAAAA	GAGGGAAAAT	ACATTCATT	CACACCTAAT	540
	CANTGGGCCC	ACCTCCCTTC	GGGTGTGTTC	GATGAGTATA	. ACAATGACAA	GTTTGTCCAT	660
75	ATBARTGGG	TAAATTAAAA	TAAAGTGACA	AGGTGTTCAT	CTGACATCAC	AGGCATTITT	720 780
	CCATCCACCT	ፈፈገልሞጋጥልሞኮ	TAGCACCCAA	AATGCAACTG	CATCAATAAT	TTTTAAAGAA GTTCATGCAA	840
	ACTOTATOT	CITCICITTGA	ATTTTGTAAT	GCAAGTACCC	: ACAACCAAGA	AGCACCAAAC	900 960
80	TTTCACCACA	CCTTTCCCAT	GAATGGGACT	GAGCTTCCAC	CTCCTCCCAC	CTCTGCTGAC ATTCTCGCTT	1020
	CTACACCCTC	CTCACAAAGT	GCTCTGTTTA	GTGCTGGATG	TGTCCAGCAA	GATGGCAGAG	1080
	ስምምር አምስር ርሚ	TOTOTOGGCAT	TGCCAGTTTC	GACAGCAAAG	GAGAGATCAG	GATTGTTGAA AGCCCAGCTA	1200
0.5	でなべてなるなです	ACAGCAATGA	TGATCGAAAG	TTGCTGGTTT	CATATCTGCC	CACCACTGTA	1260
85	AAACTTGAATT	CANANGCTTA	TGGCTCTGTG	ATGATATTAG	TGACCAGCGC	A GGTGGTTGAA B AGATGATAAG	1320 1380
	CITCTTGGC	ATTGCTTACC	CACTGTGCT	AGCAGTGGT	CAACAATTC	CTCCATTGCC	1440

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1500
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                                                                                          1560
        TCTGGAACTG GAGACATTTT CCAGCAACAT ATTCAGCTTG AAAGTACAGG TGAAAATGTC
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 5
        ATGTTTCTAG TTACGTGGCA GGCCAGTGGT CCTCCTGAGA TTATATTATT TGATCCTGAT
                                                                                          1740
        GGACGAAAAT ACTACACAAA TAATTTTATC ACCAATCTAA CTTTTCGGAC AGCTAGTCTT
                                                                                          1800
        TGGATTCCAG GAACAGCTAA GCCTGGGCAC TGGACTTACA CCCTGAACAA TACCCATCAT TCTCTGCAAG CCCTGAAAGT GACAGTGACC TCTCGCGCCT CCAACTCAGC TGTGCCCCCA
                                                                                          1860
                                                                                          1920
        GCCACTGTGG AAGCCTTTGT GGAAAGAGAC AGCCTCCATT TTCCTCATCC TGTGATGATT
                                                                                          1980
10
        TATGCCAATG TGAAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTCAC TGCCACAGTT GAGCCAGAGA CTGGAGATCC TGTTACGCTG AGACTCCTTG ATGATGGAGC AGGTGCTGAT
                                                                                          2040
                                                                                          2100
        GTTATAAAAA ATGATGGAAT TTACTCGAGG TATTTTTTCT CCTTTGCTGC AAATGGTAGA
                                                                                          2160
        TATAGCTTGA AAGTGCATGT CAATCACTCT CCCAGCATAA GCACCCCAAC CCACTCTATT CCAGGGGGTC ATGCTATGTA TGTACCAGGT TACACAGCAA ACGGTAATAT TCAGATGAAT
                                                                                          2220
                                                                                          2280
15
        GCTCCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGGCTT TAGCCGAGTC
                                                                                          2340
        AGCTCAGGAG GCTCCTTTTC AGTGCTGGGA GTTCCAGCTG GCCCCCACCC TGATGTGTTT
                                                                                          2400
        CCACCATGCA AAATTATTGA CCTGGAAGCT GTAAAAGTAG AAGAGGAATT GACCCTATCT
                                                                                          2460
        TGGACAGCAC CTGGAGAAGA CTTTGATCAG GGCCAGGCTA CAAGCTATGA AATAAGAATG
                                                                                          2520
        AGTAAAAGTC TACAGAATAT CCAAGATGAC TTTAACAATG CTATTTTAGT AAATACATCA
                                                                                          2580
20
                                                                                          2640
        AAGCGAAATC CTCAGCAAGC TGGCATCAGG GAGATATTTA CGTTCTCACC CCAGATTTCC
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                                                                                          2880
25
        CATACTITAA GCAGGAAAAA GAGAGCAGAC AAGAAAGAGA ATGGAACAAA ATTATTATAA
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ATACAGATAA GATTTTTACA TGGTAGATCA ACAATTCTTT TTGGGGGTAG ATTAGAAAAC
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        CCTTACACTT TGGCTATGAA CAAATAATAA AAATTATTCT TTAAAGTAAT GTCTTTAAAG
                                                                                          3180
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        AATAGCCCCA AGCAGAGAAA AGGAGGGTAG GTCTGCATTA TAACTGTCTG TGTGAAGCAA
                                                                                          3300
        TCATTTAGTT ACTTTGATTA ATTTTTCTTT TCTCCTTATC TGTGCAGTAC AGGTTGCTTG
                                                                                          3360
        TTTACATGAA GATCATGCTA TATTTTATAT ATGTAGCCCC TAATGCAAAG CTCTTTACCT
                                                                                          3420
                                                                                          3480
        CTTGCTATTT TGTTATATAT ATTTCAGATG ACATCTCCCT GCTAATGCTC AGAGATCTTT
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TTTATGACAA AGGTCTATTG AATTTATTTG TNTGTAAGTT TCTACTCCCA TCAAAGCAGC
35
                                                                                          3540
                                                                                          3600
        TTTCTAAGTT TATTGCCTTG GGTTATTATG GAATGATAGT TATAGCCCCN TATAATGCCT
                                                                                          3660
        TACCTAGGAA A
40
        Seq ID NO: 8 Protein sequence:
         Protein Accession #: NP_006527.1
                                                 31
45
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         IKEMITEASF YLFNATKRRV FFRNIKILIP ATWKANNNSK IKQESYEKAN VIVTDWYGAH
                                                                                            120
                                                                                            180
        GDDPYTLQYR GCGKEGKYIH FTPNFLLNDN LTAGYGSRGR VFVHEWAHLR WGVFDEYNND
KPFYINGONO IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI
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         MFMQSLSSVV EFCNASTHNQ EAPNLQNQMC SLRSAWDVIT DSADFHHSPP MNGTELPPPP
                                                                                            300
50
        TFSLVQAGDK VVCLVLDVSS KMAEADRLLQ LQQAAEFYLM QIVEIHTFVG IASFDSKGEI
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                                                                                            360
         GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLEELSRLT GGLKFFVPDI SNSNSMIDAF
                                                                                            480
         SRISSGTGDI FQQHIQLEST GENVKPHHQL KNTVTVDNTV GNDTMFLVTW QASGPPEIIL
                                                                                            540
         FDPDGRKYYT NNFITNLTFR TASLWIPGTA KPGHWTYTLN NTHHSLQALK VTVTSRASNS
        AVPPATVEAF VERDSLHFPH PVMIYANVKQ GFYPILNATV TATVEPETGD PVTLRLLDDG
55
                                                                                            660
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Seg ID NO: 16 Protein seguence:

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55	CCCCCCCC GCTCCGATCT GCCTCCTGAG TTTAATAGAG	TTTTTTTTG CTGCTCACTG TAGCTGGGAC	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG	CTCCCGGGTT CACCACCACG CCAGGATGGT	CATGCCATTC CCCGGCTAAT CTCGATCTCC	TCCTGCCTCA TTTTTGTATT TGACCTCGTG	4860 4920
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	CCCCCCCCC GCTCCGATCT GCCTCCTGAG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC	TTTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT	CTCCCGGGTT CACCACCACG CCAGGATGGT GGATTACAGG AATGTAATCA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT	4860 4920 4980 5040 5100
55 60	CCCCCCCCC GCTCCGATCT GCCTCCTGAG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG	TTTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT	CTCCCGGGTT CACCACCACG CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAGG	4860 4920 4980 5040 5100 5160
	CCCCCCCCC GCTCCGATCT GCCTCCTGAG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG	TTTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT	CTCCCGGGTT CACCACCACG CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAGG	4860 4920 4980 5040 5100
	CCCCCCCCC GCTCCGATCT GCCTCCTGAG TTTAATAGAG ATCGCCTGC CTTGTTTTCC TGATCATACG GGGAGAAAGA	TTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG	CTCCGGGTT CACCACCACG CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAGG GTAAGCCTAG	4860 4920 4980 5040 5100 5160 5220
	CCCCCCCCC GCTCCGATCT GCCTCCTGAG TTTAATAGAG ATCGCCTGC CTTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT	TTTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA TTCCTGCTGT	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC	CTCCGGGTT CACCACCACG CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAGG GTAAGCCTAG TGAAACACCC	4860 4920 4980 5040 5100 5160 5220 5280
	CCCCCCCC GCTCCGATCT GCCTCCTGG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG GGGAGAAAG TTGCTGAAAT ACTGTGTTTT	TTTTTTTTG CTGCTCACTG TAGCTGGGG ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA TTCCTGCTGT GCTCACTCCC	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG	CTCCGGGTT CACCACCACG CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT TAGGACAGTCG GGAATTCTCT TAACGGCTAC GCTACCTCCC	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGGAAAGT AGAGCCAGG GTAAGCCTAG TGAAACACCC CAAGACTTTA	4860 4920 4980 5040 5100 5160 5220 5280 5340
60	CCCCCCCC GCTCCGATCT GCCTCCTGG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG GGGAGAAAG TTGCTGAAAT ACTGTGTTTT	TTTTTTTTG CTGCTCACTG TAGCTGGGG ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA TTCCTGCTGT GCTCACTCCC	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG	CTCCGGGTT CACCACCACG CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT TAGGACAGTCG GGAATTCTCT TAACGGCTAC GCTACCTCCC	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGGAAAGT AGAGCCAGG GTAAGCCTAG TGAAACACCC CAAGACTTTA	4860 4920 4980 5040 5100 5160 5220 5280
60	CCCCCCCC GCTCCGATCT GCCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA	TTTTTTTG CTGCTCACTI TAGCTGGGAC ACGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA TTCCTGCTGT TTCCTGCTGT TAAACTTTCT	AAAGCTCCGC TACAGGGGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT CCAGTATCAC	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC GCTACCTCCC TTCCCTGTTT	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC	4860 4920 4980 5040 5100 5160 5220 5280 5340 5400
	CCCCCCCC GCTCCGATCT GCCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGATCATACG GGGAGAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC	TTTTTTTG CTGCTCACTG AGGTGGAC ACGGGCTTC GTTTAAAGTC AATTGGATCA ACTCAGGGCA TTCCTGCTGT GCTCACTCC TAAACTTCT TTTGTTCTT	AAAGCTCCGC TACAGGCGCC TACAGGCGCC CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAAACCT CCAGTATCAC AAAACCACCT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTGAACAT AAGACAGTCC TAACGGCTAC TTACCGCTACTCCC TTCCCTGTTT GGTCTGCATG	TCCTGCCTCA TTTTGTATT TGACCTCCTG CGCTCCCGGC GTGTGAAAGT AGAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA	4860 4920 4980 5040 5100 5160 5220 5280 5340 5460
60	CCCCCCCC GCTCCGACG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC	TTTTTTTE CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC AATTGGATCA ACTCAGGGA TTCCTGCTGT GCTCACTCCC TAAACTTCTTTTTCTCTCACTCACTCACTC	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATCAAAATTT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT CCAGTATCAC AAAACCACCT TAATTTTAGG	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCC TAACGGCTAC GCTACCTCCC TTCCCTGTTT GGTCTGCATG GATTCATTTC	TCCTGCCTCA TTTTGTATT TGACCTCCTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAGG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCT TATGCCCGAA TATATTTCA	4860 4920 4980 5040 5100 5160 5220 5280 5340 5460 5520
60	CCCCCCCC GCTCCGACG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC	TTTTTTTE CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC AATTGGATCA ACTCAGGGA TTCCTGCTGT GCTCACTCCC TAAACTTCTTTTTCTCTCACTCACTCACTC	AAAGCTCCGC TACAGGCGCC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATCAAAATTT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT CCAGTATCAC AAAACCACCT TAATTTTAGG	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCC TAACGGCTAC GCTACCTCCC TTCCCTGTTT GGTCTGCATG GATTCATTTC	TCCTGCCTCA TTTTGTATT TGACCTCCTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAGG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCT TATGCCCGAA TATATTTCA	4860 4920 4980 5040 5100 5160 5220 5280 5340 5460
60	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT	TTTTTTTG CTGCTCACTI TAGCTGGGAC ACGGGGTTC CTGGGCCTCC GTTTAAAGTC ACTCAGGGCA TTCCTGCTGT GCTCACTCCC TTAAACTTCT TTTGTTCTTT TTTTTCTCTC ATTATTATTTT	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT CCTTATATGT	CTCCGGGTT CACCACCA CCAGGATGGT GGATTACAGG AATGTAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT CCCAGTATCAC AAAACCACT TAATTTAGG GTAAGGTGAA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TITTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC GCTACCTCCC TTCCCTGTTT GGTCTGCATG GATTCATTTC ATTTATGGTA	TCCTGCCTCA TTTTGTATT TGACCTCCTG CSCTCCCGGC GTGTGAAAGT AGAAGCCAGG GTAAGCCTAG TGAAACACCT CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTTGAGTGTG	4860 4920 4980 5040 5100 5160 5220 5340 5460 5520 5580
60	CCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTT CTAGTGCGA TAACCATCTC TTTGTAATCT CATATGTAGT CAAGAAAATA	TTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTCA ACTCAGGGCA TTCCTGCTGT GCTCACTCCC TAAACTTTCT TTTGTTCTTT TTTTCTCTCA ATTATATTT TATTTTTAAA	AAAGCTCCGC TACAGGCGC ACTOTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAATT CCTTATATGT GCTTTCATTT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT CCAGTATCAC AAAACCACCT TAATTTAGG GTAAGGTGAA TTCCCCCAGT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TITTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC TTCCCTGTTT GGTCTGCATG GATTCATTTC ATTTATGGTA GAATGATTTA	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTTA	4860 4920 4980 5040 5100 5160 5220 5340 5460 5520 5580 5640
60 65	CCCCCCCCC GCTCCGACC GCTCCTGAG TTTAATAGAG ATCCGCCTGC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CATATGTAGT CAGGAAAATA TGTAAATTA	TTTTTTTTE CTGCTCACTE TAGCTGGAC ACGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA TCCTGCTGT GCTCACTCCC TAAACTTCT TTTTCTCTT TTTTCTCTCA ATTATTATT TATTTTTATAT TATTTTTTATATT TATTTTTT	AAAGCTCCGC TACAGGCGC TACAGGCGC CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAATT CCTTATATGT TTTCTTTCATTT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT CCAGTATCAC TAATTTAGG GTAAGGTGAA TTCCCCCAGT TTATTAAGGAA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTGAACAT AAGACAGTCC TAACGGCTAC TTCCCTGTTT GGTCTGCATG GATTCATTC ATTTATGGTA GAATGATTTA GCAGCTGCT	TCCTGCCTCA TTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTCA TTTGAGTGTG GAATTTTTA AAAATGCAGT	4860 4920 4980 5040 5160 5220 5280 5340 5460 5520 5520 5640 5700
60 65	CCCCCCCCC GCTCCGACC GCTCCTGAG TTTAATAGAG ATCCGCCTGC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CATATGTAGT CAGGAAAATA TGTAAATTA	TTTTTTTTE CTGCTCACTE TAGCTGGAC ACGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA TCCTGCTGT GCTCACTCCC TAAACTTCT TTTTCTCTT TTTTCTCTCA ATTATTATT TATTTTTATAT TATTTTTTATATT TATTTTTT	AAAGCTCCGC TACAGGCGC TACAGGCGC CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAATT CCTTATATGT TTTCTTTCATTT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT CCAGTATCAC TAATTTAGG GTAAGGTGAA TTCCCCCAGT TTATTAAGGAA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTGAACAT AAGACAGTCC TAACGGCTAC TTCCCTGTTT GGTCTGCATG GATTCATTC ATTTATGGTA GAATGATTTA GCAGCTGCT	TCCTGCCTCA TTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTCA TTTGAGTGTG GAATTTTTA AAAATGCAGT	4860 4920 4980 5040 5160 5220 5280 5340 5460 5520 5520 5640 5700
60	CCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CAGGAAAATA TGTAAATATA GGGGTTGTT	TTTTTTTG CTGCTCACTI TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC ACTCAGGGCA TTCCTGCTGT TGCTCACTCC TAAACTTCT TTTTTCTCTCA ATTATTATTT TATTTTTAAA CAGAATGTT TTGCAATGT	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT CCTTATATGT GCTTTCATTT TTTCTTACTT TTTAAACAGAG	CTCCGGGTTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT ATCAAAACCT TAATTTAGG GTAAGGTATACAC TAATTTTAGG GTAAGGTGAA TTCCCCCAGT TTTATAGGAAT TTTATAGTATT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TITTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC TTCCCTGTTT GGTTCGCATG GATTCATTCA ATTTATGGTA GAATGATTTC GGTACTCC GGTACTCC GGTACTCC TTCCCTGTTT GGTCTCATTC GATTCATTCC GTATTATGGTA GCAGCTGTC GCTATTAAAA	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GCTCCCGGC GTGGAAAGT AGAAGCCAGG GTAAGCCTAG TGAAACACCT CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTTGAGTGTG GAATTTTTTA AAAATGCAGT AAAATGCAGT	4860 4920 4980 5040 5100 5160 5220 5280 5340 5460 5520 5580 5640 5700
60 65	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CAAGAAAATA TGTAAATATA GGGGTTTGTT TGCTTTTAAA	TTTTTTTG CTGCTCACTI TAGCTGGGAC ACGGGGTTC CTGGGCCTCC GTTTAAAGTC ACTCAGGCA TTCCTGCTGT GCTCACTCC TTAAACTTCT TTTTTCTCTC ATTATTTTTTTT	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAATT CCTTATATGT GCTTTCATTT TTTATATT TTAAACAGAG TGCTTAAAAA	CTCCGGGTTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCAA GTCTGAGAAT CAGTTTTATCA ATCAAAACCT CCAGTATCAC AAAACCACCT TAATTTAGGAA TTCCCCCAGT TTATAAGGAA TTTTAGTATT AAGCAAAAT TAAGAAAAT TAAGAAAAT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC TTCCCTGTTT GGTCTGCATG GATTCATTTC ATTTATGGTA GAATGATTA GCAGCTGTCT GCTGTTTAAAA TGGATGCATA	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GCTCCCGGC GTGTGAAAGT AGAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTTGAGTGTG GAATTTTTTA AAAATGCAGT AAGTAATATT AAGTAATATT	4860 4920 4980 5040 5100 5160 5220 5280 5340 5460 5520 5580 560 5700 5760 5820
60 65	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTTTAATTC CAATATATAGT CAAGAAAATA TGTAAATATA GGGGTTTGTT TGCTTTTAATT TGCTTTTAATTAAA TACAGATGTGT TAGTTAATATAA	TTTTTTTTE CTGCTCACTE TAGCTGGAC ACGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA ACTCAGGGCA TTCCTGCTGT GCTCACTCCC TAAACTTCT TTTTCTCTTA TTTTTTTATAT TATTTTTATAT TAGCAATGTT TTGCAATGTT TTGCAATGTT GAAACTTGGG GGGAGATGTA	AAAGCTCCGC TACAGGCGC TACAGGCGC ACTOTGTTAG CAAAGTGCTG GTCTTCTTTA ATCTTGAAAT CAAAATATTG AACCAGAAGC CAACAGAGCA GAACATGCTG AATGAAAATT CCTTATATG TCTTTATATT TTTATACAGAG TGCTTAAAAT TTGTTAAATT TTAAACAAAAT TTAAAACAAT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA ACTCAACCAA CTCTAAGAACCT CAGTATCAC AAAACCAC TAAATTTAGG GTAAGGTGAA TTCCCCCAGT TTATAAGGAA TTTTAGTATT AAGCAAAAT ATTAACTTGG	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TITTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC TTCCCTGTTT GGTCTGCATG GATTCATTCC ATTTATGGTA GAATGATTTA GCAGCTGTCT GCTATTAAAAA TGGATGCATA TTGGATGCATA TTGGATGCATA TTTCTTGTTT	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTTA AAAATGCAGT AAGTTACTT TTGCTGTATT TTGCTGTATT TTGCTGTATT TTGCTGTATT	4860 4920 4980 5040 5100 5160 5220 5280 5340 5460 5520 5580 5600 5700
60 65	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTTTAATTC CAATATATAGT CAAGAAAATA TGTAAATATA GGGGTTTGTT TGCTTTTAATT TGCTTTTAATTAAA TACAGATGTGT TAGTTAATATAA	TTTTTTTTE CTGCTCACTE TAGCTGGAC ACGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA ACTCAGGGCA TTCCTGCTGT GCTCACTCCC TAAACTTCT TTTTCTCTTA TTTTTTTATAT TATTTTTATAT TAGCAATGTT TTGCAATGTT TTGCAATGTT GAAACTTGGG GGGAGATGTA	AAAGCTCCGC TACAGGCGC TACAGGCGC ACTOTGTTAG CAAAGTGCTG GTCTTCTTTA ATCTTGAAAT CAAAATATTG AACCAGAAGC CAACAGAGCA GAACATGCTG AATGAAAATT CCTTATATG TCTTTATATT TTTATACAGAG TGCTTAAAAT TTGTTAAATT TTAAACAAAAT TTAAAACAAT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA ACTCAACCAA CTCTAAGAACCT CAGTATCAC AAAACCAC TAAATTTAGG GTAAGGTGAA TTCCCCCAGT TTATAAGGAA TTTTAGTATT AAGCAAAAT ATTAACTTGG	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TITTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC TTCCCTGTTT GGTCTGCATG GATTCATTCC ATTTATGGTA GAATGATTTA GCAGCTGTCT GCTATTAAAAA TGGATGCATA TTGGATGCATA TTGGATGCATA TTTCTTGTTT	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTTA AAAATGCAGT AAGTTACTT TTGCTGTATT TTGCTGTATT TTGCTGTATT TTGCTGTATT	4860 4920 4980 5040 5100 5160 5280 5340 5400 5520 5580 5700 5700 5820 5820 5880
60 65	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA ACCGTGTTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CAAGAAAATA TGTAAATAT GGGGTTTGTT TGCTTTAAAT TACAGATGTG TAGAGAATAA TACAGATGTG TAGAGAATAA	TTTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC AATTGGATCA ACTCAGGCA ACTCAGGCA TTCCTGCTGT GCTCACTCCC TAAACTTCT TTTTCTCTCA ATTATTATTT TATTTTTAAA ACAGAATGTT TGCAATGTT GAAACTTGG GAAACTTGG GAGATGTA ATTATTCTAA	ARAGCTCGCC TACAGGCGC ACTGTGTTAG CARAGTGCTG GTCTTCTTT ATCTTGAAAT CARATATTG ARCCAGAAGC TCACTCACG CARAGAGCAA GAACATGCTG GATTGAAAT TCTTATATGT TCTTATATGT TTTTATATCTT TTTATAACAGAG TGCTTAAAAT ATAAAACAAT ATAAAACAAT	CTCCGGGTT CACCACAC CCAGGATGGT GGATTACAG AATTCAACCAA GTCTGAGAAT CAGTTTTATC CAGTATCAC AAAACCACT TAATTTAGG GTAAGGTGAA TTCCCCCAGT TTATAAGGAA TTTAGGAAAATT AAGCAAAAATT	CATTECCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TITTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTACC TTCCCTGTTT GGTTCTGCATG GATTCATTCA ATTTATGGTA GCAGCTGTCT GCTACTTCATTTCAT	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GCTCCCGGC GTGGAAGGT GAAGCCCAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTTA AAAATGCAGT GAAGTACTT AAGTAATATT TTGCGTGTAT TTGCTGTATT CTGGCATGGA	4860 4920 4980 5040 5100 5160 5220 5340 5460 5520 55640 5700 5760 5820 5940
60 65 70	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CAAGAAAATA TGCTAAAATTA TACAGAATTG TAGAGAATTA AATAGAAATA	TTTTTTTG CTGCTCACTI TAGGTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC ACTCAGGGCA TTCCTGCTGT GCTCACTCC TTTGTTCTT TTTTTCTCTC ATTATTATT TATTTTTAAA CAGAATGTTT TTGCAATGTT GAAACTIGGC GGGAGATGAA ATTATTTAA	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAATT TCTTAATTT TCTTAATTT TTAAACAGAG TGCTTAAAAAT ATAAAACAAT GATGATCACT TCTTTGTTGTT TTTTTTTTTT	CTCCGGGTTT CACACCAC CCAGGATGGT GGATTACAGG AATGTAATCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT CAGTATCAC AAAACCACT TAATTTAGGAA TTCCCCCAGT TTATAAGGAA TTTTAGTAT AAGCAAAAT ATTAACTGG TTGCAAAAT ATTAACTGG TTGCAAAAT TTTAAGGGAA TTGCAAAAT TTTAATGGGG	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC TTCCCTGTTT GGTCTGCATG GATTCATTTC ATTTATGGTA GAATGATTA GCAGCTGTCT GCTATTAAAA TCGATGCATA TTTCTTGTTT ATGCTATGGA ATTATTCTTGTTT ATGCTTATGGA ATTATTTTGGTA ATGCTTATGGA ATTATTTTGGTA ATGCTTATGGA AATTATTTTGG	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GCTCCCGGC GTGGAAAGT AGAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTTGAGTGTG GAATTTTTTA AAAATGCAGT TAGGTGATTT TTGCTGTATT TTGCTGTATT TTGCGCATGGA ACAATGTTTC	4860 4920 4980 5040 5160 5280 5340 5400 5520 5520 5580 5760 5880 5880 5940 6000
60 65	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC TGATCATACG GGGAGANAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTTTAATTC CAATATATAGT CAAGAAATA TGTAAATATA GGGGTTTGTT TGCTTTTAAAT TACAATGTG TAGAGATTAA AATAGAAATA AATTACAAAT	TTTTTTTTE CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA ACTCAGGGCA TTCCTGCTGT TTTGTTCTTT TTTTCTCTCA ATTATTATAT ACAGAATGTTT TGCAATGTT TGAACTTTGG GGGGGATGTA ATAATTCTAA ATAATTCTAA ATAATTCTAA TGCAATTATA TGTACTATA TGTACTAATATT TGCAATTTT TGCAATTTT TGCAATTTT TGCAATTTT TGTACATCAATTTT TGTACATCATTTT TGTACATCATTTT TGTACATCATT	AAAGCTCCGC TACAGGCGC TACAGGCGC ACTOTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAATT TCTTAATTT TTTCTTACTT TTAAACAGAG TGCTTAAAAT ATAAAAAAT TTAAACAAT GATGATCACT TCTTTGTTGT TTTTTTTTTT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA ACTCAACCAA CAGTTTTATC ATCAAAACCT TAATTTAGG GTAAGGTGAA TTCCCCCAGT TTATAAGGAA TTTTAGTATTAGGAA ATTAACTTGG TTGCAAAATT ATTAACTTGG TTGCAAAATT ATTAATGGGA ATTTAATGGG	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC CCTTCCCTGTTT GGTCTGCATG GATTCATTTC ATTTATGGTA GAATGATTTA GCAGCTGTCT GCTATTAAGTA TTGCTTATGGT ATTCTTGTT ATGCTTATGG AATATTTTGG AATATTTTGG TGGGAAGAGA	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT TGAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATATTTTCA TATGAGTGTG GAATTTTTTA AAAATGCAGT AAGTAATATT TTGCTGTATT TTGCTGTATT CTGGCATGGA ACAATGTTTC TCACTATTTT	4860 4920 4980 5040 5160 5280 5340 5400 5520 5520 5580 5760 5880 5880 5940 6000
60 65 70	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC TGATCATACG GGGAGANAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTTTAATTC CAATATATAGT CAAGAAATA TGTAAATATA GGGGTTTGTT TGCTTTTAAAT TACAATGTG TAGAGATTAA AATAGAAATA AATTACAAAT	TTTTTTTTE CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA ACTCAGGGCA TTCCTGCTGT TTTGTTCTTT TTTTCTCTCA ATTATTATAT ACAGAATGTTT TGCAATGTT TGAACTTTGG GGGGGATGTA ATAATTCTAA ATAATTCTAA ATAATTCTAA TGCAATTATA TGTACTATA TGTACTAATATT TGCAATTTT TGCAATTTT TGCAATTTT TGCAATTTT TGTACATCAATTTT TGTACATCATTTT TGTACATCATTTT TGTACATCATT	AAAGCTCCGC TACAGGCGC TACAGGCGC ACTOTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAATT TCTTAATTT TTTCTTACTT TTAAACAGAG TGCTTAAAAT ATAAAAAAT TTAAACAAT GATGATCACT TCTTTGTTGT TTTTTTTTTT	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA ACTCAACCAA CAGTTTTATC ATCAAAACCT TAATTTAGG GTAAGGTGAA TTCCCCCAGT TTATAAGGAA TTTTAGTATTAGGAA ATTAACTTGG TTGCAAAATT ATTAACTTGG TTGCAAAATT ATTAATGGGA ATTTAATGGG	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC CCTTCCCTGTTT GGTCTGCATG GATTCATTTC ATTTATGGTA GAATGATTTA GCAGCTGTCT GCTATTAAGTA TTGCTTATGGT ATTCTTGTT ATGCTTATGG AATATTTTGG AATATTTTGG TGGGAAGAGA	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT TGAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATATTTTCA TATGAGTGTG GAATTTTTTA AAAATGCAGT AAGTAATATT TTGCTGTATT TTGCTGTATT CTGGCATGGA ACAATGTTTC TCACTATTTT	4860 4920 4980 5040 5100 5120 5220 5280 5340 5460 5520 5540 5700 5700 5760 5820 5820 5820 6060
60 65 70	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGAGAAAGA TTGCTGATTT CTAGTGCCGA TAACCATCTC TTTGTAATC CATATGTAGT CAAGAAAATA GGGGTTTGTT TGCTTTTAAA TACAATGT TAGAGAAATA AATAGAAATA	TTTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC CATTANAGTC AATTGGATCA ACTCAGGCA TTCCTGCTGT GCTCACTCCC TANACTTCT TTTTCTCTT TTTTTTTTTT	ARAGCTCGCC TACAGGCGC ACTGTGTTAG CARAGTGCTG GTCTTCTTT ATCTTGAAAT CARATATTG ARCCAGAAGC CARAGAGCAA GAACATGCTG GAATGCTG GAATGCTG GATTCAATT TTTCTTACTT TTTATATGT TTAAAACAAT ATAAAACAAT GATGATACCT TCTTTGTTGT ATTTATATGT ATTTATATGT ATTTATATATA	CTCCGGGTT CACCACAC CCAGGATGGT GGATTACAG GTCTGAGCAA GTCTGAGCAA GTCTGAGCAA CAGTTTTATC AATCAACCAC TAATTTATAG GTAAGGTGAA TTCCCCCAGT TTATAGGAA TTTAGGAA ATTTAGTATT AAGCAAAATT ATTAACTTGG TTGCAAAATT ATTAATGGGA ATTGAAAATT ATTAATGGGA ATTGTAATGT ATTAATGGGA ATTGTAATGT ATTGAATAGT ATTGAATAGT ATTGAATAGT ATTGAATAGT ATTGAATAGT ATTGAATAGT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGCTAC GCTACCTCC TTCCCTGTTT GGTCTGCATG GATTCATTC ATTTATGGTA GCAGCTGCT GCTATTATAGAT TTATGGTA TTCTTGTTT ATGCTTATGGT ATGTTTATGGTA ATGTTTATGGT ATGTTTATGGT ATGTTTATGGT ATGTTTATGG AATATTTTGG TGGGAAGGA ATAATAAAT	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GCTCCCGGC GTGGAAGGCAGG GTAAGCCAGG GTAAGCCTAG TGAAACACCT TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTTA AAAATGCAGT GAAGTACTT AGGTAATATT TTGAGTATT CTGGCATGGA ACAATGTTT TCACTGTATT CTGGCATGGA ACAATGTTTT TCACTGTTTT TCACTGTTTT TCACTGTTTT TTGACTGTGATT TTGACTGTATT TTGACTGTTTT TTGACTGTGTATT TTGACTGTGTATT TTGACTGTGTATT TTGACTGGGT TCACTATTTT TTGACTGGGT	4860 4920 4980 5040 5100 5120 5220 5340 5460 5520 5580 5760 5880 5940 6060 6060 6120
60 65 70	CCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATAGTAGT CAAGAAAATA TGCTTTTAAA TACAGATGTG TAGAGATTAA ATTACAAATA ATTACAAATA ATTACAAATG ATTAAAAGTA	TTTTTTTG CTGCTCACTI TAGGTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTAGGATCA ACTCAGGCA TTCCTGCTGT TTTTTCTCTCA ATTATTTTTTTTTT	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT CCTTATATGT GCTTTCATTT TTTCTTACTT TTAAAACAAT ATAAAACAAT GATGATCACT TCTTTGTTGT ATTAATATTG AGTATCATTG GTTATATTAT GGTTATATTAT	CTCCGGGTTT CACACCAC CCAGGATGGT GGATTACAGG AATGTAATCA GTCTGAGAAT CAGTTTTATC ATCAAACCT TAATTTAAC GTAAGACT TAATTTAAC GTAAGGAA TTCCCCCAGT TTATAGGAA ATTTATAGGAA ATTTAAGTAT AAGCAAAAT ATTAACTGG TTGCAAAAT ATTAATGGG ATTGTAATGT ATCACATATT CAGAGTATTC CAGAGTATTC	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC GCTACCTCCC TTCCCTGTTT GGTCTGCATG GATTCATTTC GATTCATTTC GCATGTATAGAT TGCTTATAGAT TGCTTATAGAT TTCTTGTTT ATGCTTATGG AATAATTTCG AATAATAATT	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GTGTGAAAGT AGAAGCCTAG GTAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTTGAGTGTG GAATTTTTA AAAATGCAGT AAGTAATATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TCTGCATGTTC TCACCATGTTTC TCACCATGTTTC TCACCATGTTTC TCACCATGACAC ACACTGACAC	4860 4920 5040 5160 5220 5280 5340 5460 5520 5580 5640 5700 5820 5820 5820 5820 6000 6000 6120
60 65 70	CCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATAGTAGT CAAGAAAATA TGCTTTTAAA TACAGATGTG TAGAGATTAA ATTACAAATA ATTACAAATA ATTACAAATG ATTAAAAGTA	TTTTTTTG CTGCTCACTI TAGGTGGGAC ACGGGGTTTC CTCGGCCTCC GTTTAAAGTC AATTAGGATCA ACTCAGGCA TTCCTGCTGT TTTTTCTCTCA ATTATTTTTTTTTT	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT CCTTATATGT GCTTTCATTT TTTCTTACTT TTAAAACAAT ATAAAACAAT GATGATCACT TCTTTGTTGT ATTAATATTG AGTATCATTG GTTATATTAT GGTTATATTAT	CTCCGGGTTT CACACCAC CCAGGATGGT GGATTACAGG AATGTAATCA GTCTGAGAAT CAGTTTTATC ATCAAACCT TAATTTAAC GTAAGACT TAATTTAAC GTAAGGAA TTCCCCCAGT TTATAGGAA ATTTATAGGAA ATTTAAGTAT AAGCAAAAT ATTAACTGG TTGCAAAAT ATTAATGGG ATTGTAATGT ATCACATATT CAGAGTATTC CAGAGTATTC	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC GCTACCTCCC TTCCCTGTTT GGTCTGCATG GATTCATTTC GATTCATTTC GCATGTATAGAT TGCTTATAGAT TGCTTATAGAT TTCTTGTTT ATGCTTATGG AATAATTTCG AATAATAATT	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GTGTGAAAGT AGAAGCCTAG GTAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTTGAGTGTG GAATTTTTA AAAATGCAGT AAGTAATATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TCTGCATGTTC TCACCATGTTTC TCACCATGTTTC TCACCATGTTTC TCACCATGACAC ACACTGACAC	4860 4920 4980 5040 5100 5120 5220 5340 5460 5520 5580 5760 5880 5940 6060 6060 6120
60 65 70	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC TGATCATACG GGGAGANAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAACCATCTC TTTTAATATC CAATATATAGT CAAGAAATA TGTAAATATA GGGGTTTTAAA TATACAATTAA AATAGAAATA AATATACAAATA GAAGCACGC ATTAAAATAA AATATACAAATA AATATATAAATA AAGGGGTTTTA	TTTTTTTTE CTGCTCACTG CTGGGCTCC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA ACTCAGGGCA ACTCACTCCC TAAACTTCT TTTTCTCTCT ATTATTATAT ACAGAATGTT TAATTTTTAAA CAGAATGTT TGCAATGTT GAAACTTCGG GGGGGATGTA ATAATCTAA ATAATCTAA ATAATCTAA CTCAATTATG TGTGACATC TTTACAAGATG TTTACAAGATG TTTACAAGATG CTTTACAAGATG CTTTACAAGGAC CTTTACAAGATG CTTTACAAGGAC CTTTACAAGAGAC CTTTACAAGAGAC CTTTACAAGAGAC CTTTACAAGAC CTTTACAAGAC CTTTACAAGAC CTTTACAAGAC CTTTACAAGAC CTTTACAACAC CTTTACACAC CTTTACACACAC	AAAGCTCCGC TACAGGCGC TACAGGCGC ACTOTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC CAAAGAGCA GAACATGCTG GATCAACAG GAACATGCTG TCTTATATGT TCTTAACAGAG TGCTTAAAAT TTTAAACAGAT TATAAACAAT GATGATCACT TCTTTGTTGT TCTTTGTTGT TCTTTGTTGT TCTTTGTTGT TCTTTGTTGT TCTTTGTTGT TCTTTGTTGT TCTTTGTTGT TCTTTGTTGT CGTTATATTG GTTATATTG CAGTGTTAGTC	CTCCGGGTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCA ACTCAACCAA GTCTGAGAAT CAGTTTTATC ATCAAACCT TAATTTTAGG GTAAGGTGAA TTCCCCCAGT TTATAAGGAA TTTTAGTATT AAGCAAAATT ATTAATTGG TTGCAAAATT ATTAATTGG ATTAATGGG ATTGCAAAATT ATTAATGGG ATTGTAATGT ATAACTTGG ATTGCAAAATT ATTAATGGG ATTGTAATGT ATACATATGT ATACATATGT AAGGGTAATTC AAGGGAAAATT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCACC TTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC GCTACCTCCC TTCCCTGTTT GGTCTGCATG GATTCATTCA ATTATGGTA GCAATGATTA TTCTTGTTT ATGCTTATGG AATTATTTGG AATTATTTGG AATTATTTGG AATTATTTGG AATTATTTGG AATTATTTGG AATTATTTGG AATTATTGG AATTATTTGG ATGGAAGAGA AATAATAAATT CATGAATAGT	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAGG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA AAATGCAGT GAATTTTTA AAATGCAGT GAATTTTTA TTGCTGTATT TTGCTGTATT TCGCATGGCA ACAATGTTT TTGATCGGGT TCACTATTT TTGATCGGGT AAGTAAAAGCA AAGAAAAGCA	4860 4920 4980 5140 5120 5220 5280 5400 5460 5520 5580 5700 5700 57820 5880 5940 6060 6120 6120 6124
60657075	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGAGAAAGA TTGCTGATTT CTAGTGCCGA TAACCATCTC TTTGTAATC CATATGTAGT CAAGAAAATA TGCAAAATA TACAAATT GGGGTTTGTT TGCTTTAAA AATAGAAATA AGGGGTTTTAAAAGTA AGGGGTTTATA	TTTTTTTTE CTGCTCACTE CTGCGCCTCC CTCGGCCTCC CATTANAGTC AATTGGATCA ACTCAGGCA TTCCTGCTGT GCTCACTCCC TANACTTCT TTTTCTCTCA ATTATTTTTANA ACAGANGTTT TGAATGTT GAAACTTGC GGGAGATGTA ATTATTTTAAA CTCAATTAGT TTGCAATTAGT TTTGCAATTAGT TTTGCAATTATC TTTTCAGATGT TTTTCAGATGT TTTTCAGATGT TTTTCAGATGT TTTTAGAGAC CTTTTAGAGGT CAGTCTTGA	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC CAAAGAGCAA GAACATGCTG GAATGCTG GAATGCTG GAATGAAAT TTTCTTACTT TTTCTTACTT TTTAAAACAAT ATAAAACAAT GATGATCACT TCTTTGTTGT AGTTATATTAT GGTTATATTAT GGTTATATTAT GGTTATATTAT CAGTGTTAGT CAGTGTTAGT TCTCTGCACTT TCTGCCACTT TCTGCCACTT TCTGCCACTT TCTGCCACTT	CTCCGGGTT CACCACAC CCAGGATGGT GGATTACAG ACTICAACCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT TAATTTTAGG GTAAGGTGAA TTCCCCCAGT TTATAGGAA TTTAGGAAAAT ATTAACTTGG TTGCAAAATT ATTAACTTGG ATTGTAATG ATTGTAATG ATTGAATGT ATTGAATGT ATGAATATGT ATGAATATGT ATGAATATGT ATGAATATGT ATGAATATGT ATGAATATGT AAGGGAAAAT ATGAATATGT AAGGGAATATC AAGGGAATAGA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGCTAC GCTACCTCCC TTCCCTGTTT GGTCTGCATG GATTCATTTC ATTTATGGTA GCAGCTGTCT GCTATTATGGTA TTCTTGTTT ATGCTTATGGT ATGTTATAAA TTTCTTGTTT ATGCTTATGG AATATTTTGG TCGGAAGGA ATAATATTTC ATGAATAAAT CATGAATAAAT CATGAATAAT TCATGAATAGT ATGAATAAT ATGCCTGA	TCCTGCCTCA TTTTTGTATT TGACCTCGTG GSCTCCCGGC GTGGAAGGC GTAAGCCTAG GGAACACCT CAAGACTTTA ATAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTTA AAAATGCAGT GAAGTACTT AGGAGTACTT AGGAGTACTT TTGGCTGTAT TTGGTGTATT CTGGCATGGA ACAATGTTTT TTGACTGTTT TTGACTGTATT TTGACTGTAT ACACTGACAC AAGAAAAGCA AAGAAAAGCA	4860 4920 4980 5040 5100 5100 5220 5340 5460 5520 5580 5760 5880 5940 6060 6120 6120 6120 6300
60 65 70	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA ATGCGCCGA TTAGTGCCGAA TTGCTGAAAT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CAAGAAAATA TGCAGATAAT TACAGATGTT TGCTTTTAAA TACAGATGTG TAGAGAATAA AATAGAAATA AATAGAAATA AATACAAAT GAAGCACAGC ATTAAAAGTA AGGGTTTTT GGCATATTTG CAAGATGTA CAAGAATTAT	TTTTTTTG CTGCTCACTI TAGGTGGGAC ACGGGGTTTC CTCGGCCTCC AATTGGATCA ACTCAGGCA ACTCAGGCA TTCCTGCTGT TGTTCTTCT TTTTTCTCTCA ATTATTTTTAAA CAGAATGTT GAAACTTGGC GGGAGATGTA ATTATTTAAA CTCAATTATG TTTGCAATTATG TTTGCAATTATG TTTGCAATTATG TTTGCAATTATG TTTACAGAGC TTTACAGAGC CTTTACAGGAC CTTTACAGGAC CAGTCTTGAA	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT TCTTATATGT GCTTTCATTT TTTTACTTATTT TTAAAACAAAT AGAAAACAAT AGAAGACACT TCTTTGTTGT ATTAATATATAT AGTATATATAT AGTATATATT CAGTGTAGTT CCGTGTTAGCTCT TCTTGCCACTT GGTGCTCTGTT GGTGCTCTGTT GTTACTCTGTT TCTTGCCACTT TCTTGCCACTT	CTCCGGGTTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT TAATTTAAG GTAAGGAAA TTCCCCCAGT TTATATGAG GTAAGGAAAAT ATTAACTGGG ATTGAAAAT ATTAATGGG ATTGAAAAT ATTAATGGG ATTGTAATGT ATAATGT CAGAGTATTC AAGGAAAAA ACACACT AAGGAAAAT ATTAATGT ATCACATATTC AAGGAAAAAA ACACATATTC AAGGAAAAG ACAGGATAATGA ACAGGATAAGA ACAGGATAAGA ACAGGATAAGA ACAGGATAAGA ACAGGATAAGA ACAGGATAAGA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC CATGACCACAC GGAATTCTT TAACGCTAC GCTACCTCC TTCCCTGTTT GGTCTGCATG GATTCATTC ATTTATGGTA GCAGCTGTC GCTATTATGGTA TGCATTATATGTA TGCATTATGGTA ATTATTTTTTTTTT	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GCTCCCGGC GTGTGAAAGT AGAAGCCTAG GTAAGCCTAG GTAAGCCTAG TGAAACACCT TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTA AAAATGCAGT AAGTATATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TCAGCATGGA ACATGTTC AAGTAATATT TCAGCATGACAC AAGAAAAGCA ACTTTAATGA CCCATGCAGG ACTTTAATGA CCCATGCAGG	4860 4920 5040 5160 5220 5280 5340 5460 5520 5760 5820 5760 5820 6060 6060 6120 6180 6240 6360
60657075	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA ATGCGCCGA TTAGTGCCGAA TTGCTGAAAT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CAAGAAAATA TGCAGATAAT TACAGATGTT TGCTTTTAAA TACAGATGTG TAGAGAATAA AATAGAAATA AATAGAAATA AATACAAAT GAAGCACAGC ATTAAAAGTA AGGGTTTTT GGCATATTTG CAAGATGTA CAAGAATTAT	TTTTTTTG CTGCTCACTI TAGGTGGGAC ACGGGGTTTC CTCGGCCTCC AATTGGATCA ACTCAGGCA ACTCAGGCA TTCCTGCTGT TGTTCTTCT TTTTTCTCTCA ATTATTTTTAAA CAGAATGTT GAAACTTGGC GGGAGATGTA ATTATTTAAA CTCAATTATG TTTGCAATTATG TTTGCAATTATG TTTGCAATTATG TTTGCAATTATG TTTACAGAGC TTTACAGAGC CTTTACAGGAC CTTTACAGGAC CAGTCTTGAA	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT TCTTATATGT GCTTTCATTT TTTTACTTATTT TTAAAACAAAT AGAAAACAAT AGAAGACACT TCTTTGTTGT ATTAATATATAT AGTATATATAT AGTATATATT CAGTGTAGTT CCGTGTTAGCTCT TCTTGCCACTT GGTGCTCTGTT GGTGCTCTGTT GTTACTCTGTT TCTTGCCACTT TCTTGCCACTT	CTCCGGGTTT CACCACCAC CCAGGATGGT GGATTACAGG AATGTAATCAA GTCTGAGAAT CAGTTTTATC ATCAAAACCT TAATTTAAG GTAAGGAAA TTCCCCCAGT TTATATGAG GTAAGGAAAAT ATTAACTGGG ATTGAAAAT ATTAATGGG ATTGAAAAT ATTAATGGG ATTGTAATGT ATAATGT CAGAGTATTC AAGGAAAAA ACACACT AAGGAAAAT ATTAATGT ATCACATATTC AAGGAAAAAA ACACATATTC AAGGAAAAG ACAGGATAATGA ACAGGATAAGA ACAGGATAAGA ACAGGATAAGA ACAGGATAAGA ACAGGATAAGA ACAGGATAAGA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC CATGACCACAC GGAATTCTT TAACGCTAC GCTACCTCC TTCCCTGTTT GGTCTGCATG GATTCATTC ATTTATGGTA GCAGCTGTC GCTATTATGGTA TGCATTATATGTA TGCATTATGGTA ATTATTTTTTTTTT	TCCTGCCTCA TTTTTGTATT TGACCTCCTGC GCTCCCGGC GTGTGAAAGT AGAAGCCTAG GTAAGCCTAG GTAAGCCTAG TGAAACACCT TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTA AAAATGCAGT AAGTATATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TCAGCATGGA ACATGTTC AAGTAATATT TCAGCATGACAC AAGAAAAGCA ACTTTAATGA CCCATGCAGG ACTTTAATGA CCCATGCAGG	4860 4920 4980 5040 5100 5100 5220 5340 5460 5520 5580 5760 5880 5940 6060 6120 6120 6120 6300
60657075	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG GGGAGANAGA TTGCTGAAAT ACTGTGTTT CTAGTGCCGA TAGACATCTC CATATGTAGT CAGAAATA TGTAAATATA GGGGTTTGTT TGCTTTTAAA TAGAGATATA AATAGAAATA AATAGAAATA AATAGAAATA AATAGAAATA AATAGAAATA AATAGAAATA AATAGAAATA AATAGAAATA AATAGAAATA GAGGGTTTTA GGCAATATTG CAAGATGAT CAGTGTCCC	TTTTTTTTE CTGCTCACTG CTGGGCCTCC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA ACTCAGGCA ACTCAGTCC TAAACTTCT TTTTCTCTCT TTTTTCTCTCA ATTATTATTT TAATTTTTAAA CCAAATATCTAG CGGAGATGTA ATAATCTAA CTCAATTATG TTTACAGATG TTTACAGATG TTTACAGATG TTTACAGATG CTTTAGAGGCC CAGTCTTGAT CAACCATAAA CCAACAACA	AAAGCTCCGC TACAGGCGC ACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGCA CAAAGAGCAA GAACATGCTG CAAAGAGCAA GAACATGCTG TTTAATGT TTTAATATT TTAAACAGAG TGCTTAAAAT ATAAAACAAT GATGATCACT ATTAATATAT GATGATCACT TCTTTGTTGT ATTAATATAT AGTATCTATG GTTATAATT CAGTGTTAGTC TCTTGCCACTT TGGCCACTT TTAAGAGCTGA	CTCCGGGTT CACCACAC CCAGGATGGT GGATTACAGG AATGTAATCA GTCTGAGAAT CAGTTTTATC ATCAAACCT TAATTTTAGG GTAAGGTGAA TTCCCCCAGT TTATTAGGAA TTTTAGTATT AAGCAAAAAT ATTAACTTGG TTGCAAAATT ATTAATGGGA ATTGTAATGT ATTAATGGGAATGGA ATGTAATGT ATTAATGTG ATGTAATGT ATGAAAATT ATTAATGTG ATGTAATGT ATGAAAATT ATTAATGTG ATGTAATGT AAGGAAAAAC ACAGGATAGA ACAGGATAGA ACAGGATAGA TCATTCAAAAT TCATTCAAAT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC TCCCTGTTT GGTCTGCATG GATTCATTTA GAATGATTAT GTATTATGGTA TGCATGTAT ATGCTATTA ATGCTATTA ATGCTATTGG AATTATTTTGTT ATGCTATTGG TGGGAAGAGA ATAATATTTTGG TGGGAAGAGA ATAATAATT CATGAATAAAT TATGCTTAAA TAATGCCTGA AGAGTTAAA TAATGCTTAA GAATCTTTTC AATCTTATTG AATCTTATTAG AATCTTTTC AATCTTATTAG	TCCTGCCTCA TTTTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT TGAAGCCTAG GTAAGCCTAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTA AAAATGCAGT GAAGTTACTT TAGCTGAATT TTGCTGTATT TTGCTGTATT TTGCTGTATT TTGATCGGGT TCACTATTTT TTGATCGGGT TCACTATTTT TTGATCGGGT ACATTGACAC AAGAAAAGCA ACTTTAATGA ACTTTAATGA CCCATGCAGG CTTATATCAAA	4860 4920 4980 5040 5100 5120 5220 5280 5400 5460 5520 5700 5700 57820 5880 5940 6060 6120 6240 6360 6340 6340
60657075	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG GGGAGAAAGA TTGCTGAATT CTAGTGCCGA TAACCATCTC TTTGTAATTC CATATGTAGT CAAGAAAATA TGTAAATATA GGGGTTTGTT TGCTTTTAAA ATTACAATTG TAGAGATTAA ATTACAAATA AATTACAAATA AATTACAAATA AATGAAATTA AGGGATTTTA AGGGATTTTA AGGGATTTTA AGGGATTTTA CAAGATGTGCCCC ATTAAAATTG AGGTTTTTA AGGGATTTTA AGGGATTTTA AGGGATTTTA AGGGATTTTA AGGGATGATC AGGTTTTCAT	TTTTTTTTE CTGCTCACTE CTGCTCACTE ACCGGGCTTC CTCGGCCTCC CATAAAGTC ACTCAGGCA ACTCAGGCA TCCTGCTGT GCTCACTCCC TAAACTTCT TTTTCTCTT TTTTCTCTCA ATTATTATT TTGCAATGTT GAAACTTGGA ATAACTTCA ATAATTCTA TTGCAATGTT TGCAATTATA TTGCAATTATA TTGCAATTATA TTTTAAGAGGTG TTTAAGAGGTG CTTTAAGAGGTG CTTTAAGAAC CTCAATTATA CTCAATTATA CTCAATTATA CTCAATTATA CTCAATTATA CTCAATTATA CTCAATTATA CTCAATTATA CTTTAAGAAGT TTTAAGAAGT CTTTAAGAAC CTTTAAAAAC CTTACAAAC CTTCAAAAC CTTCAAAAAC CTTCAAAAAAAA	ARAGCTCGGC TACAGGGGC ACTGTGTTAG CARAGTGCTG GTCTTCTTT ATCTTGAAAT CARAATATTG ARCCAGAAGC CARAGAGCAA GARCATGCTG GAATGCTG GAATGCTG GAATGAAAAT TCTTATATGT TTTCTTACTT TTTCTTACTT TTTATACATGAAAT ATARACAGAG TGCTTAAAAT ATARACACT TCTTTGTTGT ATTATATATAT GGTTATATAT GGTTATATAT GTTATATATT CAGTGTAGTC TCTGCCACTT GGTGCCCCTT GGTGCCCCCACA	CTCCGGGTT CACCACAC CCAGGATGGT GGATTACAG GTCTGAGAAT CAGTTTTATC ATCAAAACCT CCAGTATCAC AAAACCACT TAATTTTAGG GTAAGGTGAA TTCCCCCAGT TTATAAGGAA TTTATAGGAA ATTAACTTGG TTGCAAAATT ATTAACTTGG ATTGTAATGT ATGAATATT ATGAATATT ATGAATATT ATGAATATT ATGAATATT ATGAATATT ATGAATATGT AAGGGAAAAT CAGGGATATC AAGGGAAAAC ATGTAATGT CAGGGATATC AAGGGAAAAC ACAGGATATCAAAC TCATTCCAAA	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT GAATCTCT TAACACAGTCG GGAATTCTCT TAACGCTAC GCTACCTCCC TTCCCTGTTT GGTTCTGCATG GAATGATTAA ATTTATGGTA GCAGCTGCT GCTATTAAAA TGGATGCATA TTCTTGTTT ATGCTTATGG AATATTTTGG TGGGAAGGA ATAATATTTGG TGGGAAGGA ATAATATTTGG TGGGAAGGA ATAATATTTGG TGGGAAGGA ATAATATTTGG TGGAAGGA ATAATATTTGG TGGGAAGGA ATAATATTTGG TGGAAGGA ATAATATTTGG TGGAAGGA ATAATATTTGG AATCTTTTC CAATCTATTAG CAATCTATTAG CCAGTTAACTT	TCCTGCCTCA TTTTTGTATT TGACCTCGTG GCTCCCGGC GTGTGAAAGT AGAAGCCAGG GTAAGCCTAG TGAAACACCT CAAGACTTTA ATAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTTA AAAATGCAGT GAAGTACTT AAGTAATATT CTGGCATGGA ACAATGTTTC TCACTATTTT TTGACTGTAT CTCACTATTTT TTGACTGTAT CTCACTATTTT TTGACTGTAT CTCACTATTTT TTGACTGTAT CCACTACTTTATTAAAAACTAAAACCAAGAAAAGCA AGAAAAGCA AGAAAAGCA ACTATTAATGAAC CTATATCAAA	4860 4920 4980 5040 5100 5120 5220 5280 5400 5520 5540 5700 5760 5880 5940 6060 6120 6120 6300 6360 6420 6480
60657075	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA ATGCTGATTT CTAGTGCCGA TTAGTGCCGA TAACCATCTC CATATGTAGT CAAGAAATA TGTAAATAT TGTAATATA TGCTTTTAAT TGCTTTTAAT TGCTTTTAAT TGCTTTTAAT TGCTTTTAAA TACAGATGTT TGCTTTTAAA ATTACAGATGT TAGAGAATAA AATAGAAATA AATAGAATTA CAAGATGTT CAAGATGTT CAAGATGTT CAAGATGTT CAAGATGTC AGCCTTACA AGCCTTACA AGCCTTACA CATTATTTT	TTTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC AATTGGATCA ACTCAGGCA ACTCAGGCA ACTCAGTGT GCTCACTCCC TAAACTTCT TTTTCTTCTT TATTTTTTAA ACAAATGTT GAAACTTTGAATGTT GAAACTTGGC GGGAGATGTA ATTATATAT TTGCAATTGT CTCAATTATG TTTCGACATC TTTAGAAGGT CTTTAGAGAGT CTTTAGAGAGT CAACCATAAA CCTACAAACG TTTAATATA CTTAATATA CTACAAACG TTTAATATA CTACAAACG TTTAATATA CTACAAACG TTTAATATA CTACAAACG	AAAGCTCCGC TACAGGCGC AACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT TCTTTATATGT GCTTTATATGT TTTATACTAT TTTAAAACAAT TCATAGAAACAAT AGTATACACT AGTATATATT AGTATCATT TCTTTGTTGT ATTAATATTAT AGTATCATT TCTTGCCACTT TGGTGCTCTGT TTAAGACTGA GTTAAACACT TCTTGCCACTT TGGTGCTCTGT TTAAGACTGA TTAAAGACTGA TTAAAGACTGA	CTCCGGGTTT CACACCAC CACGACTGGT GGATTACAGG AATGTAATCA GTCTGAGAAT CAGTTTTATC CAGTATTAATCA AAACCACT TAATTTAAGG GTAAGGTAATCAC TAATTTAGG GTAAGGTAATTAAGGAAAAT ATTAACTGGA ATTGAAAAT ATTAATGGG ATTGTAATGT CAGAGTATTC AAGGAAAAT ATTAATGGG ATTGTAATGT CAGAGTATTC AAGGGAAAAC ACAGGATAGA ACTTCACAGT TCACTTCACAGT TCACTTCACAGT TCACTTCACAGT TCATTCACAAT AATTTCAATT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC CATGACCCAC CATGACCAC GGAATTCTCT TAACGCTACC GCTACCTCCCTTTCCCTGTTT GGTCTGCATG GATTCATTCA ATTTATGGTA GCAGCTGTC GCTATTAAAA TGGATGCATA TGGTATTATGGTA ATGCTTATGG AATATTTTGG TGGGAAGGA ATAATTAAAT CATGAATAAAT CATGAATAAAT CATGAATAAT CATGATTAAA TAACCCTGA GAATCTTTTC AATCTTTTC AATCTTTTC CAGTAACTT TTTTTTTTTT	TCCTGCCTCA TTTTTTTTTTTTTTTTTTTTTTTTTTTTT	4860 4920 5040 5160 5220 5280 5340 5460 5520 5580 5760 5820 5760 5820 6000 6020 6120 6120 6240 6360 6420 6420 6540
60657075	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCCTGC CTGTTTTCC TGATCATACG GGGAGAAAGA ATGCTGATTT CTAGTGCCGA TTAGTGCCGA TAACCATCTC CATATGTAGT CAAGAAATA TGTAAATAT TGTAATATA TGCTTTTAAT TGCTTTTAAT TGCTTTTAAT TGCTTTTAAT TGCTTTTAAA TACAGATGTT TGCTTTTAAA ATTACAGATGT TAGAGAATAA AATAGAAATA AATAGAATTA CAAGATGTT CAAGATGTT CAAGATGTT CAAGATGTT CAAGATGTC AGCCTTACA AGCCTTACA AGCCTTACA CATTATTTT	TTTTTTTTG CTGCTCACTG TAGCTGGGAC ACGGGGTTTC CTCGGCCTCC AATTGGATCA ACTCAGGCA ACTCAGGCA ACTCAGTGT GCTCACTCCC TAAACTTCT TTTTCTTCTT TATTTTTTAA ACAAATGTT GAAACTTTGAATGTT GAAACTTGGC GGGAGATGTA ATTATATAT TTGCAATTGT CTCAATTATG TTTCGACATC TTTAGAAGGT CTTTAGAGAGT CTTTAGAGAGT CAACCATAAA CCTACAAACG TTTAATATA CTTAATATA CTACAAACG TTTAATATA CTACAAACG TTTAATATA CTACAAACG TTTAATATA CTACAAACG	AAAGCTCCGC TACAGGCGC AACTGTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT TCTTTATATGT GCTTTATATGT TTTATACTAT TTTAAAACAAT TCATAGAAACAAT AGTATACACT AGTATATATT AGTATCATT TCTTTGTTGT ATTAATATTAT AGTATCATT TCTTGCCACTT TGGTGCTCTGT TTAAGACTGA GTTAAACACT TCTTGCCACTT TGGTGCTCTGT TTAAGACTGA TTAAAGACTGA TTAAAGACTGA	CTCCGGGTTT CACACCAC CACGACTGGT GGATTACAGG AATGTAATCA GTCTGAGAAT CAGTTTTATC CAGTATTAATCA AAACCACT TAATTTAAGG GTAAGGTAATCAC TAATTTAGG GTAAGGTAATTAAGGAAAAT ATTAACTGGA ATTGAAAAT ATTAATGGG ATTGTAATGT CAGAGTATTC AAGGAAAAT ATTAATGGG ATTGTAATGT CAGAGTATTC AAGGGAAAAC ACAGGATAGA ACTTCACAGT TCACTTCACAGT TCACTTCACAGT TCACTTCACAGT TCATTCACAAT AATTTCAATT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC CATGACCCAC CATGACCAC GGAATTCTCT TAACGCTACC GCTACCTCCCTTTCCCTGTTT GGTCTGCATG GATTCATTCA ATTTATGGTA GCAGCTGTC GCTATTAAAA TGGATGCATA TGGTATTATGGTA ATGCTTATGG AATATTTTGG TGGGAAGGA ATAATTAAAT CATGAATAAAT CATGAATAAAT CATGAATAAT CATGATTAAA TAACCCTGA GAATCTTTTC AATCTTTTC AATCTTTTC CAGTAACTT TTTTTTTTTT	TCCTGCCTCA TTTTTTTTTTTTTTTTTTTTTTTTTTTTT	4860 4920 5040 5160 5220 5280 5340 5460 5520 5580 5760 5820 5760 5820 6000 6020 6120 6120 6240 6360 6420 6420 6540
60 65 70 75 80	CCCCCCCCC GCTCCGATCT GCTCCGAGC TTTAATAGAG ATCCGCCTGC CTTGTTTTCC TGATCATACG GGGAGANAGA TTGCTGAAAT ACTGTGTTTT CTAGTGCCGA TAGACATCTC CATATGTAGT CAAGAAATA TGTAAATATA GGGGTTTGTT TGCTTTAAAT TAGACATCTG TAGACATGTG TAGACATTGT TAGACATTGT TAGACATTGT TAGACATTGT TAGACATTTAAA ATTATCAAAT GAAGACATAA AGGGGTTTA AGGGGTTTA AGGGGTTTA GGCAATATTG CAAGATGATC AGTGTGCTCC AGCCTTACAT CATTATTATTA	TTTTTTTTE CTGCTCACTG CTGGGCTCC CTCGGCCTCC GTTTAAAGTC AATTGGATCA ACTCAGGGCA ACTCAGGGCA ACTCAGGCCA TTTGCTCTT TTTTCTCTCA ATTATTATAT TATATTATAT	AAAGCTCCGC TACAGGCGC TACAGGCGC ACTOTGTTAG CAAAGTGCTG GTCTTCTTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC CAAAGAGCAA GAACATGCTG CAAAGAGCAA GAACATGCTG TTTATATGT TTTATATGT TTAAACAGAG TGCTTAAAAT ATAAAACAT GATGATCACT ATTAATTATGT GTTATATTT TCTTTATGTT TCTTTATGTT TCTTTAGTT TCTTTATGTT TCTTTATGTT TCTTTATGTT TCTTTATGTT TCTTTATGTT TCTTTATGTT TCTTTTGTTGT TCTTTGTGTT TTTAATATAT GGTGTTATATG GTTATAATTAT GGTGTCTCTT TTAAGACTGA GTTGAACCAA TCAAGACTGA	CTCCGGGTT CACCACAC CACCACAC CCAGGATGGT GGATTACAGG AATGTAATCAA GTCTGAGAAT CAGTTTTATCA ATCAAACCT TAATTTAGC AAAACCACT TAATTTAGGAA TTCCCCCAGT TTATAGGAA TTTAGTAT ATGCAAAAT ATTAATGGG ATGCAAAAT ATTAATGGGA ATGCAAAAT ATTAATGGG ATGCAAAAT ATTAATGGG ATGCAAAAT TATAATGT CAGAGTATCA AAGGAAAAA ACAGGATAGA TCAGGTATTCAAAA ATTTCAAAT TCATTGGAT TGATTTGGTT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TTTTGAACAT AAGACAGTCG GGAATTCTCT TAACGGCTAC GCTACCTCCC TTCCCTGTTT GGTCTGCATG GAATGATTAT GAATGATTA TATGATAT ATGCTATTA ATGCTATTA ATGCTATTGG TGGGAAGAGA ATAATATTTTGG TGGGAAGAGA ATAATATTTTCATGTT TATGATTAAA TAATGCTGA TAATGATTAAA TAATGCTGA GAATCTTTTC AATCTTATTAG CAGTAACTT TTTGTTTTTT TTTGTTTTTT TTTGTTTTTT TTTGTTTTTT	TCCTGCCTCA TCTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTA AAAATGCAGT CAGGATTACTT AAGTAATATT TTGCTGTATT TTGCTGTATT TTGATCGGAT ACATGATCA ACATGATCA ACATGATCA ACATGACAC AAGAAAAGCA ACTTTAATGA CCCATGCAGG CCTATATCAAA CTATTGTAAC TTAATGAAA CTATTGTAAC TCATTAATGAA CTATTGTAAC TTCATAATGAA CTATTGTAAC TTCATAATGGT TCATAATGGT TCATAATGGT	4850 4920 4980 5140 5120 5220 5280 5400 5460 5520 5580 5700 5700 57820 5880 6060 6120 6060 6120 6360 6420 6480 6540 6640 6660
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60 65 70 75 80	CCCCCCCCC GCTCCGATCT GCTCCTGAG TTTAATAGAG ATCCGCTGC TGATCATACG GGAGAAAGA TTGCTGATTT CTAGTGCCGA TTAGTGCCGA TAACCATCTC TTTGTAATC CATATGTAGT CAAGAAAATA TACAGATGT TGCTTTAAA TACAGATGT TAGAGAAATA AATAGAAATA AATAGAAATA AATAGAAATA AGGGGTTTTA CAAGATTAT CAAGATTATA CAAGATTAA AGGGATTTAA AGGGATTTAA AGGGATTTAA AGGGATTTAA AGGGATTTAT CAAGATGTC CAAGATGAT CAAGATGAT CAAGATGAT CAAGATGAT CAAGATGAT TAAGAAATA TGAAGACAT AGGGATACA TGAGAAGAACA TGAGAAGAT TGAGAAGAT TTCTTGTGTA	TTTTTTTTE CTGCTCACTE TTAGCTGGGAC ACGGGGTTTC CTCGGCCTCC CATTANAGTC AATTGGATCA ACTCAGGCA TTCCTGCTGT GCTCACTCCC TANACTTCT TTTTCTCTT TTTTTTTTTT	AAAGCTCCGC TACAGGCGC AACTGTGTTAG CAAAGTGCTG GTCTTCTTT ATCTTGAAAT CAAAATATTG AACCAGAAGC TCACTCACCG CAAAGAGCAA GAACATGCTG AATGAAAAT CCTTATATGT TCTTTATTT TTTCTTACTT TTTAAAACAAAT AGAAAATATCACT AGTTATATATG GTTATAATATG GTTATAATATG TCTTTGTTGT TTTAAAACAAT AGTATATTATG GTTATAATATG TCTTGTTGT TTAAAACAAT TCTTTGTTGT TTAAAACAAT TCTTTGTTGT TTAAAACAAT CCTTCAGTAT CCTTCAGTAT GCCAGAATGG CCTTCAGTAT	CTCCGGGTT CACACCAC CACACCAC CAGGATGGT GGATTACAGG AATGTAATCA GTCTGAGAAT CAGTTTTATC CAGTATCAC AAAACCAC TTAATTTAGG GTAAGGGA TTCCCCAGT TTATAGGAA ATTTAAGGA ATTTAAGTAAT ATTAACTTG ATTAATGGG ATTGTAATGT ATTAATGGG ATTGTAATGT CAGAGTATAC ACAGGTAGAA ACTTCCACAGT TCATTCAAA AATTTCAATT TCATTTGATT TGATTTGGTT TTGGATATGT TTGGATATGGT TTTGGATATGT TTTGGATATGGT TTTGGATATGGT TTTGGATATGGT TTGGATATGGAT TTGGATATGGAT TTGGATATGGT TTGGATATGGAT	CATGCCATTC CCCGGCTAAT CTCGATCTCC CATGACCCAC TITTGAACAT AAGACAGTCG GGAATTCTCT TAACGCTACC TTCCCTGTTT GGTCTGCATG GATTCATTCA ATTTATGGTA GCAGCTGCT GCTATTATGGTA TTCTTGTTT ATGCTTATTGG AATATTTGG AATATTTGG AATATTTGG AATATTTTG GAATGATTAAA TCATGAATAAAT CATGAATAAAT CATGAATAATT CATGAATAATT CATGAATAATT TATGTTTATGG GAATCTTTTC AATCTATTAG CCAGTAACTT TTTGTTTTTTA GAATATTTGG AATATTTGG AATCTATTAG AATATTTGG AATCTATTAG AATATTTGG AATCTATTAG AATCTATTAG CCAGTAACTT CCTGGAACGT ACCTGGATCG ATCCTGGATCG ATCCTGGATCG ATCCTGGATCG ATCCTGGATCG ATCCTGGATCG ATCCTGGATCG ATCCTGGATCG GCTTTCTCAT	TCCTGCCTCA TCTTGTATT TGACCTCGTG CGCTCCCGGC GTGTGAAAGT AGAAGCCAG GTAAGCCTAG TGAAACACCC CAAGACTTTA ATAAAACCTC TATGCCCGAA TATATTTTCA TTTGAGTGTG GAATTTTTA AAAATGCAGT CAGGATTACTT AAGTAATATT TTGCTGTATT TTGCTGTATT TTGATCGGAT ACATGATCA ACATGATCA ACATGATCA ACATGACAC AAGAAAAGCA ACTTTAATGA CCCATGCAGG CCTATATCAAA CTATTGTAAC TTAATGAAA CTATTGTAAC TCATTAATGAA CTATTGTAAC TTCATAATGAA CTATTGTAAC TTCATAATGGT TCATAATGGT TCATAATGGT	4860 4920 5040 5160 5220 5280 5340 55580 5640 5760 5880 6000 6120 6180 6240 6360 6420 6440 6540 6600 6600 6600 6720

ATAGAACACT GCCTGCACAT AGTAAAAGAA TTATAAGTGT GAGGTAGTTG GTAAAATTAT GTAGTTGGAT ATACTACCGA ACAATATCTA ATCTCTTTTT AGGGAAATAA AGTTTGTGCA 6900 TATATATAAT CCCGAAACAT G 5 Seg ID NO: 32 Protein seguence: Protein Accession #: NP_001932.1 51 10 MAAAGPRRSV RGAVCLHLLL TLVIFSRDGE ACKKVILNVP SKLEADKIIG RVNLEECFRS
ADLIBSDPD FRVLNDGSVY TARAVALSDK KRSFTIWLSD KRKOTOKEVT VLLEHOKKVS 60 120 KTRHTRETVL RRAKRRWAPI PCSMQENSLG PFPLFLQQVE SDAAQNYTVF YSISGRGVDK 180 EPIMIFYIER DTGNLFCTRP VDREEYDVFD LIAYASTADG YSADLPLPLP IRVEDENDNH PVFTEAIYNF EVLESSRPGT TVGVVCATDR DEPDTMHTRL KYSILQQTPR SPGLFSVHPS 240 300 15 TGVITTVSHY LDREVVDKYS LIMKVQDMDG QFFGLIGTST CIITVTDSND NAPTFRQNAY EAFVEENAFN VEILRIPIED KOLINTANWR VNFTILKGNE NGHPKISTDK ETNEGVLSVV 420 KPLNYEENRQ VNLEIGVNNE APFARDIPRV TALNRALVTV HVRDLDEGPE CTPAAQYVRI 480 KENLAVGSKI NGYKAYDPEN RNGNGLRYKK LHDPKGWITI DEISGSIITS KILDREVETP 540 KNELYNITVL AIDKDDRSCT GTLAVNIEDV NDNPPEILQE YVVICKPKMG YTDILAVDPD 20 EPVHGAPFYF SLPNTSPEIS RLWSLTKVND TAARLSYQKN AGFQEYTIPI TVKDRAGQAA 660 TKLLRVNLCE CTHPTQCRAT SRSTGVILGK WAILAILLGI ALLFSVLLTL VCGVFGATKG 720 KRFPEDLAQQ NLIISNTEAP GDDRVCSANG FMTQTTNNSS QGFCGTMGSG MKNGGQETIE 780 MMKGGNQTLE SCRGAGHHHT LDSCRGGHTE VDNCRYTYSE WHSFTQPRLG EKLHRCNQNE DRMPSODYVL TYNYEGRGSP AGSVGCCSEK QEEDGLDFLN NLEPKFITLA EACTKR 25 Seq ID NO: 33 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 64-2583 30 31 GGCAGGTCTC GCTCTCGGCA CCCTCCCGGC GCCCGCGTTC TCCTGGCCCT GCCCGGCATC CCGATGGCCG CCGCTGGGCC CCGGCGCTCC GTGCGCGGAG CCGTCTGCCT GCATCTGCTG 120 CTGACCCTCG TGATCTTCAG TCGTGATGGT GAAGCCTGCA AAAAGGTGAT ACTTAATGTA CCTTCTAAAC TAGAGGCAGA CAAAATAATT GGCAGAGTTA ATTTGGAAGA GTGCTTCAGG 35 180 240 TCTGCAGACC TCATCCGGTC AAGTGATCCT GATTTCAGAG TTCTAAATGA TGGGTCAGTG 300 TACACAGCCA GGGCTGTTGC GCTGTCTGAT AAGAAAAGAT CATTTACCAT ATGGCTTTCT GACAAAAGGA AACAGACACA GAAAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA 360 420 40 TCGAAGACAA GACACACTAG AGAAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 480 ATTCCTTGCT CTATGCAAGA GAATTCCTTG GGCCCTTTCC CATTGTTTCT TCAACAAGTT GAATCTGATG CAGCACAGAA CTATACTGTC TTCTACTCAA TAAGTGGACG TGGAGTTGAT 540 600 AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660 CCTGTGGATC GTGAAGAATA TGATGTTTTT GATTTGATTG CTTATGCGTC AACTGCAGAT 720 GGATATTCAG CAGATCTGCC CCTCCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 45 780 CACCCTGTTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC 900 CTGARATACA GCATTTTGCA GCAGACACCA AGGTCACCTG GGCTCTTTTC TGTGCATCCC AGCACAGGGG TAATCACCAC AGTCTCTCAT TATTTGGACA GAGAGGTTGT AGACAAGTAC 960 50 TCATTGATAA TGAAAGTACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA 1080 ACTTGTATCA TAACAGTAAC AGATTCAAAT GATAATGCAC CCACTTTCAG ACAAAATGCT 1140 TATGRAGGAT TTGTAGAGGA AAATGCATTC AATGTGGAAA TCTTACGAAT ACCTATAGAA GATAAGGAT TAATTAACAC TGCCAATTGG AGAGTCAATT TTACCATTTT AAAGGGAAAT 1200 1260 GAAAATGGAC ATTTCAAAAT CAGCACAGAC AAAGAAACTA ATGAAGGTGT TCTTTCTGTT 1320 GTARAGCCAC TGAATTATGA AGAAAACCGT CAAGTGAACC TGGAAATTGG AGTAAACAAT GAAGCGCCAT TTGCTAGAGA TATTCCCAGA GTGACAGCCT TGAACAGAGC CTTGGTTACA 55 1380 GTTCATGTGA GGGATCTGGA TGAGGGGCCT GAATGCACTC CTGCAGCCCA ATATGTGCGG 1500 ATTAAAGAAA ACTTAGCAGT GGGGTCAAAG ATCAACGGCT ATAAGGCATA TGACCCCGAA 1560 AATAGAAATG GCAATGGTTT AAGGTACAAA AAATTGCATG ATCCTAAAGG TTGGATCACC 1620 60 ATTGATGAAA TTTCAGGGTC AATCATAACT TCCAAAATCC TGGATAGGGA GGTTGAAACT 1680 CCCAAAAATG AGTTGTATAA TATTACAGTC CTGGCAATAG ACAAAGATGA TAGATCATGT 1740 ACTGGAACAC TTGCTGTGAA CATTGAAGAT GTAAATGATA ATCCACCAGA AATACTTCAA 1800 GAATATGTAG TCATTTGCAA ACCAAAAATG GGGTATACCG ACATTTTAGC TGTTGATCCT 1860 GATGAACCTG TOCATGGAGC TCCATTTTAT TTCAGTTTGC CCAATACTTC TCCAGAAATC
AGTAGACTGT GGAGCCTCAC CAAAGTTAAT GATACAGCTG CCCGTCTTTC ATATCAGAAA 1920 65 1980 AATGCTGGAT TTCAAGAATA TACCATTCCT ATTACTGTAA AAGACAGGGC CGGCCAAGCT 2040 GCAACAAAT TATTGAGAGT TAATCTGTGT GAATGTACTC ATCCAACTCA GTGTCGTGCG 2100 ACTTCAAGGA GTACAGGAGT AATACTTGGA AAATGGGCAA TCCTTGCAAT ATTACTGGGT 2160 ACTICAGGA GIACAGGA ATTAGCALACT TRAGTATGTG GAGTTTTTGG TGCAACTAAA GGGAAACGTT TTCCTGAAGA TTTAGCACAG CAAAACTTAA TTATATCAAA CACAGAAGCA 2220 70 2280 CCTGGAGACG ATAGAGTGTG CTCTGCCAAT GGATTTATGA CCCAAACTAC CAACAACTCT 2340 AGCCAAGGTT TTTGTGGTAC TATGGGATCA GGAATGAAAA ATGGAGGGCA GGAAACCATT GAAATGATGA AAGGAGGAAA CCAGACCTTG GAATCCTGCC GGGGGGCTGG GCATCATCAT 2400 ACCCTGGACT CCTGCAGGGG AGGACACACG GAGGTGGACA ACTGCAGATA CACTTACTCG 2520 75 GAGTGGCACA GTTTTACTCA ACCCCGTCTC GGTGAAGAAT CCATTAGAGG ACACACTGGT TAAAAATTAA ACATAAAAGA AATTGCATCG ATGTAATCAG AATGAAGACC GCATGCCATC 2580 2700 CCAAGATTAT GTCCTCACTT ATAACTATGA GGGAAGAGGA TCTCCAGCTG GTTCTGTGGG CTGCTGCAGT GAAAAGCAGG AAGAAGATGG CCTTGACTTT TTAAATAATT TGGAACCCAA ATTTATTACA TTAGCAGAAG CATGCACAAA GAGATAATGT CACAGTGCTA CAATTAGGTC 2760 2820 80 TITGTCAGAC ATTCTGGAGG TITCCAAAAA TAATATTGTA AAGTTCAATT TCAACATGTA 2880 TGTATATGAT GATTTTTTC TCAATTTTGA ATTATGCTAC TCACCAATTT ATATTTTTAA 2940 AGCCAGTTGT TGCTTATCTT TTCCAAAAAG TGAAAAATGT TAAAACAGAC AACTGGTAAA 3000 TCTCAAACTC CAGCACTGGA ATTAAGGTCT CTAAAGCATC TGCTCTTTTT TTTTTTTACG 3060 GATATITTAG TAATAAATAT GCTGGATAAA TATTAGTCCA ACAATAGCTA AGTTATGCTA 3120 85 ATATCACATT ATTATGTATT CACTTTAAGT GATAGTTTAA AAAATAAACA AGAAATATTG 3180 AGTATCACTA TGTGAAGAAA GTTTTGGAAA AGAAACAATG AAGACTGAAT TAAATTAAAA 3240 ATGTTGCAGC TCATAAAGAA TTGGGACTCA CCCCTACTGC ACTACCAAAT TCATTTGACT

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	TTGGAGGCAA	AATGTGTTGA	AGTGCCCTAT	GAAGTAGCAA	TTTTCTATAG	GAATATAGTT	3360
	GGAAATAAAT	GTGTGTGTGT	ATATTATTAT	TAATCAATGC	AATATTTAAA	ATGAAATGAG	3420
	AACAAAGAGG	AAAATGGTAA	AAACTTGAAA	TGAGGCTGGG	GTATAGTTTG	TCCTACAATA	3480
5	GAAAAAAGAG	AGAGCTTCCT	AGGCCTGGGC	TCTTAAATGC	TGCATTATAA	CIGAGICIAI	3540 3600
5	GAGGAAATAG	TTCCTGTCCA TGTGGGAAGG	ATTIGIGIAA	TOCASTOCAS	CAGTACCTTT	GCTTTGCAGT	3660
	CTCTTTCAAG	ATTTCTGCAT	CCACAAGTTA	GTAGCAAACT	GGGGAATACT	CGCTGCAGCT	3720
	GGGGTTCCCT	GCTTTTTGGT	AGCAAGGGTC	CAGAGATGAG	GTGTTTTTTT	CGGGGAGCTA	3780
	ATABCABAAA	CATTTTAAAA	CTTACCTTTA	CTGAAGTTAA	ATCCTCTATT	GCTGTTTCTA	3840
10	TTCTCTCTTA	TAGTGACCAA	CATCTTTTTA	ATTTAGATCC	AAATAACCAT	GTCCTCCTAG	3900
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	ATTGTCCTTA	AACCTAAGCC CTCCTCACTG	CCACAAACTT	GACACCIGAT	CAGGICIGGG	AGCIACAAAA	4080
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-		id Accessio		equence			

5 Seq ID NO: 35 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 146-1273.

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Seq ID NO: 38 Protein sequence: Protein Accession #: NP 057667

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WO 02/086443

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Protein Accession #: NP_001784.2

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50 55	Nucleic According sequences of the control of the c	Id Accession Lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCGGGATC CACGGCCTT AGCAATTTC AGCAGTTCA GTTCGGCTG CTACAAGGG CCTGCCCAG GTCCCAGGAC TGCTGTGGGC TGCTGTGGGC TCCCAGGAC TTCCCGACTTC TTCCCGACAGAC	#: NM_0000 21 TCGGACCTGC CGGCTTTTAC CTGCAGAGG TACGCCGCTG CGCGTGTGC CAGGGTGTGC GATGCACTG GGCAACACTC CTGGCCCGAC CTGGTGGACA ATCAAGAATG TTCTTCTGG GTTGTGCACGA	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGT GCAGCTTTC GCTCTGGGGG GCACAGGGGG CTGGTGTCCC CAGCTGCCCA CTGACCCTGA TCAACGACTTCA TCACTGGTGG	CAGGGGGGA GAGGCCAG GCGAGCCCAG GCTTACTGGAT AGTGCAGTAC TGAATGCTC TGCAATTCTC TGCAATTCTC TAGGGTTGC AAGGCTGAAG GCAGCTGAAG GCAGCTGAAG CAGCATCTTG CGTGCCTGTG	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGACACCTAC ACCCGACCTC	120 180 240 300 360 420 480 540 600 660 720 780
50 55	Nucleic Act Coding sequence GGGCTGGAGG GAGGCGGGG CCACTGGCC CCATTGGCCG TCTCTGGAGC CACGGACAGA ACCATGTCTT CAGACGGACAT TCAGACGGACAT TCAGACGCACT TCAGACGCACT TCAGACGCACT TCAGACGCACT TCAGACGCACT TCAGACGCACT TCAGACGCACT TGCCCTCGT TGGATGACTC	Id Accession Lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATTC CAGCAGATTTC AGCCAGTGCA AGTTCGACTGCA GTTCGCCTG CTACAAGGG CTTCCAGGCCT TCCCAGGAC TCCTGCCCAG TCCTGCCCAG TCCTGCGACATTCC TTCCCGAGAG AGCCTCTGCT	1 #: NM_0000 333 21 1 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG TACGCCGCTG CGCAGGTGTGC CAGGGTGTGC CTGGCCGAC CTGGCCGAC CTGGCCGAC ATCAAGAATG TTCTTCTTCT GTGCACAG CCACGAGACCC CTGGTGCACA	31 CAAGGCCACC TGCCTAGGAT CGCCCGAGT ACATTGTGT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCCA CTGACCCTGA TCAATGACTT CTGCTGGTG	CAGGGGGGA GCAGCCCAG GCAGCCCAG CTTACTGGAT CGAAGGGCTA TGATGTGATCTC CAAGGTCTGC AAGGCTGAAG GGAGCTGAAG GGAGCTGAAG CAGCATCTTG CGTGCCTGTG TGAGCCCAGG	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGACACTAC ACCCGACCTC AGCCAATCCT	120 180 240 300 360 420 480 540 660 720 780 840
50 55 60	Nucleic Act Coding sequence Coding sequence	Id Accession uence: 99-8: 11 GGGGCTGGGC TCCTAGCTGA GGCGCCTT CAGCAATTTC AGCCAGTGCA GTTCGGCCTG GTCCCAGGAC GTCCCAGGAC TCCCAGGAC TCCGACTTC TCCGGAGA ACCTCTGCTG	#: NM_0000 333 21 1 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG TACGCCGCTG CGCAGGTGTCC CAGGGTGTCC CAGGGTGTCC CTGGCCCGAC CTGGCCCGAC CTGGTGGACA ATCAAGAATG TTCTTCTTCG GTGTGCACGA CCACGAGACC CGCAGGACC CGCAGGACC CGCAGGACC CGCAGGACC CGCAGGACC CCAGGAGCC CCCAGTGCCC CCCAGTGCCC CCAGTGCCC CCAGTGCC CCACTC CCA	31 CAAGGCCACC TGCCTAGGAT CGCCCGAGT ACATTGTGT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCCA TCAATGACTT CTGCTGGTGG TGGTGCTGC TGGTGCTGTC TGTGTGTG	GCAGGGGGGA GCAGCCCAG GCAAGGCCCAG CTTACTGGAT CGAAGGGCTG TGATGTACT TGATGTATC TGAATTCTC CAAGGTCTGA GGAGCTGAAG GGAGCTGAAG GGAGCTGAAG CAGCATCTTG CGTGCCTGTG TGAGCCAAGC CTACAAGGTC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CAGGCCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGACACTAC ACCCGACCTC CAGCCGACCTC CAGTACACTC CAGTACACTC	120 180 240 300 360 420 480 540 600 660 720 780
50 55	Nucleic Actional Sequence Coding Sequence Coding Sequence Coderate	Id Accession Lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCGGGATTC CACGGCCTT AGCAATTTC AGCAGTGCA GTTCGGCTG CTACAAGGGG CTCCCAGGAC TGCTGTGGGG GTCCCAGGAC TCCCGGACTT TCCCGGACAGAC GTCCGGACAGAC GTCGGACAGAC GTGGACAGC GTGGACAGC	#: NM_0000 21 TCGGACCTGC CGGCTTTTAC CTGGCAGAGG TACGCCGCTG CGGAGTGTCC CAGGGTGTGC GATGCACTG CTGGCCGAC CTGGCCGAC ATCAAGAAT TTCTTCTTCG GTGTGACAG CCACGAGACC CCACGAGACC CCACTGCCGA	31 CAAGGCCACC TGCCTAGGAT CGCCCGAGT ACATTGTTT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA TCAACCTGA TCAATGACTT CTGCTGGTGG TGGTGCCC TGGTGCCGA TCAATGACTT CTGCTGGTGG TGGTGCTGACTGG TGGTGCCGC TGGTGCCGA	CAGGGGGGA GAGGCCAG GCGAGCCCAG GCGAGCCCAG GCTTACTGGAT CGAAGGGCTG AGTGCAGTAC TGAATTCTC CAAGGTCTGC AAGGCTGAAG GCAGCATCATG CAGCACTTG CAGCCAAGC CAGCACTAGAG CAGCATCATG CAGCATCAGG CAGCATCAGG CAGCATCAGG CAGCATCAGG CAGCATCAGG CAGCATGAAG CAGCATGAAG CAGCATGAAG CAGCATGAAG CAGCAGGT CACAGGTC CAGCAGGT CAGCAGGT CAGCAGGT CAGCAGGT CAGCGT CAGCAGGT CAGCAGGT CAGCAGGT CAGCAGGT CAGCGT CAGCT CAGCGT CAGCT CAGCGT CACCGT CAGCGT CAGCGT CAGCGT CAGCGT CAGCGT CAGCGT CAGCGT CAGCGT CAGCT CAGCGT CAGC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGACACTAC ACCCGACTC AGCCCATCC GCCATCCC GTCCCAGCTC GTCCCAGCTG GTCCCAGCTG	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60	Nucleic Act Coding sequence Coding sequence	Id Accession Lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATTC CAGCAGATTTC AGCCAGTGCA GTTCGGCCTG GTCCCAGGG TCTCCAGGGG TCTCCAGGGG CTGCCCAG GTCCCAGGG GTCCCAGGG GTCCCAGGACTTC TCCCGGAGA AACCTCTGCT GGTGGACAGC GGTGGACAGC GCTGGCCAG TGTGGCGCTG GCGACAACAGC	#: NM_0000 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG TACGCCGCTG CGCAGGTCC CAGGGTGTGC CATGGCCGAC CTGGCCGAC CTGGTGACA ATCAAGAATG TTCTTCTTCG GTGTGACA CCACGAGAC CCAGTGGCC CACGTGCCCA CCACTGCCGA CACCTGCCGA CACCTGCCGA CACCTGCCGA CACCGGGACG CACGGGGAC CACGGGACG CACGGGACC CACGGGACC CACGGGACC CACGGGACC CACGGGACC CACGGACC CACGGGACC CACGGACC CACGGGACC CACGCGACC CACGGCACC CACGCGACC CACGCGACC CACGCGACC CACGCGACC CACGCACC CACCC CACGCACC CACCC CACCCACC	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCCA ACTGACCTGA TCAATGACTT CTGCTGGTGG TGCTGGTGG TGTGACTGC GTGAGCGCA GCCACTGAC CTGTGACTGAC	CAGGGGGGGA GCAGCCCAG GCAGCCCAG CTTACTGGAT CGAAGGGCTG TGATGTGATC TGCAATTCTC CAAGGTCTGC AAGGCTGAAG GGAGCTGAAG GGAGCTGAAG CAGCATCTTG CGTGCCTGTG TGAGCCAAGC CTACAAGGTC CGAGTACCAA GAAGTCAAG	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CATGTGGCTG ATCCTGATCA ATCCTGATCA ACCAGGGGG CGAGTTGCCT AGGACACTAC ACCCGACCTC AGCAATCCT CAGTACACTC CTCCCAGCTC CTCCCAGCTC CTCCCAGCTC AGCACTGCCC ACCCCTC AGCACTCC AGCACTCC AGCACTCC AGCACTCCC ACCCCACCTC AGCACTCCC ACCCCACCTC AGCACTCCC	120 180 240 300 360 480 540 660 720 780 840 900 960 1020
50 55 60	Nucleic Activation States Nucleic Activation Sequence Coding Sequence Code Code Code Code Code Code Code Cod	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCGGGATTC CACGGCCTT AGCAATTTC AGCAGTGCA GTTCGACTGA GTCCCAGGAC TCTCCAGGAC TCTCCAGGAC TCCCAGGAC TCCCAGGAC TCCCGGACTTC TTCCCGGAGA GACCTCTGCT TGTGGACGG GCTGGGACAG GCTGGGACAG GCTGCGACAGC GCCAACAGC	#: NM_0000 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG TACGCCGCTG CGGGTGTGC CAGGGTGTGC CAGGGTGTGC CTGGCCGAC ATCAGAATA TTCTTCTTCG GTGTGACAGA CCACGAGGCC CCACGAGGCC CCACGAGGCC CCACGAGGCC CCACGAGACA CCACACA CCACGAGACA CCACACACA	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTTT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA TCAACCTGA TCAATGACTT CTGCTGGTGG TGGTGCCCA GCCCACTGA CCTGACCTGA	CAGGGGGGA GAGGCCAG GCGAGCCCAG GCGAGCCCAG GCGAGGGCTG GGAGGGCTG GAGGGTGAG GCAATTCTC CAAGGTCTGAAG GAGCCTGAAG CAGCATCTTG CGTGCCTGTG TGAGCCAAGG CTACAAGGTC GCAGGTGAAG GCAGCTGAAG GCAGCTGAAG CAAGCCAAGC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGCAACTC ACCCGACTC AGCCAATCCT GTCCAGTCGCTG GTGACTGTGA ACCACTGCCC GTGACTGCCC GTGGCCTGCC	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080 1140
50 55 60 65	Nucleic Act Coding sequence GGGCTGGAGG GAGGCGGGGG CCGCTTTG CCATTGGCCG TCTCTGGAGC CACCGACAGA ACCATGTCTT CAGACGGATAT CAGACGGATAT CAGACGACAT TCAGCTATT CACAGCTATT CACAGCTACT TGGAGTACA TCGGATGACTC TGGAGTACA TCTGACGGG GTGAGACCAG TTGCCCTCTT TAGAAGGGC TTGCCCTCT TAGAAGGGC GGAGTGTGCC GGAGTGTGCC	Id Accession Lence: 99-8: 11	#: NM_0000 333 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CAGGGTGTGC CAGGGTGTGC CAGGGTGTGC CTGGCCGAC CTGGCCGAC CTGTGCCCGAC CTGTGCACAC ATCAAGAATG TTCTTCTTCT GTGCACAGA CCACGAGGCC CCACTGCCGA CCACTGCCGA ACCAGGAGAC CCACTGCCGA ACCAGGAGAC CCACTGCCGA ACCAGGAGAC CCACTGCCGA ACCAGGAGAC CCACTGCCGA ACCAGGAGAC ACCAGGAGAC ACCAGGAGAC CCACTGCCGA ACCAGGAGAC A	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGTT GCAGCTTTCT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGCCCA TCAACGCTGC TGACCTGA TCAATGACTT CTGCTGGTGG GTGACCTGA GCTGGTGC TGGTGCTGC TGGTGCTGC TGGTGCTGC TGGTGCTGC TGGTGCTGC TGGTGCTGC TGGTGCTGC TGGTGCGCA TCAACACCCA TCACAGCCCA TCACAGCCCA	CAGGGGGGA AGGCTGAGG AGGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAAGGCTGAAGGCTGAAGCAGCTAGAGCCTACAGGCTAAGCCTACAGGCTAAGCCTACAGGCTAAGCCTACAGGCCTACAGGCCTACAGGCCTACAGGCCTACAGGCCTCAGGAGCTCAGGAGCTCAGGAGCTCAGGAGCCTCCAGGGCCTCCTG	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG ATCCTGATG AGGCAGGGG GAGTTGCCT AGGCACTAC ACCCGACCTC AGCCAATCCT CAGTACACT CGTGCCTG GTCCAGCTG GTGACTGGA ACCGGCGGG GTGACTGCC GTGCCAGCTG GTGACTGCC GTGCCTGCC GTGGCCTGG GTGGCCCCG	120 180 240 300 480 540 660 720 780 840 900 960 1020 1140 1200
50 55 60	Nucleic Act Coding sequence GGGCTGGAGG GAGGCGGGGG CCGCTCTG CCATTGGCCG TCTCTGGAGC CACAGAA GTGACCTAT ACCATGTTA ACCATGTTT CAGAGCGAAA TCAAGCTAAT TCACAGCTAAT CGGATGACT TGGAGTACA CTCTGACGG GTGAGACCA TTGCCCTCTA TAGAAGGGCC CACAGCAGCA CACAGCAGCA	Id Accession Lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATTC CAGCAGATTTC AGCCAGTGCA GTTCGGCCTG CTACAAGGGG CCTGCCCAGGA GTCCCAGGAC TCCTGGCTGC TGCTGGCTGGACAG GTCCGACTGC GTGGACAGC GTGGACAGC GCTGGACAGC GCTGGCCAGACAGC GGCCAACAGC GAGTGCACAC GGAGTGCACAC	#: NM_0000 333 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CAGGGTCC CAGGGTGTGC CAGGGTGTGC CTGGCCGAC ATCAAGAATG TTCTTCTTCG GTGTGCACA CCACTGCGA CCACTGCGA CCACTGCGA CCACTGCGA ATCAAGAATA CCACGAGACC CCACTGCGA ATCAGAGAC CCACTGCGA ATCAGAGAT CGCAGAGAC CCACTGCGA ATCAGGAGAC CCACTGCGA CCCACTGCGA CCCACGGGAGG CCCACGGGAGG CCCACGGGAGG CCCCGCAGGGCAGG CCCGGGCAGG	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CAGCTGCCCA ACTGACCTGA TCAATGACTT CTGCTGGTGG TGGTGGTGTC CTGTGACTGG GTGAGCGCA GGCACTGAC CTGTGAGCGCA GCCACTGAC CTGTGAGCGG CACAGGCCA TGACATGGCG GTCACAGGCG TGACATGGCG GTTCAGTGTT	CAGCCTCAG GCAGCGGGG GCAGCCCAG CTTACTGGAT CGAAGGGCTA TGATGTGATC TGATGTGATC TGATGTGATC TGAGGTCTGC AAGGCTGAAG CGAGCTGAAG CGAGCTGAAG CGAGCACTTGT TGACAATCTG CGAGCATCTGC TGAGCACTCTGC TGAGCACCTGTG TGAGCCCAGG CTACAAGGTC CGAGTGAAC GCAGCTCCTG GCAGCTCCTG GGTCCTCAGT GGTCCTCAGT GCTGCGTGAC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CAGGGCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGACACTAC AGCCAACCTC AGCCAATCCT CAGTACACTC GTCCCAGCTG GTGACTGTGA ACCACTGCCG GTGGCCTGGC GGGGCCCA TTGGAGCCTG	120 180 240 300 480 540 660 720 780 840 900 960 1020 1080 1120 1200 1260
50 55 60 65	Nucleic Act Coding sequence GGGCTGGAGG GAGGCGGGGG CCGCTTTG CCATTGGCCG TCTCTGGAGC CACCGACAGA ACCATGTTA ACCATGTTT CACAGCGAAT TCAGACGGA TCAGCTATT CACAGCTAT TCAGAGTACT TGGAGTACT TGGAGTACA TCTGACGGG GTGAGACCAG TTGCCCTCT TAGAGTACA CCTGACGGC CACAGCAGAC CACAGCAGAC CCCACGACCA CCCACGACCA CCCACGACCA CCCTGATGGC CCACAGCAGCA CCCTGATGGC CCCTGATGGC CCACAGCAGCA CCCTGATGGC CCACAGCAGCA CCCTGATGGC CCACAGCAGCAC CCCTGATGGC CCACAGCAGCAC CCCTGATGGC CCACAGCAGCAC CCCTGATGGC CCCTCTCT CCCTCTCT CCCTCTCT CCCTCTCT CCCTCTCT CCCTCTCT CCCTCTCT CCCTCTCT CCCTCTCT CCCTCT CCCT	Id Accession Lence: 99-8: 11	1 #: NM_0000 333 21 1 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CGCGAGGTCC CAGGGTGTGC CAGGGTGTGC CTGGCCGAA ATCAAGAATG TTCTTCTTCT GTGCACGA CCACGAGACC CCACTGCCA ATCAAGAATG TTCTCTTCTC	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGTT GCAGCTTTCT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGACCCTGA TCAATGACT CTGCTGGTGC CTGATGCCCA TGACCTGGTGG TGTGCCCA TGACCTGA CCTGTACTGG GTAGACGCG AGCCACTGAC GCACAGCCC CCACAGCCCA CCACAGCCCA CCACAGCCCA CTACATGGTGT TATTTGCCCC AGCAGACCCT TATTTGCCCC AGCAGACCCT TATTTGCCCC AGCAGACCCCT	CAGGGGGGA GCAGGCCCAG GCAGCCCAG GCAGCCCAG GCAGCCCAG GCAGCCCAG GCAACTCTC GCAACTCTC CAAGGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG CAGCATCTTG CATGCCTGTG GCAGCTCAAG GCAGCTCAAG GCAGCTCAG GCAGCTCAG GCAGCTCAG GCAGCTCGG GCAGCTCCGG GCTCCTCAGT GCTGCGTGAG GCACCTCCTG GCTGCGTGAG GCCCCCGGT	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATCAC CAGGGCCATCC CATGTGGCTG AGCCAGGGGG GAGTTGCCT AGGCAGCTAC ACCCGACCTC AGCCAATCCT CAGTACACT CAGCCAATCCT CAGTACACTC GTCCCAGCTGG GTGACTGGGC GTGACTGGGC GTGGCCCA TTGGAGCCTA ATCCTGGGCCCA TTGGAGCCTT ATCCTGGGCC	120 180 240 300 360 420 480 540 600 720 780 840 960 1020 1140 1200 1260 1320
50 55 60 65	Nucleic Act Coding sequence GGGCTGGAGG GAGGCGGGGG GAGGCGGTCTG CCATTGGCCG TCTCTGGAGC CACAGACATCAA ACCATGTCTT CACAGCGAAA TCAAGCTAAT CAGAGCGAAC TCGGATGACT TGGAGTAC TCGGATGACT TGGAGTACA CTCTGACGGG TTGCCCTCTA TAGAAGGGCA TTGCCCTCTA TAGAAGGGCC CACAGCAGCA GCACGGACTA CCTGATGGC CACAGCAGCA CCCTGATGGC CCACATCCAT	Id Accession Lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATTC CAGCAGATTTC AGCCAGTGCA GTTCGGCCTG GTCCCAGGG GTCCCAGGG GTCCCAGGAC TGCTGCCCAG GTCCCAGGAC TGCTGGCCTG TGCGACTGC TGCGACTGC GGGGCGGCGCACAGC GCTGGCACAGC GGTGCCACAGC GGAGTGCCAC TGGGACAGC GGAGTGCCC TGGGACAGC TGGGACAGC TGGGCTGGCC TGGGACAGC TGGGCTGGCC TGGGACTGCC TGGACTGGC TGAGGTGCCC TGGACTGGC TGAGGTGACC TGGACTGGC TGAGGTGACC TGGACTGAC TCGCACTGAC CCTCCTTTCC	#: NM_0000 333 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CAGGGTGCC CAGGGTGTGC CAGGGTGTGC CTGGCCGAC CTGGTGACACTC CTGGTGACAC CTGGTGACA ATCAAGAATG TTCTTCTTCG GTGTGCACGA CCACTGCGA CCACTGCGA ATCAGAGCC CCACTGCGA ATCAGGAGC CCACTGCGA ATCAGGAGC CCACTGCGG CCACTGCGC ATCGGGGAGG CTGGCACG CTTCCGGGAGG GTGAGCACC CCTTCTGTTG TGGAACTTGG	31 CAAGGCCACC TGCCTAGGAT CGCCCGAGT ACATTGTGT GCAGCTTCT GCTTTGCAC GCTCTGGGGG CCAGGGGC CTGGTGTCCC CAGCTGCCA TCAATGACTT CTGCTGGTGG TCATGACTGC GTGAGCGCA GCCACTGAC GCACAGGGC CACAGCGC TGACTGAC TGACTGAC TGACTGAC TGACTGAC TGACTGAC TGACTGAC TGACTGAC TGACTGAC TGACTGAC TGACATGAC TTATTTGGCCG TTCAGTGTT TATTTGGCCG AGCAGACCCT TGCCTGAGGCC TGCCTGAGGCC	CACAGGGGGGA GCAGGCCCAG GCAGCCCAG GCAGCCCAG GCAGCCCAG GCAGCCCAG GCAGCCCAG GCAGCCCAG GCAGCCCAGC GCAGCCCAGC GCAGCCCAGC GCAGCCCAGC GCAGCCCCCCAG GCCCCCCGG GCCCCCGCG GCCCCCGCCCCCCCC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG ATCCTGATCA GGGACGGGG CAGTTGCCT AGGACATCCT AGGACATCCT AGCAATCCT AGCAATCCT CAGTACACTC GTCCCAGCTG GTCACACTCC GTGCCAGCTG CTGACTGCCC CTGGCCTGGC	120 180 240 300 360 420 600 600 720 780 840 900 1020 1080 11200 1260 1320 1380
50 55 60 65 70	Nucleic Act Coding sequence 1	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATTC CAGCAATTTC AGCAGTGCA GTTCGGCCTG CTACAAGGGG CTTCCAGGAC GTCCCAGGAC TCCCAGGAC TCCGGACTTC TGCGGCTG GTGGACAGC GCTGGACAGC GCTGGACAGC GCTGGACAGC GGAACTGCC TGTGGTGGCG TGTGGACAGC GGAACTGCC TGGAGTGCC TGAGGTGCACT GAGGTGCACT GAGGTGCACT GAGGTGCCC TGAGGTGACC TCCACTTACC GACTTGCC TGAGGTGACC CCTCCTTTCC	#: NM_0000 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG TACGCCGCTG CAGGGTGTC CAGGGTGTC CAGGGTGTC CTGGCCGAC CTGGCCGAC CTGGTGACA ATCAAGAATG TTCTTCTTG GTGTGACAC CCAGTGGCC CACTGCGA CCACTGCGA ATCAGAATA GCCACTGCGC ATCGGGAGAC CTGGGCACG CTACTGTGCCAC ATCAGAATA GGCTACCGTG CTTGGCAGG CTTGGGCACG CTTGGCAGG CTTGGCAGG CTGGCACG CTTGTTG CGACTTCGTTG TGGAACTTCG GAGCCACCGC	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGTT GCTTTGCCAC GCTCTTGGCAC GCACGGGGG CCAGGTGTCCC CAGCTGCCA CTGACCTTGA TCAATGACTT CTGCTGGTGC TGGTGCTGT CTGTGGTGC TGGTGCTGA CCATGACTTT CTGCTGGACGC TGAGCGCCA TGACATGAC TTGACTGGC GTCACTGAC TTATTGGCCG AGCAGACCCT TGCCTGAGGC AGCAGACCT TGCCTGAGGC AGCAGACCT TGCCTGAGGC AGCAGACCT AGCAGACCT AGCAGAGCCA AGAAGGTGGT	CAGGGGGGA GAGGCTGCGG GCGAGCCCAG GCTAACTGGAT CGAAGGGCTG CGAGGTCT CGAGGTCTGC AAGGCTGAAG CGAGCTGAAG CGAGCTGAAG CTACAAGGCTGG GGAGCTGAAG CTACAAGGCCAAG CTACAAGGTCTG GGAGCTGAG CCAAGTACCAA ACAGGCTCCTG GGTCCTCAGT GCTCCTCTG GGTCCTCAGT CCAGTGCCTAGC CAGTTCCTG GCTCCTGGGTCCCCTG CCTGCGTGCCCCCTC	GCAAGGACA CTTCTGGTGG CACAGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG ATCCTGATCA GGCAGGGG CGAGTTGCCT AGGACACTCC AGGCAATCCT CAGTACACTC GTCCAGCTG GTGACTGAC GTGACTGC GTGACTGC GTGGCTGG GTGGCCTGC GTGGCCTGC GGTGGCCTGC GGTGGCCCG CCGGTTGGACCT ATCCTGGGCC CGGTTGGACCT ATCCTGGGCC CGGTTGGACC CGGTTGACCC CGGTTGGACC CGGTTGACC CGGTTGGACC CGGTTGAC CGCC CGGTTGGAC CGCC CGGTTGGAC CGCC CGGTTGAC CGCC CGGTTGCAC CGCC CGC	120 180 240 300 360 480 540 660 660 720 780 900 960 1020 1140 1200 1320 1380 1440 1500
50 55 60 65	Nucleic Act Coding sequence 1	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCGGGATTC CACGGCCTT AGCAATTTC AGCAGTGCA GTTCGGCTG GTACAAGGG CTACAAGGG CTCCCAGGAC TCCTGGGCTT TCCCGGAGA TCTCGGCTG GTCCAGGAC TGCTGGGC GCTGGCACT TCCCGGACA GACTCGCT GGACTGC GGACTGCC AGGTGCCAC AGGTGCCAC AGGTGCCAC TGGGGCTGGC TAGGCTGGCC TAGGTGCCC TAGGTGCCC TAGGTGCCC TAGGTGCCC TAGGTGCCC TAGGTGCCC TAGGTGCCC TAGGTGCCC TAGGTGCCC TAGGTGCC TAGGTGCCC GACTGCCTTG GGATGGCCT GGATGGCTTG GGATGGCTTG GGATGGCTTG GGATGGCTTG GGATGGCTTG	#: NM_0000 21 TCGGACCTGC CGGCTTTTAC CTGGCAGAGG TACGCCGCTG CGGGTGTGC CAGGGTGTGC CAGGGTGTGC CTGGCCGAC CTGGCCGAC CTGGCCGAC CTGGCCGAC CTGGCCGAC CTGGCCGAC CTGGCCGAC CTGGCCGAC CTGGCCGAC CCACTGCCGA CCACTGCCGA ATCAGAATA CGCACTGCCGA ATCAGACTTCTTCG CTGGCCGGC CCACTGCCGA CTGGCCGGC CCACTGCCGA CTGGCCGGC CCACTGCCGA CCACTGCCGA CCACTGCCGA CCACTGCCGA CCACTGCCGA CCACTGCCGA CCACTGCCGAC CCACTGCCGAC CCACTGCCGAC CCACTGCCGAC CCACTGCCGAC CCACTGCCGGCACG CCTTCTGTTG TGGAACTTCG CAGCCGCCACCCC CACCCGGCACACCCC CACCCGGCCACCCC CACCCGCCCACCCCC CACCCGGCCAC	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGTT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA TCAACCTGA TCAATGACT CTGTGGTGG GTACGCGCA TGACCTGAC GTTAGCGGCA TGACTGGC GTTAGCGGCA TGACTGGC TGAGGCCA TGACATGGC TTTAGGCGG TTATTGGCCG AGCAGACCT AGCAGGCCA AGAAGGTGCT TGCCTGAGGC AGAAGCCT TGCCTGAGGC AGAAGGTACC TGTGAGGCG AGAAGGTACC TGTGAGGCG AGAAGGTACC TGTGAGGCG AGAAGGTACC TGCCTGAGGC TGCCTGAGGC TTGAGTACC TGCCTGAGGC TTGAGTACC TGCCTGAGGC TTGAGTACC TGAGGTACC TGAGGTAC TGAGGTACC TGAGGTAC TGAGTAC TGAGCT TGAGTAC TGAGTAC TGAGTAC TGAGTAC TGAGTAC TGAGTAC TGAGTAC TGAGTAC	CAGGGGGGA GAGGCCAG GCGAGCCCAG GCGAGCCCAG GCGAGCCCAG GCGAGCCAG GCGAGCCAG GCGAGCCAG AGGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG CCAAGCCTGC GCAGCCCCGC GGTCCCCGG GCCCCGGTC CCCTGCCCTCC CCTGCCCTCC CCCCCCCC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGGCCATCC CATGTGGCTG ATCCTGATCA ACCCGACCTC AGGCAATCAC AGCCAACTAC ACCCGACCTC AGCCAACTC GTGCCAGCTG GTGACTGAT ACCAGCCTG GTGACCTG GTGGCCTGG GTGGCCTGC GTGGCCTGC GTGGCCCACTT ATCCTGGGCC CGGTTGGAT ATCCTGGACC CGGTTGGAAT GATGTGACC CTACACTCCC CGTTTGGAAT CACTCTCTC CTACACTCTC CTACACTCTC CTACACTCTC CTACACTCT CTTTTTTTT	120 180 240 360 420 540 600 600 720 780 900 960 1020 1140 1260 1320 1380 1440 1560
50 55 60 65 70	Nucleic Act Coding sequence Coding sequence	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATTC CAGCAGATTTC AGCCAGTGCA GTTCGCCTG CTACAAGGG CCTGCCCAG GTCCCAGGC TTCCAGGAC TCCTGGGCTG TTCCGGACATTC TCCGGACATC TCCGGACATC GCCAGCC GCTGGCCCAG GCTGGCCCAG GCTGGCCCAG GCTGGCCCAG CTCTGCCT GCCAACAGC GCAACAGC GAACTGCC CGAGTGAC TCGCCTTTCC GAACTGCC CCCCTTTCC GACTGCC CCCCTTTCC GACTGGCCTG CCCAGCTGCC CCCCTTTCC GACTGGCCTC CCCAGTGCC CCAGGTCGCC CCCAGTGCC CCAGGTCGCC CCAGGTCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGTCCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGTCCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGTCGCC CCAGGT	1 #: NM_0000 333 21 1 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CGCGAGGTCC CAGGGTGTGC CAGGGTGTGC CTGGCCGAC CTGGTGACACTC CTGGCCGAC CTGGTGACACTC CTGGCCGAC CTGCTGACACACT CTGGCCGAC CACAGAGAC CTCTCTCTCG GTGTCACGA CCCACTGCCGA ATCAGAGACC CCACTGCCGA ATCAGAGAC CCCACTGCCGC ATCGGGCAG GCTACCGTC CTGGCCAG CCTGCTGCC CGTTCTGTTG CCTGGACCTC CTGGACCTC CTGGACCTCC CAGCCGCA ACCCCTGCAA	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGTT GCAGCTTTCT GCAGCTTCT GCACCTGGGG GCACAGGGGC CTGACCTGA TCAATGACT CTGCTGGTGC CTGTGGTGC CTGTGGTGC CTGTGGTGG CCACTGACCTGA CCACTGACCTGA GCCACTGAC GTCACTGAC GTCACTGAC GTCACTGAC GTCACTGAC GTCACTGAC CCAAGCCC TGACAGCCC TGACAGCCC TGACAGCCC TGACAGCCC TGACAGCCC TGACAGCCC TTATTTGGCC ACAAGCCCT TGCCTGAGGC ACAAGCTCT TCTAGTACCC CCGTGGTTCC CCGTGGTTCC	GCAGGGGGA GAGGCTGCAG GCGAGCCCAG GCTTACTGGAT CGAAGGGCTG AGTGCAGTTCTC CAAGGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG CAGCATCTTG CAGCATCTTG CAGCATCTTG GCAGCTCAAG GCAGCTCAG GCAGCTCAG GCAGCTCCAG GCTCCTCAGT GCTGCCTGTG GCTGCGTGAG CAGCTCCTC CATTGCCCTCT CCTCACACCC CACTGGACCA CCACTGCCCC CACTGGACCA CCACTGCCCC CACTGGACCA CCACTGCACCC CACTGGACCA CCACTGCACCC CACTGGACCA CACTGCAC CACTGGACCA CACTGGACCA CACTGCAC CACTGGACCA CACTGCAC CACTGACCA CACTGCAC CACTGCAC CACTGCAC CACTGCAC CACTGCAC CACTGCAC CACTGA	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG AGGCAGGGG GAGTTGCCT AGGCAACCT AGGCAATCCT AGGCAATCCT AGGCAATCCT CAGTACACT AGCCAATCCT CAGTACACTC GTCCCAGCTG GTGACTGGA ACCACTGCCC GTGGCCTGG CCGCCACTT ATCCTGGGCCCA TTGGAGCCT CCGCCACTT ATCCTGGGCC CGGTTGGAAT GATGTGACC CTACACTCTCC CGGTTGGAAT CATCTCTCC CGGTTGGAAT CATCTCTCC CAGCTTCCC CGGTTGGAAT CATCTCTCC CAGCTTCCC CTACACTCTCC CAGCTTCCC CGGTTGGAAT CATCTCTCC CAGCTCCT CACACTCTCC CGGTTGCCCT CACACTCTCC CGGTTGCCCT CACACTCTCC CGGTTGCCTC CGGTTGCCTC CGGTTGCCTC CGGTTCCCT CACACTCTCC CGGTTCCCT CACACTCTCC CGGTTCCCT CACACTCTCC CGGTTCCCT CACACTCTCC CGGTTCCCC CGGTTCCCCC CGGTTCCCCC CGGTTCCCCC CGGTTCCCCC CGGTTCCCCC CGGTCCCCC CGCCCCC CGCCCC CGCCCC CGCCCC CGCCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCC CGCCCC CGCCCCC CGCCCC CGCCC CGCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCCC CGCCC CGCCCC CGCCC CGCCC CGCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC CCCC	120 180 240 300 360 420 540 660 720 780 900 900 1080 1140 1200 1200 1380 1440 1500 1500
50 55 60 65 70	Nucleic Act Coding sequence 1	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA GGCGCCTT CAGCAATTTC AGCCAGTGCA GTTCGGCTGA GTCCCAGGAC GTCCCAGGAC TGCCCAG GTCCCAGGAC TGCGGCGC TGCGCACTGC TGCGGAGA GACCTCTGCT TGCGGGGA GACTGCC GGACTGC GGACTGCC GGACTGCC TGCGGCGC GGACTGCC TGCGCTGCC TGGGCCT GGACTGCC GGACTGCC TGAGGTGCACT GGACTGGCC TGAGGTGCACT GGACTGGC TGAGGTGCACT GGACTGGC TGAGGTGCACT GGACTGGC CCCACTTAC GACTGGCT GGACTGGC CCCACTTGC CCACTTGC CACAGGCTGC CACAGGCCTGC CACAGGCCTGC CACAGGCCTGC CACAGGCCTGC CACAGGCCTGC CACAGGCCTGC CACAGGCCTGC CACAGGCTGCC CACAGGCCTGC CACAGGCCTGC CACAGGCCTGCC AACAGACCTG	# : NM_0000 333 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CAGGGTCC CAGGGTGTCC CAGGGTGTCC CAGGGTGTCC CTGGCCGAC CTGGCCGAC CTGGCCGAC CTGGTGACA CACAGAGAC CCACTGCCGA CCACTGCCGA CCACTGCCGA ATCAGGACC CCACTGCCGA ATCAGGACC CCACTGCCGA ATCAGGACC CCACTGCCGA ATCAGGACC CCTGCGCAC CCTGCGCAC CCTGCGCAC CCTGCCGC CATCCGCGCAC CCACTCCCGC CCTCTCTTTG CCTGGCACCC CCACTCCCGC CAGCCCCCCCCAC CAGCCCCCCCACA CAAGCCACCCC	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGTT GCTTTGCCAC GCTCTGGGGG GCACAGGGCC CAGCTGCCA CTGACCTGA CTGACCTGA CTGACCTGA CTGACCTGA CTGACCTGA CTGACCTGA CTGACCACGA CTGACCACGAC CTGACCACGAC CTGAGCGCCA GCCACTGAC CTGAGCGCCA CTACAGCCCA TGACATGGC ACAGGCCA ACAGCCCA ACAGGCCA ACAGGCCA ACAGGCCA ACAGGCCA CTGACTGGT TTTTTGGCC ACCTGAGGC ACAGGCCC ACCTGAGTACCC ACCTGATTCC ACCTGCTCC ACCTGCCCC ACCTGCTCC ACCTGCCCCC ACCTGCCCCC ACCTGCTCC ACCTGCCCCC ACCTGCTCC ACCTGCCCCC ACCCCCCCCCC	CAGGGGGGA GAGGCTGCAG GCGAGCCCAG GCGAGCCCAG GCGAGCCCAG GCGAGCCCAG AGTGCAGTAC CAAGGCTGC AAGGCTGAAG GCAGCTGAAG CTACAAGCCTAGC GCAGCTCAGC CTACAAGGCTCGC GGTCCTCG GGTCCTCGGTCCCTG GGTCCTCGGTCCCTG GCTCCTGGGTCCCCTCCCCTCCCT	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGGCCATCC CATGTGGCTG ATCCTGATCA ACCCGACCTC AGGCAATCAC AGCCAACTAC ACCCGACCTC AGCCAACTC GTGCCAGCTG GTGACTGAT ACCAGCCTG GTGACCTG GTGGCCTGG GTGGCCTGC GTGGCCTGC GTGGCCCACTT ATCCTGGGCC CGGTTGGAT ATCCTGGACC CGGTTGGAAT GATGTGACC CTACACTCCC CGTTTGGAAT CACTCTCTC CTACACTCTC CTACACTCTC CTACACTCTC CTACACTCT CTTTTTTTT	120 180 240 300 360 480 540 660 660 720 780 840 900 960 1080 1140 1290 1320 1380 140 1500 1560 1680
50 55 60 65 70	Nucleic Act Coding sequence 1	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGGATT CAGCAGTTCC AGCCAGTGCA GTTCGACTGCA GTTCGCCTGGCCT CTACAAGGG CTTCCAGGCCT CTACAAGGG GTCCCAGGAC TCCTGGCCTG TCCGACATTC TCCGGAGA GTCCTGGGC GCTGGCCTG GCGACAGC GCTGGCCTG CGCACAGC GCTGGCCTG CGCACAGC GCAACAGC GGAGCTGCC CCCTTTCC GACTGGCCT GAGGTGAC CCCCTTTCC GACTGCCTC CCCCTTTCC GACTGGCTGC CCCCTTTCC GACTGGCCTC CCCCTTTCC GACTGGCCC CCCCTTTCC GACTGGCCC CCCCTTCCC CCCCTTCCC CCCCTGGTGCC CCCTGGTGCC CCCTGGTGCC CCTCGGTCC CCCTGGTCC CCTCGTCCC CCTCCTTCCC CCTCGTCCC CCTCCTTCCC CCTCGTCCC CCTCCTCCC CCTCCTCCC CCTCCTCCC CCTCCT	#: NM_0000 333 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CGCGAGGTCC CAGGGTTGCC CAGGGTGGC CAGGGTGGC ATCACACTC CTGGCCGAC ATCAAGAATG TTCTTCTTCG GTGGACA ATCAAGAATG TCCTCTCTCG ATCGGGAGG CCACTGCCGA ATCAGAGACC CCACTGCCGA ATCAGAGACC CCACTGCCGA ATCAGAATA GGCTACCTG CTGGGCAGG ATCCAGAATA CAGGACACCG CAGCCGGCA ACCCCTGCAA CAGCCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CAGCACCAC CGGGACCACC CGGGCCACC CGGAGCCACC CGGGACCACC CGGAGCCACC CGGAGCCACC CGGAGCCACC CGGGACCACC CGGAGCCACC CGGAGCCACC CGGAGCCACC CGGAGCCACC CGGAGCCACC CGGACC CGGAGCCACC CGGACC CGGAGCCACC CGGACC CGGAGCCACC CGGAGCCACC CGGAGCCACC CGGAGCCACC CGGAGCCACC CGGAGCCACC CGCACC CCCCCCCC	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGTT GCAGCTTTCT GCAGCTTCT GCACCTGG GCACAGGGG CCACAGGGG CCAGAGCCCA TGACCTGA GTTGCTGT GTGTGCTGT GTGACCTGA GCACAGGGC AGAGCGCA TGACATGGCG GTCACAGGGCA TGACATGGCG TTTATTGGCG AGCAGACCT TATTTGGCG AGCAGACCT TGCTGAGGCCA TGACATGGC TTTATTGGCC AGCAGACCCT TGCTGAGGC AGAACGTGT TCTGAGTGT TTATTTGCCC AGCTGAGCC CGTGGTCC AGCTGCCCAG CCACATCATTCC AGCTGCCCG GCATCATTCGA	GCAGGGGGA GAGGCTGCAG GCGAGCCCAG GCTTACTGGAT AGTGCAGTAC TGCAATGTGAT TGCAATTGTAT TGCAATTGTAT TGCAGTTGC AAGGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG CCTACAAGGTCTG GCAGCTCAAG GCAGCTCAG GCAGCTCAG GCTCCTG GCTCCTGG GCTCCTGCTGCTCCTCAGT CCTCACACTC CCTCACACTC CACTGGACCAC GCAGCAGCACC CCTTGGACCAC CCTTGGATGAC CTTGGATGAC CTTGATGAC CTTGGATGAC CTTGAC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGCAACCT AGGCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCACCTG GTGACCTGG CGTGGCCCA TTGGAGCCTG CCGCCACTT ATCCTGGGCC CGGTTGGAAT CATGTGAAC CGGCACTT CAGTGTGCCC CGGTTGGATT CATCTTGGAC CGGCACTT CACTCTGCC CGGTTGGATT CATCTTGCC CGGTTGGATT CATCTTGC CAGGGGTTG CCAGCTGCTG CAGGGGTTG CCAGCTGCTG CGAGTGTCCT CAGGGGGTTG GTTCAGGCTG GTTCAGCTG	120 180 240 300 360 420 540 660 720 780 900 900 1080 1140 1260 1320 1380 1440 1500 1680 1740 1680 1740
50 55 60 65 70	Nucleic Act Coding sequence 1	Id Accession lence: 99-8: 11 GGGGCTGGGC TCCTAGCTGA CGCCGGATTC CAGCAGATTTC AGCCAGTGCA GTTCGGCCTG GTCCCAGGG GTCCCAGGG GTCCCAGG GTCCCAGG GTCCCAGG GTCCCAGG GTCCCAGG GTCCCAGG GTCCCAGG GTCCCAGG GTCCCAGGC TGGGACAG GTGGACAGC GGAGTGCACAG GGAGTGCAC AGGTGCACTG GAGTGCCC GGAGTGCC GAGTGGCC GAGTGGCC GAACAGC GGAACAGC GGAACAGC GGAACAGC GGAACTGACC GGAGTGCCC CCCCGTTCC GACTGGCT CCCCGTGTCC CCACTGGCC CCACTGGCCC CCACTGGCCC CCCTGGTCCC CCACTGTGCCG CCACTGTGCCG CCACTGTGCCG CACTGTGCCG	#: NM_0000 333 21 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CAGGGTCC CAGGGTGTGC CAGGGTGTGC CAGGGTGTGC CAGGGTGTGC CAGGGTGTGC CAGGGTGCC CAGGGACACACTC CTGGCCGAC CTGGCCGAC CACGGGAGC CCACTGCGA CACAGGAC CCACTGCGA ATCAGAATA GGCTACCGG CATCCGGAGAC CTGGCAGAC CTGGCAGAC CTGGCAGAC CACTGCGA ATCAGATAC CACTGCGA ATCAGATAC CACTGCGA ATCAGATAC CAGGGACC CCCTCTCTTT CGGACTGC CAGCCGGCA CAGCCGCC CAGCCGGCA CAGCCAGC	31 CAAGGCCACC TGCCTAGGAT CGCCCGAGT ACATTGTGT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA ACTGACCTGAC	GCAGGGGGA GAGCTGCGG GCGAGCCCAG CTTACTGGAT CGAAGGGCTG AGTGCAGTAC TGATGTGATC CAAGGTCTGC AAGGCTGAAG GGAGCTGAAG CTACAAGGTCTG TGAGCTAAG CTACAAGGTCAA GCAGCTCAC GAGGTCCAC CGAGTACCA GCAGCTCCTG GCTCCTG GCTCCTGGGTAC CAGGTCCTAC CCTCCACACT CCTCACACT CCACTGCCTC CCTCACACT CCACTGCCCC CCTCACACT CCACTGCCCC CCTCACACT CCACTGCCCC CCTCACACT CCACTGCCCC CCTCACACT CCTCACACT CCACTGCCCC CCTTGACCC CCTTGACCC CCTTGACGCC CCTTGCATGCC CCTTGCAGGGC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GGGCATGCCCT AGCGATGACC CGCGCCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTCCCT AGGACACTCC AGCCAATCCT CAGTACACTC GTCCAGCTG GTGACTGACT ACCCGACCTC AGCCATCCT CAGTACACTC GTCCAGCTG CTGACTGGCC GTGGCCCACTT ATCCTGGGCC CGGTTGGACT ATCCTGGGCC GGTTGACCTC CGGTTGACCT CGGGGCTT CAGGGGGTT CAGGGGGTT CTTCAGGCT CGTTCAGGCT CTTCAGGCTT ATCCCAGTT CAGGGGGTTA CATTCAGGCTT AGTGCCAGTT ATCCCAGTT CAGGGGGTTA ATCCCAGTT CAGGGCTTA ATCCCAGTT CAGGGCTTA ATCCCAGTT CAGGCTTA ATCCCAGTT CAGGGCTTA ATCCCAGTT CAGGCTTA ATCCCAGTT CAGGCTT CAGGCTTA ATCCCAGTT CACACTCCT CAGGGGGTTA CATTCAGGCTT AGTGCCAGTT CAGGCTT AGTGCCAGTT CAGGCTT AGCCCAGTT CTCAGGCTT AGCCCAGTT CTCAGGCTT AGCCCAGTT CTCAGGCTT AGCCCAGTT CTCAGGCTT CAGGCTC CTCAGCCCACT CTCAGCCCACT CTCAGCCCACT CTCAGCCCACT CTCAGCCCACT CTCAGCCCACT CTCAGCCCACT CTCAGCCCC CTCACTCCACT CTCAGCCCC CTCACTCCACT CTCAGCCCC CTCACTCCCC CTCACTCCC CTCACTCCC CTCACTCC CTCACTCCC CTCACTCC CTCACTCC CTCACCC CTCACTCC CTCACCC CTCACTCC CTCACCC CTCACTC CTCACCC CTCACTC CTCACCC CTCACTC CTCACCC CTCACTC CTCACC CTCACT	120 180 240 300 360 420 540 660 720 780 840 900 1020 1080 1140 1260 1320 1560 1560 1680 1740 1680 1740 1860
50 55 60 65 70	Nucleic Act Coding sequence 1	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATTC CAGCAATTTC AGCAGTGCA GTTCGGCCTG CTACAAGGGG CTTCCAGGAC GTCCCAGGAC TCCCAGGAC TCCGACTTC TCCGGAGAC TCTCGGCTT GTGGACAGC GCTGGCCAG GCTCGACAGC GCTGGCACAG GCTGGCACAG CGCAACAGC GGAACTGAC CGCAACAGC GGAACTGAC CCTCTTTCC GAGTGGCC TCAGGTGGC TAGGGTGGCC TCAGGTGGCT GCCACTTCC CACTGGCT CCCGGTGCC CCTGGTGCC CCTGGTGCC CCCTGGTGCC CCCCGGGAG	#: NM_0000 333 21 1 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CAGGGTGCC CAGGGTGCC CAGGGTGCC CAGGGTGCC CTGGCCGAC CTGGCCGAC CTGGCCGAC CTGGTGACA ATCAAGAATG TTCTTCTTC GTGTGCACGA CCACGAGGCC CCACTGCCGA CCACTGCCGA ATCAGAATA GGCTACCGTG CTGGCAGG ATCAGAATA GGCTACCGTG CTTGGGCAGG CTGGCAGG CTGGCAGG ACCCTGCAG ACCCCTGCAA CCACGCAC ACCCCTGCAC CGGAGTCACC CGGAGTCACC CGGAGTCACC CCGGAACTC CCGGAAACTC CCGGAAACTC CCGGAAACTC	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTTT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA TCAATGACTT CTGCTGGTGG GTGACCTGA TCAATGACTT CTGTGACTGG GTGACCCA GGCCACTGAC CTGAGCGCA GGCACATGAC CTGTGACTGC GTCAGTGCT TATTTGGCCG AGCAGACCT TACTTGGTT TGCTGAGTGT TGCTGAGTGT TGCTGAGTGT CAGTAGTT TATTTGGCCG AGCAGACCT AGCAGACCT TGCCTGAGG CCACTGGTTC CAGTTCCTG GCATCATTGT CAGCATTCGA GAGTGGTCC CACTTGCTGT	GCAGGGGGA GAGCTGCGG GCGAGCCCAG GCTACTGGAT CGAAGGGTG AGTGCAGTAC TGATGTGAT TGATGTATC TGAAGTCTGC AAGGCTGAAG CAGAGCTGAAG CAGAGCTGAAG CAGAGTCTGC GGAGCTGAAG GCAGGTGAAG GCAGGTGAAG CCAGTACCAA GACAGCTCGG GGTCCTCTG GGTCCTCTG GGTCCTCTG GCTCCTGGCTGAC CAGCTCCTC CCTGCGTGAC CAGCTCCTC CCTCACACTC CCTCACACTC CCTCACACTC CCTCACACTC CCTTAGATGAC GCAGGGGTGAC CCTTGGATGAC CCTTGGATGAC CCTTGGATGAC CCTTGGATGAC CTTGGATGAC CTTGGATGAC CTTGGATGAC CTTGGATGAC CCTTGGATGAC CCTTGAGGGC CCTTGAGGGC CCCTGAGGGCT CCCAGGGCTG CCCAGGGCTG CCCAGGGCT CCCAGGGCTG CCCAGGGCC CTTGGATGAC CCTTGAGGGC CCCTGAGGGC CCCTGAGGGC CCCTGAGGGC CCCTGAGGGC CTCAGGGCC CTTGGGGGC CCCAGGGCTG CCAGGGCC CTTGGGGGC CCCTGAGGGC CCCAGGGCC CTTGGGGCC CCCAGGGCC CTTGGGGCC CTCAGGGCC CTCAGGGCC CTCAGGGCC CCTGAGGGC CCCAGGGCC CTCAGGGCC CTCAGGCC CTCAGC CTCAGCC CTCAGCC CTCAGC CTCAGC CTCAGGC CTCAGC CTC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC GGGCCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGCAACCT AGGCAATCCT AGCCAATCCT GTCCAGCTG GTCCAGCTG GTGACTGTGA ACCACTGCC GTGGCCTGC GTGGCCTGC GGTGGCCTG CCGGCCTGC GGTGGCCTG CCGGCACTT ATCCTGGGC CGGTTGGAC CGGGTTGGAC CGGGTTGGAC CGGGTTGGAC CGGGTTGGAC CGGGTTGGAC CGGGTTGGAC CGGGTTGGAC CGGGTTGGAC CGGGTTGGAC CGGGTTGGC	120 180 240 300 360 480 540 660 660 720 780 900 960 1020 1140 1260 1320 1380 1450 1560 1560 1740 1800 1800 1920
50 55 60 65 70	Nucleic Act Coding sequity 1	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATT CAGCAATTTC AGCCAGTGCA GTTCGCCTGGCCT CTACAAGGG CTTACAAGGG GTCCCAGGACT TCCGGACT TTCCCGAGAC TTCCGGACT TTCCGGACA TTCCGGACA GCTCGGCCT GCCAACAGC GCTGGACACG CTCAGACAGC GCTACACGC GCTAGCCTGGCCT GGAGCTGCC CGCACAGC CGAACTGCC CGCACAGC CGAGCTGCC CCCCTTTCC GACTGGCCT GACTGGCTGC CCCCTGTGCC CCCCGGGAG ACCGGCGC CCCCCGGGAG AACGCGAGTGC CCCCCCGGAG AACGCGAGTGC CCCCCCGGAG AACGCGAGTGC CCCCCCGGAG AACGCGAGTGC CCCCCCGGAG AACGCGAGTGC CCCCCCGGAG AACGCGAGTGC CCCCCGGAG AACGCGAGTGC CCCCCGGGAG AACGCGAGTGC CCCCCGGGAG AACGCGAGTGC CCCCCGGGAG AACGCGAGTGC CCCCCGGGAG AACGCGAGTGC CCCCCGGGAG AACGCGAGTGC CCCCGCGGAG AACGCGAGTGC CCCCCGGGAG AACGCGAGTGC CCCCCGGAG AACGCGAGTGC CCCCCGGAG AACGCGAGTGC CCCCGCGAG AACGCGAGTGC CCCCGCGAGA AACGCGAGTG	1 #: NM_0000 333 21 1 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CGGCTTTAC CTGGCAGAGG CAGGGTTGC CAGGGTTGC CAGGGTTGC CTGGCCGAC ATCAAGAATG TTCTTCTTCG GTGCACAG CACAGGACC ATCAGGAGAC CCACTGCCGA ATCAAGAATG CCCAGTGCCA ATCAGAGACC CCACTGCCGA ATCAGAGACC CCACTGCCGA ATCAGAATA CGCTACTGC CGTTCTGTTG CCTGGCAGG CAGCCCCCCAC CAGCCCCCCCAC CAGCCCCCCCC	31 CAAGGCCACC TGCCTAGGAT CGCCCCGAGT ACATTGTGTT GCAGCTTTGCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA TGACCTGA TCATGCTGT CTGTGGTGG GCACAGGGCA TGACATGGC GTTAGACCTGA GCCACTGAC TGACCTGA GCCACTGAC TGACCTGA GCCACTGAC TGACTGGC TTGACCTGA TGACTGGC TTGAGCGCA TGACATGGC TTATTTGGCC AGAAGCTCT TCAGTGTT TATTTGGCC AGAAGCTCT TCAGTGTT CTGAGTGC CAGTGCTC CAGTGCTCC CAGTGCTCC CAGTGCTCC CAGTTCCTGT CAGCATTCGA GAGTGGGTC CACTTGCTGT GGGGACCCGT	GCAGGGGGA GAGGCTGCAG GCGAGCCCAG GCGAGCCCAG GCTTACTGGAT AGTGCAGTAC TGAATGTCT TGCAATTCT TGCAATTCT TGCAGTTGC AAGGCTGAAG GCAGCTGAAG GCAGCTGAAG GCAGCTGAAG CCTACAAGCTCAG GCAGCTCAG GCAGCTCCTG GGTCCTCAGT GCTCCTGAGTCCCTCAGT CCTCACACTC CCTCACACTC CACTGGACCA CCTTGGATGAC CCCTTGGATGAC CCCTTGGAGGCC CCCTTGGATGAC CCCTTGACT CCCTTGACT CCCTTCT	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG AGGCAAGCGGG CGAGTTGCCT AGGCAACCTC AGCCACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCAACCTC AGCCACCTG ACCCAGCTGC CGGGCCACTT ATCCTGGGCCA CTGGAGCCTG CCGCCACTT CAGTGGACCTG CAGCTGCCC CGGTTGGAAT CATCTGGAC CGGCACTT CACTCTGCC CGGTTGGACT CAGCGGCCT CAGCGGCCT CAGCGCCCT CAGCGGCTT CAGCGGCTT CTCAGGCT CGGGTTGCT CGGGTTGCT CGGGTTGCT CGGGTTGCT AGTGCCAGTT CGGGTTGCT AGTGCCAGTT CGGGTTTGC CGGGTTTGC CGGGTTTGCC CGGTTGTGC AGTGCCAGTT CGGGTTTGTG CGGGTTTGTG CGGGTTTGTG CGGGTTTGTG CGGGTTTGTG CGGGTTTGTG CGGGTTTGTG CGGGTTTGTG CGGGTTTTC	120 180 240 300 360 420 660 720 780 900 900 1080 1140 1260 1380 1440 1560 1680 1740 1680 1740 1880 1980
50 55 60 65 70 75	Nucleic Act Coding sequence 1	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATT CAGCAATTTC AGCCAGTGCA GTTCGGCCTG GTCCCAGGG GTCCCAGGG GTCCCAGGG GTCCCAGGAC TGTGGGCT TGGGCTG TGGGCAGA GTCCGACTGC TGGGCAGA GTCCGGACTGC TGGGCAGA GACTGGC GGTGCCAGA GCCAACAGC GGTGCCACAG GGTGCCACAGC GGTGCCACAG GGTGCCACTGC TGGACTGGC TGGACTGGC TGGACTGGC TGAGTGCC TGGACTGGC TGAGTGCCC TGGACTGGC TGAGTGCCC TGGCCTTGC GACTGGC GACTGGCC CCCGGTGCC CCACTGGCC CCACTGGCC CCACTGGCC CCACTGGCC CCACTGGCC CCACTGGCC CCACTGGCC CACAGGCGC CCACGGGAG CCCCGGGGAG CCCCGGGGAG CACGCGGGAG GAGCGCACGGC GAGCCGGGAG GAGCCACAGGC GAGCCACAGGC CCACGGGAG CCACGGGAG GAGCCACAGGC GAGCACAGGC CCACGGGAG GAGCCACAGGC GAGCACACGC CCACGGGAG GAGCCACACGC CCACGGGAG GAGCCACACGC CCACGGGAG GAGCCACACGC CCACGGGAG GAGCCACACGC CCACGGCAC GAGCCACACGC CCACGGCAC GAGCCACACGC CCACGCACACACGC CCACGCACACACC CCACGCACACACC CCACGCACACACA	#: NM_0000 333 21	31 CAAGGCCACC TGCCTAGGAT CGCCCGAGT ACATTGTGT GCAGCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA TCAATGACTT CTGCTGGTGG TCATGACTGC GCTTGACTGG GCACAGGCCA GGCCACTGAC GCACAGCGC AGACATGCC AGACATGCC AGACATGCC AGACATGCC AGACATGC AGACATGC CCATGGTT TATTTGGCG GCTCAGGCC AGAGGCCA AGACATGCC AGAGACCC AGACATGCC AGAGACCC CCATGGTTC CCATGGTTC CACTTGCTGT CAGCTTCC AGCTCCCG GCATCATTGT CAGCATTCGA GAGTGCGC CACTTGCTGT GGCGACCCCT AGTCCAGCC AGTCCAGCC AGTCCAGCC AGTCGCCGC AGATGGGTCC CACTTGCTGT GGCGACCCCT AGTCCAGCC AGTCCAGC AGTCCAGCC AGTCCAGC AGCC AGTCATGC AGTCCAGC AGTCCAGC AGTCCAGC AGTCCAGC AGTCAGC AGTCCAGC AGTCCAGC AGTCAGC AGTCCAGC AGTCCAGC AGTCCAGC AGTCCAGC AGTCCAGC AGTCAGC AGTCCAGC AGTCAGC AGTCCAGC AGTCCAGC AGTCCAGC AGTCCAGC AGTCAGC AGTCCAGC AGTCAGC AGTCCAGC AGTCAGC AGTCCAGC AGTCAGC AG	GCAGGGGGA GAGCTGCAG GCGAGCCCAG GCGAGCCCAG GCTTACTGGAT AGTGCAGTAC AGTGCAGTAC AGAGTCTGC AAGGTCTGC AAGGTCTGC AAGGTCTGC AAGGTCTGG GCAGCTGAAG CCTACAAGGTCAG GCAGCTCAGA GCAGCTCCTG GGTCCTCAG GCTCCTAGT GCTGCGTGAC CCAGTGCCCTCT CCTCACACTC CCACTGGCTAC GCAGCGGGTAC CCACTGGCTAC CCACTGGCTAC CCACTGGCTAC CCACTGGCTAC CCACTGGCTAC CCACTGCCCC CCTTGCACCC CCTTGCACCC CCTTGCAGTAC CCTTGGATCAC CCTTGGATCAC CCTTGGATGAC CCTTGACTC CCTTGACT CCTTGACT CCTTC CCTTC CTTTC CTTT CTTT CTTT CTTT CTTT CTTT CTTT CTT CT C	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC CGCGCCATCC CATGTGGCTG AGGCAGGGG GGAGTTGCCT AGGCAACCT AGGCAATCCT AGGCAATCCT AGGCAATCCT CAGTACACT AGCCAATCCT CAGTACACT GTCCCAGCTG GTGACTGCC GTGACCTG GTGACTGCC GTGACCTGCC GTGGCCTGGC CCGCCACTT ATCCTGGGCCC CGGTTGGAAT GATGTGACC CGGTTGGAAT GATGTGACC CGGTTGGAAT GATGTGACC CGGTTGGAAT GATGTGACC CGGTTGGAAT GATGTGACC CGGTTGGAAT CAGGGGTTG CGAGGTTCCT CAGGGGTTG CTTCAGGCTG CGGGTTGTGG AGTGCCAGTG CGGGTTTTGG AGTGCCAGTG CGGGTTTTTGG AGTGCCAGTG CGGGTTTTTGG AGTGCCAGTT CCAGACTCTA	120 180 240 300 360 420 540 660 720 780 840 900 900 1080 1140 1260 1380 1560 1560 1680 1740 1860 1860 1920
50 55 60 65 70	Nucleic Aci Coding sequitorial	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGGAT CAGCAGTTC AGCCAGTGCA GTTCGACTGCA GTTCGCCTGGCCT CTACAAGGG CTTCCAGGGCTT CAGCAGTTCA AGCCAGTGCA GTCCGAGAC TCCTGCCAGGAC TCCGACTTC TTCCCGAGA GACTCTGCT GGGACAGC GCTAGCACAGC GCTAGCACAGC GCTAGCACAGC GCAACAGC GCAACAGC CCACTGCC CACTGCC CCACTGCC CCACTGCC CCACTGCC CCACTGCC CCACTGCC CCACTGCC CCACTGCC CACTGCC CACTGCC CCACTGCC CACTGCC CCACTGCC CCACTGCC CACTGCC CCACTGCC CACTGCCC CACTCCC CACTGCCC CACTCCC CACTCCC CACTCC CACTC	1 #: NM_0000 333 21 1 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CGGCTTTAC CTGGCAGAGG CGCGAGGTCC CAGGGTGTGC CTGGCCGAC ATCAAGAATG TTCTTCTTCT CTGGCCGAC ATCAAGAATG CCACGAGGCC CACTGCCGA ATCAAGAATG TCTTCTTTCG CCAGTGGCC CACTGCCGA ATCAGAGACC CCACTGCCGA ATCAGAGATG CCTGGGCAGG CTGAGCACCG CAGTGCCC CACTGCCGA ACCCTGCAA CAGGCACCG CAGCAGTCAC AGGGTCAGA CAGGAAACTC CAGGAAACTC CAGGAAACTC CAGGAAACTC CAGGAAACTC AGGGTGGCCT CCGGAAACTC AGGGTGGCCT CCTGCAGCCTG CTGCAGCCTC CCGGAAACTC AGGGTGGCCT CCTGCAGCCTC CCTGCAGCCTC CCTGCAGCCTC CCGGAAACTC CCGGAAACTC CCGGAAACTC CCGGAAACTC CCGGAACCTC CCTGCAGCCTC CCTGCTGCAGCCTC CCTGCTGCCAGCCTC CCTGCTGCCAGC CCTGCTGCCAGC CCTGCTGCCAGC CCTCCTGCCAC CCTGCTGCCAGC CCTGCTGCCAGC CCTGCTGCCAGC CCTGCTGCCAGC CCTGCTGCCAGC CCTGCTGCCAC CCTGCTGCCAC CCTGCTGCCAC CCTGCTGCCAC CCTCTGCAC CCTGCTGCCAC CCCTGCAC CCTGCTGCCAC CCCTGCAC CCCTGCAC CCCTCCTGCAC CCCTGCAC CCCTGCAC CCCTCCTGCAC CCCTGCAC CCCTCCCTGCCAC CCCTCCCTGCCAC CCCTCCCTGCCAC CCCTCCTGCAC CCCTCCTGCCAC CCCTCCCTCCCCC CCCCTCCCCCCCCC CCCCTCCCCCC	31 CAAGGCCACC TGCCTAGGAT CGCCCGAGT ACATTGTTT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA TCAACCTGA TCATGCTG GTTAGCGG GTAGCGGCA TGACCTGA GCCACTGAC GGCCACTGAC TGACTGGC AGCAGGCCA TGACATGGC TTATTGGCG AGCAGGCCA TGACTGCT AGCATGACC AGCAGGCCA TGACTGACTGC AGCAGGCCA TGACTGTT CAGCATGCC AGCAGGCCA AGCACTGAC CCACTGCTGACC CCACTGCTGC CCACTGCTGC GAGTGGTTC CAGCTGGTTC CACTTGCTGT GGGGACCCGT AGTCCACGCA AGACCACCTA TCATCGTGGG TCACTGGGC AGACCACCTA TCATCGTGGC TCACTGGGCC TGCCCGACTGCCCG TGCACCCTACTCCTGCTGT TCACCCTACTCCTCACTTGCTGCCACTTGCTGCCACTTGCTGCCCACTTGCTGCCCCACTTGCCCCACTTGCCCCACTTGCCCCACTTGCCCCACTTCCCCCCTACTCCCCCCTACTCCCCCCTACTCCCCCC	GCAGGGGGA AGCCCTTCACACTC CACAGGCCC CCAGGACCC CCAGGACCC CCAGGACCC CCAGGACCC CCAGGACC CCAGGACCAC CCAGGACAC CCAGGACAC CCAGGACAC CCAGGACAC CCAGGACAC CCAGGACAC CCAGACAC CCAGACAC CCAGACAC CCAGACAC CCAGACAC CCAGACAC CCAGACAC CCACAC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCTT AGCGATGACC CGGCCATCC CATGTGGCTG AGGCACTC AGCCACTC AGCCACTGGCC GTGGCCTG CTGGCCTG CGGGCCTG CGGCCTG CGGCCTG CGGCTGGCC ATCTGGAC CGGTTGGAT CACTCCC CGGTTGGAT CACTCCC CGGTTGGAT CACTCCC CGGTTGCACT CAGGCTGC CGGCTGC CGGCTGC CGGTTGGAT CATCTGGCC CGGTTGGAT CCAGCTTCC CAGGGGTTG ATTCAGGCTG AGTGCCACT AGTGCCACT CCGGTTGTGG AGTGCCACT CGGGTTGTGG AGTGCCACT CCGGGCTTGTGG AGTGCCACT CCGGGCTCC CCGGTTGTGG AGTGCACTC CCACTCGGCC CCACTCGGCC CCACTCGGCC CCACTCGGCC CCACTCGGCC CCACTCTCC CCACTCGGCC CCACTCGGCC CCACTCGGCC CCACTCGGCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCCC CCCC	120 180 230 360 420 660 720 780 900 900 1020 1260 1260 1320 1440 1500 1680 1740 1680 1740 1860 1980 2040 2160
50 55 60 65 70 75	Nucleic Act Coding sequity 1	Id Accession lence: 99-8: 11 GGCGCTGGGC TCCTAGCTGA CGCCGGATT CAGCAATTTC AGCCAGTGCA GTTCGGCCTG GTCCCAGGG GTCCCAGGG GTCCCAGGG GTCCCAGGAC TGTGGACAGT GTGGACAGT GTGGACAGC GTGGACAGC GTGGACAGC GGTGCCAGGAC GGTGCCAGGAC GGTGCCAGGC GGTGGCACAG GGTGCCAC GGTGCCCAGGC GGAGTGCCC GGAGTGCCC TGGACAGC GGAGTGCCC TGGACAGC GGAGTGCCC TGGACTGGC TGGACTGGC TGAGGTGCCC TGGCCTTGC GACTGGC TGGACTGGC TGGACTGGC TGGACTGGC TGGACTGGC TGGACTGGC TGGACTGGC TGGACTGGC TGGACTGGC TGGCCTTTCC GACTGGC CCCGGTGCC CCCGGTGCC CACAGGCG CATGACAGGC CATCACAGGC CATCACAGGC CATCACAGGC CATCACAGGC CATCACAGGC CATCACAGGC GGGGAGT GAGGACAGGC CATCACAGGG GGGGAGGGG GGGGCCATGTG GGGCCATGTG GGCCCATGTG GGGCCATGTG GGGCCATGTG GGCCCATGTG GCCCATGTC GCCCATGT G	#: NM_0000 333 21 1 TGGGACCTGC CGGCTTTTAC CTGGCAGAGG CTGCGAGGTCC CAGGGTGTGC CAGGGTGTGC CTGGCACACACTC CTGGCACACACTC CTGGCACACC CTGGTGCACA ATCAAGAATG TTCTTCTTCG GTGTGCACGA CCACTGCGA ACCACTGCGA ATCAGAGACC CCACTGCGA ATCAGAGACC CCACTGCGA ATCAGAGACC CCACTGCGCA ATCAGAGACC CCACTGCGA ATCAGAGACC CCACTGCGA ATCAGAGACC CCCCTGCAG CCAGTCGC CAGCCGGCAC CCACTGCGA CCAGTCCC CAGCCGGCAC CCAGTCCC CAGCCGGCAC CCAGTCCC CAGCCGGCAC CCAGTCCC CCGGAAACTC CCGGAAACTC CCGGAAACTC CCGGAAACTC CCGGAAACTC CCGGAAACTC CCGGAAACTC CCGGAAACTC CCGCACCC CTCCCAC AGCCTGCCC CCTCCCAC AGCCTGCCC CCTCCCAC AGCCTGCCC CCTCCCAC CCGCACCC CCTCCCAC CCCGCCCC CCTCCCAC CCCCCCCC CCCCCCCC CCCCCCCC	31 CAAGGCCACC TGCCTAGGAT CGCCCGAGT ACATTGTGT GCTTTGCCAC GCTCTGGGGG GCACAGGGGC CTGGTGTCCC CAGCTGCCA TCAATGACTT CTGCTGGTGG TCATGACTGC GCTGAGCGCA GCCACTGAC GCACAGCGCA GCACAGCGCA TGACATGAC TTATTGGCG AGCACTGAC CCATGAGCCA TGACATGCC AGCAGACCA AGACATGCC AGAGACCA AGACATGCC CCATGGTTC AGCTGCCG GCATCATTG CAGCTTCCAGCCC AGACCCAT CACTTGCTG GGGACCCGT GGCACCCGT GACTTCGCC AGATCGCC AGACCACTT	GCAGGGGGA AGAGGCTGCAGGGGTACAGGGTCTGCAGGGTAGAGGCTGAGGCTGAGGCTGAGGCCAGGGCTGAGGGCCAGGGGCAGCCCGCAGGGGCCACAGGGCCAGGGGCCCGCCAGGGGCCCCCC	GCAAGGGACA CTTCTGGTGG CACAGGGAGA GGCTCCTCAT GTGCTGCCTT AGCGATGACC GGGCCATCC CATGTGGCTG ATCCTGATCA GGGCAGGGG CGAGTTGCCT AGGCAATCCT AGGCAATCCT AGGCAATCAC ACCCGACCTC AGGCCATCC GTGCCTGGC GTGGCCTGGC GTGGCCTGC GGTGGCCTGC GGTTGGCCT ATCCTGGCC CGGTTGGAC CTACACTCTG CAGGCCTGC CGGTTGGACT ATCCTGGCC CGGTTGGACT CAGGCCTG CGGCTGGC CGGCTGGC CGGTTGACA CTCCGGCCT CAGGCCTG CGGCTGGC CGGTTGGACT CCGGCCTG CGGCTGTC CAGGCGTT CCGGCTGC CGGTTGTGG AGTGCATT CCGGCTTG CCGGCTTGTG AGTGCATTC CCAGACTCTA CCCAGACTCTA CTGTCGGTC CCAGACTCTA CTGTCGGTTC CCAGACTCTA CTGTCGGTTC CCAGACTCTA CTGTCCGTTAC CTGTCGGTTC CCAGACTCTA CTGTCCGTTAC CTGTCGGTTC CCAGACTCTA CTGTCCGTTAC CTGTCGGTTC CCAGACTCTA CTGTCCGTTAC CTGTCTCGTTAC CTGTCTCGTTAC CTGTCCGTTAC CTGTCTCGTTAC CTGTCTCTAC CTGTCTCGTTAC CTGTCTCGTTAC CTGTCCGTTAC CTGTCTCGTTAC CTGTCTCGTTAC CTGTCTCGTTAC CTGTCTCTAC CTGTCTCGTTAC CTGTCTCTAC CTGTCTCGTTAC CTGTCTCGTTAC CTGTCTCTAC CTGTCTCGTTAC CTGTCTCGTTAC CTGTCTCGTTAC CTGTCTCGTTAC CTGTCTCTCTCTAC CTGTCTCGTTAC CTGTCTCTCTAC CTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	120 180 240 360 420 540 660 720 780 900 900 1080 1140 1260 1380 1560 1440 1560 1680 1740 1860 1980 2040 2100 2100 2120

	WU UZ/						
			GCCACGGTGG				2340
			GCCCATGTGG				2400
			CCTGTGGGTC				2460
_			ACCTGGGTAG				2520
5			GCCCCATGA				2580
			GAAGGTGGAG				2640
			CCTGTCTCCA				2700
	CAGCCCTGGG	GACGCTTCAC	GTGGTGCAGC	GCGGGGAGCA	CTCGCTGAGG	CTGCGCTGGG	2760
	AGCCGGTGCC	CAGAGCGCAG	GGCTTCCTTC	TGCACTGGCA	ACCTGAGGGT	GGCCAGGAAC	2820
10	AGTCCCGGGT	CCTGGGGCCC	GAGCTCAGCA	GCTATCACCT	GGACGGGCTG	GAGCCAGCGA	2880
	CACAGTACCG	CGTGAGGCTG	AGTGTCCTAG	GGCCGGCTGG	AGAAGGCCC	TCTGCAGAGG	2940
			CCTCGTGTTC				3000
			GCCTGGACTC				3060
			CCTGGCCAGG				3120
15	CCTCCCCCCC	CTCCCAGCGG	GTGACAGGGC	TAGAGCCTCG	CGTCTCTTAC	ATCTTCTCCC	3180
1.5	TONCCOCTOT	CCTCCATCCT	GTGCGGGGTC	CTGAGGCATC	TCTCACACAG	ACGCCAGTGT	3240
	COCCOCCIGI	CCTGGATGGT	GTGGTGTTCC	TACCACATCC	CACTCAACAC	AATGCTCACC	3300
			GTCCTGGAGC				3360
20			CTGCTGTCTT				3420
20			GGCATTATCT				3480
			GGCACAGCCG				3540
			CAGCACGTAC				3600
			AGCCCCATCC				3660
~-	TGATGTTGGG	AATGGCTGGA	GCGGACCCAG	AGCAGCTGCG	TCGCTTGGCG	CCGGGTATGG	3720
25	ACTCTGTCCA	GACCTTCTTC	GCCGTGGATG	ATGGGCCAAG	CCTGGACCAG	GCAGTCAGTG	3780
	GTCTGGCCAC	AGCCCTGTGT	CAGGCATCCT	TCACTACTCA	GCCCCGGCCA	GAGCCCTGCC	3840
	CAGTGTATTG	TCCAAAGGGC	CAGAAGGGGG	AACCTGGAGA	GATGGGCCTG	AGAGGACAAG	3900
	TTGGGCCTCC	TGGCGACCCT	GGCCTCCCGG	GCAGGACCGG	TGCTCCCGGC	CCCCAGGGGC	3960
			AAGGGCGAGA				4020
30			AATCCTGGGA				4080
•			GGGGACCCGG				4140
	VGCCGGGGGC	TCCCGGACAA	GTCATCGGAG	GTGAAGGACC	TGGGCTTCCT	GGGCGGAAAG	4200
	CCGNOCCTCG	ACCATOGGG	CCCCTGGAC	CTCCTGGACC	ACTEGEGGAC	CCAGGACCCC	4260
			GGAACAGCCA				4320
35			GAAGGTGGCA				4380
55	GGGGTCCCCC	CCCMCCAGGI	CAAGGCCCCG	MMCCCCCCCC	TCCN A A CARA	CCACAAAAAG	4440
	TTCCCGGAAG	CCCTGGACCC	CAAGGCCCCG	TIGGCCCCCC	TOGANAGANA	CCTCACCACA	4500
	GTGACTCTGA	GGATGGAGCT	CCAGGCCTCC	CAGGACAACC	TGGGTCTCCG	GGTGAGCAGG	4560
			GCTATTGGCC				
40	TGGGTGAGGC	TGGAGAGAAG	GGCGAACGTG	GACCCCCAGG	CCCAGCGGGA	TUUUGGGGGC	4620
40			CCTGGAGCCA				4680
			GAGCCTGGTC				4740
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TAOD

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Seq ID NO: 67 Protein sequence: Protein Accession #: NP_005620.1

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Seq ID No: 68 DNA sequence
Nucleic Acid Accession #: NM_021953.1
Coding sequence: 178-2469

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		70 D					
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80	i	11	21	31	41	51 1	
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PCT/US02/12476

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CTATAGACGT TTCTCTCCAA GGCCCTATCC CCCAATGTTG TCAGCAGATG CCTGGACAGC 2220 2280 2340 15 ACAGCCACCC ATCTCCCATT CACATGGCCC ACCTCCTGCT TCCCAGAGGA CTGGCCCTAC 2400 GTGCTCTCC TCGTCCTACC TATCAATGCC CAGCATGGCA GAACCTGCAG TGGCCAAGGG CTGCAGATGG AAACCTCTCA GTGTCTTGAC ATCACCCTAC CCAGGGGGTG GGTCTCCACC 2460 2520 ACAGCCACTT TGAGTCTGTG GTCCCTGGAG GGTGGCTTCT CCTGACTGGC AGGATGACCT 2580 2640 20 2700 2760 GTGCCTTACA CACTGCCCCC ACCCTCAGCC GTTGCCCCAT CAGAGGCTGC CTCCTCCTTC 2820 2880 AGCAGCACAG TGGGGACATC TCCCGTCTCA ACAGCCCCAG GCCTATGGGG GCTCTGGAAG GATGGGCCAG CTTGCAGGGG TTGGGGAGGG AGACATCCAG CTTGGGCTTT CCCCTTTGGA 25 3000 ATAAACCATT GGTCTGTC Seq ID NO: 95 Protein sequence: Protein Accession #: NP_036233.1 30 11 21 MEAADASRSN GSSPEARDAR SPSGPSGSLE NGTKADGKDA KTTNGHGGEA AEGKSLGSAL KPGEGRSALF AGNEWRRPII GFVESGDDKN SNYFSMDSNE GKRSPYAGLQ LGAAKKPPVT FAEKGDVRKS IFSESRKPTV SIMEPGETRR NSYPRADTGL FSRSKSGSEE VLCDSCIGNK 35 120 180 QKAVKSCLVC QASFCELHLK PHLEGAAFRD HQLLEPIRDF EARKCPVHGK TMELFCQTDQ 240 TCICYLCMFQ EHKNHSTVTV EBAKAEKETE LSLQKEQLQL KIIEIEDEAE KWQKEKDRIK SFTINEKAIL EQNFRDLVRD LEKQKEEVRA ALEQREQDAV DQVKVIMDAL DERAKVLHED 300 360 KOTREQLHSI SDSVLFLQEF GALMSNYSLP PPLPTYHVLL EGEGLGQSLG NFKDDLLNVC 420 40 MRHVEKMCKA DLSRNFIERN HMENGGDHRY VNNYTNSFGG EWSAPDTMKR YSMYLTPKGG VRISYQPSSP GRFTKETTQK NFNNLYGTKG NYTSRVWEYS SSIQNSDNDL PVVQGSSSFS 540 LKGYPSLMRS QSPKAQPQTW KSGKQTMLSH YRPFYVNKGN GIGSNEAP 45 Sec ID NO: 96 DNA secuence Nucleic Acid Accession #: NM_080668.1 Coding sequence: 83-841 51 21 50 GGCACGAGGG CAGCGAGTGG CCTTCCCGGT TGGCGCGCGC CCGGGGCGGC GGCGCTGGAG GAGCTCGAGA CGGAGCCTAG TTATGTCTGG GAGGCGAACG CGGTCCGGAG GAGCCGCTCA 120 GCGCTCCGGG CCAAGGGCCC CATCTCCTAC TAAGCCTCTG CGGAGGTCCC AGCGGAAATC 180 AGGCTCTGAA CTCCCGAGCA TCCTCCCTGA AATCTGGCCG AAGACACCCA GTGCGGCTGC AGTCAGAAAG CCCATCGTCT TAAAGAGGAT CGTGGCCCAT GCTGTAGAGG TCCCAGCTGT 300 55 CCAATCACCT CGCAGGAGCC CTAGGATTTC CTTTTCTTG GAGAAAGAAA ACGAGCCCCC 360 420 TGGCAGGGAG CTTACTAAGG AGGACCTTTT CAAGACACAC AGCGTCCCTG CCACCCCCAC CAGCACTCCT GTGCCGAACC CTGAGGCCGA GTCCAGCTCC AAGGAAGGAG AGCTGGACGC 480 CAGAGACTTG GAAATGTCTA AGAAAGTCAG GCGTTCCTAC AGCCGGCTGG AGACCCTGGG 540 CTCTGCCTCT ACCTCCACCC CAGGCCGCCG GTCCTGCTTT GGCTTCGAGG GGCTGCTGGG 600 60 GGCAGAAGAC TTGTCCGGAG TCTCGCCAGT GGTGTGCTCC AAACTCACCG AGGTCCCCAG GGTTTGTGCA AAGCCCTGGG CCCCAGACAT GACTCTCCCT GGAATCTCCC CACCACCGA 720 GAAACAGAAA CGTAAGAAGA AGAAAATGCC AGAGATCTTG AAAACGGAGC TGGATGAGTG GGCTGCGGCC ATGAATGCCG AGTTTGAAGC TGCTGAGCAG TTTGATCTCC TGGTTGAATG AGATGCAGTG GGGGGTGCAC CTGGCCAGAC TCTCCCTCCT GTCCTGTACA TAGCCACCTC 780 900 65 CCTGTGGAGA GGACACTTAG GGTCCCCTCC CCTGGTCTTG TTACCTGTGT GTGTGCTGGT 960 GCTGCGCATG AGGACTGTCT GCCTTTGAGG GCTTGGGCAG CAGCGGCAGC CATCTTGGTT 1020 TTAGGAAATG GGGCCGCCTG GCCCAGCCAC TCACTGGTGT CCTGTCTCTT GTCGTCCTGT CCTTCCTATC TCCCCAAAGT ACCATAGCCA GTTTCCAGAT GGGCCACAGA CTGGGGAGGA 1140 70 GAATCAGTGG CCCAGCCAGA AGTTAAAGGG CTGAGGGTTG AGGTGAGAGG CACCTCTGCT 1200 CTTGTTGGGA GGGGTGGCTG CTTGGAAATA GGCCCAGGGG CTCTGCCAGC CTCGGCCTCT CCCTCCTGAG TTGCCTTCTG TTGGTGGCTT TCTTCTTGAA CCCACCTGTG TAAAGAGGTT 1320 TTCAGTTCCG TGGGTTTCCC CTTTGATTCT GTAAATAGTC CCAGAGAGAA TTCGTGGGCT 1380 GAGGGCAATT CTGTCTTGGA GGAAGAAGCT GGACATTCAG CCTGTGGAGT CTGAGTTTTG 1440 AAGGATGTAG GGAGCCTTAG TTGGGTCTCA GACCATAAGT GTGTACTACA CAGAAGCTGT GTTTTCTAGT TCTGGTCTGC TGTTGAGATG TTTGGTAAAT GCCAGGTTGA TAGGGCGCTG 75 1500 1560 GCTGCTTGGA GCAAAGGGTG CATTTCAGGG TGTGGCCACC AGGTGCTGTG AGTTTCTGTG 1620 GCTCATGGCC TCTGGGCTGG TCCCTTGCAC AGGGCCCACG CTGGAGTCTT ACCACTCTGC 1680 TGCAGGGGTG GAAGGTGGCC CCTCTTGTCA CCCATACCCA TTTCTTACAA AATAAGTTAC 1740 ACCERGICIA CITEGCOCTA GARGAGARA TIGARGAGIC CCAGACCIAC TAGCATITIG 80 1800 1860 CAACTATGCT TGTAAAGTCC TCGGAAAGTT TCCTCGCGTA CCAGACAGCG GCGGGGGCTG ATAGCAATTT TAGTTTTTGG CCTCCCTATC CTCTCACATG AGAACACTGC CTGGATGCAT 1920 CTCATGATCT CTGGAGAATT TCCCCATCTT TCTCTTCTTT CCATCGTGTG GATTCAATAG 1980 TTTGGATTTG AGGGTGCCC TGCCCCCGAC TCTCCTGCCG CACCCCTGC CATTGTACCT
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2220

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10	1	11 	21 	31 	41 	51 	
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20	Nucleic Ac	98 DNA sequid Accession Lence: 58-12	1 #: Eos sec	quence			
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        RPRAWGAAAP SAPHWNETAE KNLGVLADED NTLQQNSSSN ISYSNAMQKE ITLPSRLIYY
                                                                                     120
        INQDSESPYH VLDTKARHOQ KHNKAVHLAQ ASFQIEAFGS KFILDLILNN GLLSSDYVEI
80
        HYENGKPQYS KGGEHCYYHG SIRGVKDSKV ALSTCNGLHG MFEDDTFVYM IEPLBLVHDE
                                                                                     240
        KSTGRPHIIQ KTLAGQYSKQ MKNLTMERGD QWPFLSELQW LKRRKRAVNP SRGIFEEMKY
LELMIVNDHK TYKKHRSSHA HTNNFAKSVV NLVDSIYKEQ LNTRVVLVAV BTWTEKDQID
                                                                                     300
                                                                                     360
        ITTNPVQMLH EFSKYRQRIK QHADAVHLIS RVTFHYKRSS LSYFGGVCSR TRGVGVNEYG
                                                                                     420
        LPMAVAQVLS QSLAQNLGIQ WEPSSRKPKC DCTESWGGCI MEETGVSHSR KFSKCSILEY
                                                                                     480
85
        RDFLQRGGGA CLFNRPTKLF EPTECGNGYV EAGEECDCGF HVECYGLCCK KCSLSNGAHC
SDGPCCNNTS CLFOPRGYEC RDAVNECDIT EYCTGDSGQC PPNLHKQDGY ACNQNQGRCY
                                                                                     540
                                                                                     600
        NGECKTRONQ CQYINGTKAA GSDKFCYEKL NTEGTEKGNC GKDGDRWIQC SKHOVFCGFL
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	LDRKCLQIQA	IGQLQGEIIP LNMSSCPLDS TNLIIGSIAG	KGKVCSGHGV	CSNEATCICD	FTWAGTDCSI	RDPVRNLHPP	720 780
5	Nucleic Aci	151 DNA seq d Accession dence: 250-1	#: NM_0239	15			
10	1	11	21	31	41	51	
10	 GGCACGAGGG	TTTCGTTTTC	ATGCTTTACC	AGAAAATCCA	CTTCCCTGCC	GACCTTAGTT	60
	TCAAAGCTTA	TTCTTAATTA	GAGACAAGAA	ACCIGITICA	ACTTGAAGAC	ACCGTATGAG	120
	GTGAATGGAC	AGCCAGCCAC AATCGTCCCC	CACAATGAAA	GAAATCAAAC	CAGGAATAAC	AGTGCATCAC	180 240
15	AACTGAAGAA	TGGGGTTCAA	CTTGACGCTT	GCAAAATTAC	CAAATAACGA	GCTGCACGGC	300
		ACAATTCAGG					360 420
	TTGCTGAATG	ACACAATTGT GTTTAGCAGT	GTGGATCTTC	TTCCACATTA	GGAATAAAAC	CAGCTTCATA	480
20	TTCTATCTCA	AAAACATAGT	GGTTGCAGAC	CTCATAATGA	CGCTGACATT	TCCATTTCGA	540
20		ATGCAGGATT TTTATGCAAA					600 660
	GATCGCTATC	TGAAGGTGGT	CAAGCCATTT	GGGGACTCTC	GGATGTACAG	CATAACCTTC	720
	ACGAAGGTTT	TATCTGTTTG ATGGTCAGCC	TGTTTGGGTG	ATCATGGCTG	TTTTGTCTTT	GCCAAACATC	780 840
25	CCTTTGGGGG	TCAAATGGCA	TACGGCAGTC	ACCTATGTGA	ACAGCTGCTT	GTTTGTGGCC	900
	GTGCTGGTGA	TTCTGATCGG TAAGTCAGTC	ATGTTACATA	GCCATATCCA	GGTACATCCA	CAAATCCAGC	960 1020
	AGGCAATTCA GTGGCTGTGT	TAAGTCAGTC	CTTTCTACCA	TATCACTTGT	GCAGAATTCC	TTTTACTTTT	1080
20	AGTCACTTAG	ACAGGCTTTT	AGATGAATCT	GCACAAAAAA	TCCTATATTA	CTGCAAAGAA	1140
30	ATTACACTTT	TCTTGTCTGC TTTCAAGAAG	GTGTAATGTT	TGCCTGGATC	CAATAATTTA	GAGTGAAAGC	1200 1260
	ATCAGATCAC	TGCAAAGTGT	GAGAAGATCG	GAAGTTCGCA	TATATTATGA	TTACACTGAT	1320
		TTTATTGTTT		ATATGTACAA	AGTGTAAATA	AATGTTTCTT	1380
35	TTCATTATCC	AAAAAAA	AA				
		152 Protei cession #: 1					
40	1	11	21	31	41	51	
	i .	1	1	1	1	1	
	MGFNLTLAKL GLAVWIFFHI	PNNELHGOES					60 120
45	FYANMYTSIV	FLGLISIDRY	LKVVKPFGDS	RMYSITFTKV	LSVCVWVIMA	VLSLPNIILT	180
45	FYANMYTSIV NGQPTEDNIH	FLGLISIDRY DCSKLKSPLG	LKVVKPFGDS VKWHTAVTYV	RMYSITFTKV NSCLFVAVLV	LSVCVWVIMA ILIGCYIAIS	VLSLPNIILT RYIHKSSRQF	180 240
45	FYANMYTSIV NGQPTEDNIH ISQSSRKRKH	FLGLISIDRY	LKVVKPFGDS VKWHTAVTYV FFTCFLPYHL	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL	LSVCVWVIMA ILIGCYIAIS DRLLDESAQK	VLSLPNIILT RYIHKSSRQF ILYYCKEITL	180
	FYANMYTSIV NGQPTEDNIH ISQSSRKRKH FLSACNVCLD	FLGLISIDRY DCSKLKSPLG NQSIRVVVAV	LKVVKPFGDS VKWHTAVTYV FFTCFLPYHL FSRRLFKKSN	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL	LSVCVWVIMA ILIGCYIAIS DRLLDESAQK	VLSLPNIILT RYIHKSSRQF ILYYCKEITL	180 240
45 50	FYANMYTSIV NGQPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac:	FLGLISIDRY DCSKLKSPLG NQSIRVVVAV PIIYFFMCRS 153 DNA sec id Accession	LKVVKPFGDS VKWHTAVTYV PFTCFLPYHL FSRRLFKKSN Quence 1 #: D80008	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS	LSVCVWVIMA ILIGCYIAIS DRLLDESAQK	VLSLPNIILT RYIHKSSRQF ILYYCKEITL	180 240
	FYANMYTSIV NGQPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ	FLGLISIDRY DCSKLKSPLG NQSIRVVVAV PIIYFFMCRS 153 DNA sec id Accession Lence: 149-	LKVVKPFGDS VKWHTAVTYV FFTCFLPYHL FSRRLFKKSN Quence 1 #: D80008	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS	LSVCVWVIMA ILIGCYIAIS DRILDESAQK LQSVRRSEVR	VLSLPNIILT RYIHKSSRQF ILYYCKEITL IYYDYTDV	180 240
50	FYANMYTSIV NGQPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac:	FLGLISIDRY DCSKLKSPLG NQSIRVVVAV PIIYFFMCRS 153 DNA sec id Accession	LKVVKPFGDS VKWHTAVTYV PFTCFLPYHL FSRRLFKKSN Quence 1 #: D80008	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS	LSVCVWVIMA ILIGCYIAIS DRLLDESAQK	VLSLPNIILT RYIHKSSRQF ILYYCKEITL	180 240
	FYANMYTSIV NGOPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ 1	PLGLISIDRY DCSKLKSPLG NQSIRVVAV PIIYFFMCRS 153 DNA see id Accession uence: 149-	LKVVKPFGDS VKWHTAVTYV PFTCFLPYHL FSRRLFKKSN Quence 1 #: D80008 739 21 21 GCGGAGGCCG	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS 3.1 31 31 AGGCGAGAGG	LSVCVWVIMA ILIGCYIAIS DRLLDESAQK LQSVRRSEVR 41 CTGGCGCTGT	VLSLPNIILT RYIHKSSROF ILYYCKEITL IYYDYTDV 51 AGGACTAGAA	180 240 300
50	FYANMYTSIV NGOPTEDNIH ISQSSRKKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ 1 GTTCGGCGCC CGAAAGGAGT	FLGLISIDRY DCSKLKSPLG NQSIRVVVAV PILYFFMCRS 153 DNA see id Accession nence: 149- 11 AAAGCGCGGA AAAGCGCCGA	LKVVKPFGDS VKWHTAVTYV FFTCFLPYHL FSRRLFKKSN Quence 1 #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS 3.1 31 AGGCGAGAGC ACCATTTGG	LSYCWWIMA ILIGCYIAIS DRLLDESAQK LQSVRRSEVR 41 } CTGGCGCTGT CTGAGAGCT	VLSLPNIILT RYIHKSSRQF ILYYCKEITL IYYDYTDV 51 } AGGACTAGAA GCTGGTTGGC	190 240 300
50	FYANMYTSIV NGOPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ 1 GTTCGGCGCC CGAAAGGAGT AAGGCCGCG CGASCTGCAT	PLGLISIDRY DCSKLKSPLG NQSIRVVAV PIIYFFMCRS 153 DNA see id Accession Lence: 149-' 11 AAAGCGCGGGA GAGGGCCGGA GAGGGCCCGA	LKVVKPFGDS VKWHTAVTYV PFTCFLPYHL FSRRLFKKSN Quence 1 #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT AAGGGCAACT	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS 3.1 31 31 AGGCGAGAGC ACCATTTTGG GTTCTGCGA GCCTGCCTTC	LSVCVWVIMA ILIGCYIAIS DRLLDESAQK LQSVRRSEVR 41) CTGGCGCTGT CATGAGAGCATGAAGCATGAAGCATGAAGCATGAAGAGTATGAAGGATGAAGGATGAAGGAATGAAGGAATGAAGGAATGAAGGAATGAAGGAATGAAGGAATGAAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAGGAATGAAAAGGAATGAAAGGAATGAAAGGAATGAAAAGGAATGAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGGAATGAAAAGAAATGAAAAGAAATGAAAAGAAATGAAAAAA	VLSLPNIILT RYIHKSSROF ILYYCKEITL IYYDYTDV 51 AGGACTAGAA GGTGGTTGGC GACTCAGACA GACTCAGACA	180 240 300 60 120 180 240
50	FYANMYTSIV NGOPTEDNIH ISQSSRKKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ 1 GTTCGCGCC CGAAAGGAGT AAGGCCGCG CGAAAGGAGT AAGTCTGCAT AGTTCTTGGAG	PLGLISIDRY DCSKLKSPLG NQSIRVVVAV PIIYFFMCRS 153 DNA see id Accession nence: 149- 11 AAAGCGCGGA GAGTGGGAAG GCGCCCGG GAGATGAAAG	LKVVKPFGDS VKWHTAVTYV FFTCFLPYHL FSRRLFKKSN Quence 1 #: D80008 739 21] GCGGAGGCCG GAGCCCAGAT CGTCGSCAT AAGGGCAACT CTTTGTATGA	RMYSITFTKV NSCLFVAVLV CRIPFTFSHL IRTRSESIRS 3.1 31 AGGCGAGAGC ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG	LSYCWWIMA ILIGCYIAIS DRLLDESAQK LQSVRRSEVR 41 CTGGCGCTGT CTGAGAGCT AAAGCCATGG AACGAGGATG TCTGATGTGA	VLSLPNIILT RYIHKSSROF ILYYCKEITL IYYDYTDV 51 AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA	60 120 180 240 300
50	FYANMYTSIV NGOPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ 1 GTTCGGCGCC CGAAAGGAGT AAGGCCGCG CGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC	PLGLISIDRY DCSKLKSPLG NQSIRVVVAV PILYFFMCRS 153 DNA see id Accession Lence: 149-' 11 AAAGCGCGGG GAGGGCCGG GAGGGCGCGG GAGATGAAAG CGGAGGCCCG GAGATGAAAG CGGAGGATT TGCACTGTAG	LKVVKPFGDS VKMHTAVTYV PFTCPLPYHL PFRRLFKKSN Quence 1 #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT CGTCGSCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA	RMYSITFTKV NSCLFVAVLV CRIPFTSHL IRTRSESIRS 3.1 31 AGGGGAGAGG ACCATTTGG GGTTTGGGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG	LSVCVWVIMA ILIGCYIAIS DRILDESAQK LQSVRSEVR 41 CTGGCGCTGT CGTGAGAGCT AAAGCCATGGG AACGAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCAT	VLSLPNIILT RYIHKSSROF ILYYCKETTL ILYYCKETTL ILYYCKETTL IYYDYTDV 51 AGGACTAGAA AGGACTAGAA AGGACTAGAA ACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG	60 120 180 240 300
50	FYANMYTSIV NGOPTEDNIH ISQSSRKKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ [] GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG CGACTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGG ATGGGAATAT	PLGLISIDRY DCSKLKSPLG RQSIRVVVAV PIIYFFMCRS 153 DNA see id Accession nence: 149-' 11 AAAGCGCGGA GAGTGGAAG GGCGCCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTTAGCGTCT	LKVVKPFGDS VKWHTAVTYV FFTCFLPYHL FSRRLFKKSN Quence ##: D80008 739 21 GCGGAGGCCG GAGCCCAGAT CGTCCGCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS 3.1 31 AGGCGAGAGC ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG ATTACGATTT	LSYCWWIMA ILIGCYIAIS DRILDESAQK LQSVRRSEVR 41) CTGGCGCTGT CGTGAGAGCT AAAGCCATGG ACCAGGATG TCTGAGTGA CGACACTGTT CTTCGGATCA CACATGGCT CACATGGCT CACATGGCT CACATGGCT CACATGGCTGCT	VLSLPNIILT RYIHKSSRQF ILYYCKETTL IYYDYTDV 51 AGGACTAGAA GGTGGTTGGC AACTGATCGG AACTGATCGA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAA CTCTGTTAAG	60 120 300 300 420 480
50 55 60	FYANMYTSIV NGGPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ CGAAAGGAGT AAGGCCGCGC CGAAAGGAGT AAGGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTTT TGAAGGTTGTT	PLGLISIDRY DCSKLKSPLG NQSIRVVVAV PIIYFMCRS 153 DNA see id Accession Hence: 149- 11 AAAGCGCGGA GAGGGCCCGA GAGTGGGAAG CGCGCCCG GACATGAAG CGAATGAAG CGAATGAAT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC	LKVVKPFGDS VKMHTAVTYV PFTCFLPYHL PFRRLFKKSN Quence 1 #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGGATCCT AAGGATCTCT AAGGATATGAA	RMYSITFTKV NSCLFVAVUV CRIPFTFSHL IRTRSESIRS 3.1 31 AGGCGAGAGGC ACCATTTTGG GTTCTGCGAA GCCTGCCTTC ACAAAACCAA TATCAAATTT TGACCGCTTG ATTACGATTT TGCTACTTAT TGCTACTTAT TGCTACTTAT	LSVCVWVIMA ILIGCYIAIS DRILDESAQK LQSVRSEVR 41 CTGGCGCTGT CGTGAGAGCT AAAGCATGG ACCAGGATG TCTGATGTGA CGACACTGTT CTTCGGATCA CACATGGCTCA ATGAGGTCA AGCCTATATA	VLSLPNIILT RYIHKSSROF ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL ACTOR A	60 120 180 240 300 420 480 540 600
50	FYANMYTSIV NGOPTEDNIH ISQSSRKKH PLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ I GTTCGGGGCC CGAAAGGAGT AAGGCTGGCA AGGTCTGCAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTTT TGAAGGTTT TGAAGGTTT TGAAGGTTT	PLGLISIDRY DCSKLKSPLG RQSIRVVVAV PIIYFFMCRS 153 DNA see id Accession Lence: 149-' 11 AAAGCGCGGA GAGTGGAAG GAGTGGAAG CGCACCCG GAGATGAAAG CGCAGCCCCG GAGATGGATG TGCACTGTAC GGTTAGCGTCT AATAATTATA GACATTACAC GACTATACGAG	LKUVKPFGDS VKWHTAVTY FFTCFLPYHL FSRRLFKKSN Quence #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT CGTCCGCAT TGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAGGATATGA AGGATATGA AGGATATGA AATTTGAAGT	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS 3.1 31 AGGCGAGAGGC ACCATTTTGG GATACCACTT TGACCGCTTC ACAAAACCAG TATCAAATTT TGACGCTTG TGACCACAAAA ACCACCAAAA TGATGATGAT TGATGATGAGGC	LSYCWVIMA ILIGCYIAIS DRILDESAQK LQSVRRSEVR 41 } CTGGCGCTGT CGTGAGAGCT AAAGCCATGG TCTGATGTGA TCTTGGATCA CACATGGCTG ATGAGGTCA CACATGGCTG ATGAGGTCA AGCCTATATA AGCTTAATATA	VLSLPNIILT RYIHKSSRQF ILYYCKETTL IYYDYTDV 51 AGGACTAGAA GGTGGTTGGC AACTGATCGG AACTGATCGG AACTGATCAG ATGAAGCAAA CTCTGTTAAG CTGGAGGACA TTGGAGGAGAAT TTGGAGGAGAAT TTGGAGGTCCG TATTAAAAAA	60 120 180 240 300 420 480 540 660 660
50 55 60	FYANMYTSIV NGOPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ I GTTCGGCGCC CGAAAGGAGT AAGGCCGCG CGAAAGGAGT AAGTCTGGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTT TGAAGGTTGT GTGTTCTAAAA AAATAGCCAG	PLGLISIDRY DCSKLKSPLG NQSIRVVVAV PIIYFFMCRS 153 DNA sec id Accession Lence: 149- 11 AAAGCGCGGA GAGTGGGAAG CGGCGCCG GAGATGAAAG CGAAGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACATTACAC GACATTATGAG CGACTTTTTAC	LKVVKPFGDS VKWHTAVTYV FFTCFLPYHL FSRRLFKKSN Quence 1 #: D80006 739 21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCTGTA TGATACCTGTA TGATACTGTA AGGATATGAA AATTTGAAGT CTCGATGGAA AATTTGAAGT	RMYSITFTKV NSCLFVAVLV CRIPFTFSHL IRTRSESIRS 3.1 31 AGGCGAGAGC GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG TATCACATTAT ACCACCAAAA TGATGATGAGCAG TATGAGCAGATT	LSVCVWVIMA ILIGCYIAIS DRILDESAQK LQSVRRSEVR 41 CTGGCGCTGT CGTGAGAGCT AAAGCCATGG ACCAGGGATG CTCTGGATGA CGACACTGTT CTTCGGATCA ACCATGGCTCA ACCATGGCTCA ACCATGATCA ACCTTCAGTCA CCTGATCAGACC CTGATCAGACC	VLSLPNIILT RYIHKSSROF ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL AGAGACTAGAA AGGACTAGAA ATGAAGCATAGA CTCAGACAA CTCAGTAAA CTCAGTAAA CTCAGTAAA CTCAGTAAA CTCAGAAAT TCGGAGGAGA TTGAAAGTCCC TATTAAAAAA AAAGAAGTCCCT	60 120 180 240 300 120 180 240 420 420 420 600 720
50 55 60	FYANMYTSIV NGGPTEDNIH ISQSSRKRKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG GGAGCTGCAT AGTTCTGGAG GTCAGGTGGA AAATTCGACGC ATGGGAATAT GGAGTGGTT TGAAGGTTGTT GGAGTGGTT GGAGTGGTT GGAGTGGTT GGAGTGGTT GGAGTGGTT GGAGTGGTT CGAGGTGGTT CGAGGTGGTT CGAGGTGGTT CGAGGTGGTT CGAGGTGGTT CGAGGTGGTT CGAGGTGGTT CGAGGTGGTT CGAGGTGGTT CGTCTTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA	PLGLISIDRY DCSKLKSPLG NQSIRVVVAV PIIYFMCRS 153 DNA see id Accession Lence: 149-' 11 AAAGCGCGGA GAGGGCCCG GAGATGAAAG CGACGTGATT TGCACTGTAG GGTAGCGTCT AATAATTATA GACATTACAC GACTATGGAG CACTTTTTAC CTGTCATGAC CTCTCTCTT	LKVVKPFGDS VKMHTAVTYV PFTCFLPYHL PFRRLFKKSN Quence 1 #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT CGTCCGCCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AAGATCTCT AAGATATGAA AATTTGAAGT CTCGATGGAA AATTTGAAGT CCCACTCCCACCCCC	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS 3.1 31 AGGCGAGAGGC ACCATTTTGG GCTTCTGCGAA GCCTGCCTTC ACAAAACCAA TATCAAATTT TGCCGCTTG ATTACGATTT TGCTACTTAT TGCTACTTAT TGCTACTTAT TGCTGCAAA TGATGATGGC ATGTGAGCAG GGCACTTCCA CTTCACCTCC	LSVCVWVIMA ILIGCYIAIB DRILDESAQK LQSVRRSEVR 41 CTGGCGCTGT CGTCAGAGCT AAAGCATGG ACCAGGGTTG CTTCGGATCA CACATGGTTG CTTCGGATCA ACGTCATGTA ACTTCAGTCC CTCATCAGTC CTGATCAGCC CGCTTCACTC CTCTTCACTC CTCTTCACTC CTCTTCACTC CTCTTCACTC CTCTTTCATT	VLSLPNIILT RYIHKSSROF ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL ILYYCKETTL AGACTAGAC AGACTAGAC AGACTAGAC AACTGATCAG AACTGATCAG ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TCGGAGGAGA TTGAAGTCCG TATTAAAAAA AAGGAGTCCT TATTAAAAAA TAGAAGCTA TTAGAAGCTA	60 120 180 240 300 120 180 240 300 420 480 540 660 720 780 840
50556065	FYANMYTSIV NGOPTEDNIH ISOSSIKKKH FLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ 1 GTTCGCGCC CGAAAGGAGT AAGGCCGCGA AGGCCGCAG AGGCTGCAT AGTTCTTGAG GTCAGGTGGA AAATCGACGC ATGGGAATAT GGAGTGGTT TGAAGGTTTT TGAAGGTTTT GTAAGCTTTC GTCTCTAAA AAATAGCCAG GGAGCACATC CTCCTCTGTT TGAAGCATTGT	PLGLISIDRY DCSKLKSPLG NQSIRVVVAV PIIYFFMCRS 153 DNA see id Accession nence: 149-' 11 AAAGCGCGGA GAGTGGAAG GAGTGGAAG CGAGTGGAAG CGAGTGGATT TGCACTGTAG GGTTAGCAC AATAATTATA GACATTACAC GACTATGGAG CACTTTTAC CCTGTCATGAC CTGTCATGATA CTGTCATGATA CTGTCATGATA CTGTCATCTCT TTTAAGATAAC	LKVVKPFGDS VKWHTAVTYV FFTCFLPYHL FSRRLFKKSN Quence 1 #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT CGTCGSCAT AAGGGCAACT CTTTGTATGA TGATACCTAGA TGCCAAATGC AAGATCT AGGATATGAA AATTTGAATG CTCGATGGAA CTCGATGGAA CTCGATGGAA CATGCGCCAC CTCAAGAATACC TAAGATACCTAC TAAGATACCTAC TAAGATACCTAC TAAGATACCTAC TAAGATACCTAC TAAGATACCTAC TAAGAATACC TAAGAATACC TAAGAATACC	RMYSITFTKV NSCLFVAVLV CRIPFTFSHL IRTRSESIRS 3.1 31 AGGCGAGAGC GTTCTGCGAA GCCTGCCTTC ACAAAACCAG TATCAAATTT TGACCGCTTG TGACTACTAT ACCACCAAAA TGATGATTAT ACCACCAAAA TGATGATGAGCAG ATTGAGCAG ATTGAGCAG ATTGAGCAG ATGATGAGCAG CTTCACCTCC TGGCTAAGAA	LSYCWWIMA ILIGCYIAIS DRILDESAQK LQSVRRSEVR 41 CTGGCGCTGT CTGAGAGCT AAAGCCATGG ACCACTGTT CTTCGGATCA CACATGGTCA ACGCTATATA ACTTCAGTCC CTGATCAGCC CTGATCAGCC CTGATCAGTC CTGATCAGTC CTGATCAGTC CTGATCAGTC CTGATCAGTC CTGATCAGTC CTGATCAGTC CTGATCAGTC GGCTTTTGATT GTATTATTTG	VISLPNIILT RYIHKSSROF ILYYCKETTL IYYDYTDV 51 AGGACTAGAA GGTGGTTGGC AACTGATCCG GACTCAGACA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCT TATTAAAAAA AAGGAGTCCT AACTCATGGA TTRGAAGCTA CTAACTATTA	180 240 300 120 180 240 360 420 540 600 780 840 900
50 55 60	FYANMYTSIV NGOPTEDNIH ISQSSRKKH PLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ GTTCGGGGCC CGAAAGGAGT AAGGCCGGG GCAGGTGGA AAATCGGAG AAATCGAGG ATGGAATT TGAAGGTTT TGAAGGTTT TGAAGGTTT TGAAGTTT TGAAGTTTT AGACATTCTAAAA AAATAGCAAG GGAGCACAT CCTCCTCTGTA TAGACATTGT AGGACTTTTTA	PLGLISIDRY DCSKLKSPLG MQSIRVVVAV PIIYFFMCRS 153 DNA see id Accession Lence: 149-' 11 AAAAGCGCGGA GAGTGGAAG GAGTGGAAG GAGTGGAAG GAGTGGTATA GACATTATATA GACATTATAC CGACTATGGAG CACTTTTTAC CTTCATGAC CTTCATGAC CTTCATGAC CTTCATTATATATATATATATATATATATATATATAT	LKUVKPFGDS VKWHTAVTY FPTCFLPYHL FSRRLFKKSN Quence #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT CGTCGCCAGAT CGTTGTATGA TGATACCAAC CATACCTGTA TGCGATATGA AAAGATCTCT AGGATATGAA AATTTGAAGT CTCGATGGAC CATCCCTAGCCCCA CCACCCCT TAGGAATACT TGTACACTA CTATGTTGCCC TAGGAATACTA CTTGTACACTA TGTACACTA TGTACACTA TGTACACTA TGTACACTA CTATGTTGCC	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS 3.1 31 31 AGGCGAGAGGC ACCATTTTGG GATACAAATCTT TGACCGCTTG ACTACATATT TGCTACTTAT ACCACCATAT TGATGATGGC ATGTGAGGAG ATGTGAGGAG CGCTCCC CGGCTAGGAA TCTTCCCTAC CAAGCTGGT CAAGCTGGT CAAGCTGGT CAAGCTGGT CAAGCTGGT CAAGCTGCCACCCACC CCAGCTTCCCACCCCAC	LSYCWVIMA ILIGCYIAIS IRILIDESAQK LQSVRRSEVR 41 CTGGCGCTGT CGTGAGAGCT AAAGCCATGG TCTTGATGTGA CACATGGTG ATCAGGTCA CACATGGTC CACATGGTCC CTGATCAGCC CTGATCAGAC GGCTTCACTC CTCTTTGATT GTATATATTG TCTATTTTGG TCTATTTTTG	VISLPNIILT RYIHKSSROF ILYYCKETTL IYYDYTDV 51 AGGACTAGAA GGTGGTTGGC AACTGATCAG ATGAAGCAAA CTCTGTTAAG CAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGACTCAG TTATAAAAA AAGGAGTCCT TATTAAAAAA TAGGAGTCCT TATTAAAAAT TTTAGATTTT TTTTGGTTTTT GGCCTCAAGC	60 120 180 240 300 120 180 240 300 420 480 540 660 720 840 900 900 1020
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50556065	FYANMYTSIV NGOPTEDNIH ISQSSRKKH PLSACNVCLD Seq ID NO: Nucleic Ac: Coding sequ 1 GTTCGGCGCC CGAAAGGAGT AAGGCCGCGG GCAGCTGCAT AGTTCTGGAG GTAGGGGATAT GGAGTGGTT TGAAGGTTTT TGAAGGTTTT TGAAGCTTTG TGTTCTAAAA AAATAGCCAG GGAGCACATC CTCCTCTGTA TAGACCATTGT AGGACTTTCT GTTTTTTAGA AGTCCTCCCA CCCCTACTCC GTGTGTTTT TTGGCTGGAC	PLGLISIDRY DCSKLKSPLG ROSIRVVVAV PIIYFFMCRS 153 DNA see id Accession lence: 149-' 11 AAAGCGCGGA GAGTGGAAG GAGTGGAAG GAGTGGAAG CGCGCCCG GAGATGATAT TGCACTGTAG GACTATACAG CACTTTTAC GACTATTAGAG CACTTTTAATG CTCTCATGAT TTAAGATAAC TTTTTTAATG GACTGTCTC TTAAGATAAC TTTTTTTTTAATG GACTGTCTC TTTAGCTTC TTATAGCTTC TTATAGCTTC TTTTTCTAAT TAAATGAAAG AGGAAGAAGG	LKVVKPFGDS VKMHTAVTY FFTCFLPYHL FSRRLFKKSN Quence #: D80008 739 21 GCGGAGGCCG GAGCCCAGAT CGTCGGCAT AAGGGCAACT CTTTGTATGA TGATACCAAC CATACCTGTA TGCCAAATGC AAAGATCTCT AGGATATGAA CATGCGCGA CATGCGCCGA TGAGAATACT TTGTACACTA CTAAGATGTT AAGCTGTATC TAAACATGGT TAGATCCTGT	RMYSITFTKV NSCLFVAVLV CRIPFTPSHL IRTRSESIRS 3.1 31 AGGCGAGAGG ACCATTTTGG ACCACATTTGGAA GCCTGCCTTC TGACCACATA ACCACCACA ATCAACTTT TGCTACTTAT ACCACCTCC ATGTGAGGAG ATGTGAGGAG ATGTGAGGAG ATGTGAGGAG ATGTGAGGAG ATGTGAGGAG ATGTGAGCAG ATGTGAGCAG ATGTGAGCAG AGATCACAA TTCTTCCTAC CAAGCTGGTC GAGATCACAG TGTAATCACA TGTAATCACA TGTAATCACA TGTAATCACA GAGATCACAG TGTAATCACA TACATTGAA	LSYCWVIMA ILIGCYIAIS DRILDESAQK LQSVRRSEVR 41 CTGGCGCTGT CGTGAGAGCT AAAGCCATGGT TCTTCGGATCA CACATGGTCA CACATGGTCA CTGATCAGTCC CTGATCAGTCC CTGATCAGTCC CTGATCAGTCC CTCTTTGGATT GTATAATTTG TCTTTTTTTGG TCAATCCCAC GCATCCTCA	VISLPNIILT RYIHKSSROF ILYYCKETTL IYYDYTDV 51 AGGACTAGAA GGTGGTTGGC AACTGATCGG GACTCAGGCA ATGAAGCAAA CTCTGTTAAG GAGCACTCAG CTGAAGAAAT TGGGAGGAGA TTGAAGTCCT AACTCATGGT TTTTGGTTTT CGCCTCAAGC CTGCACCCGG AGTTGTTACA AAGCACTCA	180 240 300 60 120 180 240 360 420 480 540 660 720 780 960 900 960 1080 1140 1260
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		ACAGTTGTTA					1260
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1680

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                                                                                                120
                                                                                                180
50
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                                                                                                540
                                                                                                600
        RKEWLTNYMB DRRORKLIGL PEDYLYGOTT TYLTYNDFIN KELILFSNSD NERSIPSMVD
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                                                                                                780
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                                                                                                900
        ELAPNQYVIS GEVAILNSTT IEISELPVRT WTQTYKEQVL EPMLNGTEKT PPLITDYREY
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                                                                                                960
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                                                                                                420
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AGTAGCCATA GGIGCIATIC TCARIARITI GLIACCARA HORSTING TICTICACAT GCCTACTGAT TGCACATATG GCTACTGAT ACCCACATGA TTGTCGACAT GCCTACTGAT AATCCTGAAC TTGATCTTT CCCTGAATTA ATTGGAACTG AAGAAATAAT CAAGGAGGAG GAAGAGGGAA AAGACATTGA AGAAGGCGCT ATTGTGAATC CTGGTAGAGA CAGTGCTACA AACCAAATCA GGAAAAAGGA ACCCCAGATT TCTACCACAA CACACTACAA TCGCATAGGG ACGAAATACA ATGAAGCCAA GACTAACCGA TCCCCAACAA GAGGAAGTGA ATTCTCTGGA AAGGGTGATG TTCCCAATAC ATCTTTAAAT TCCACTTCCC AACCAGTCAC TAAATTAGCC ACAGAAAAAG ATATTTCCTT GACTTCTAG ACTGTGACTG AACTGCCACC TCACACTGTG GAAGGTACTT CAGCCTCTTT AAATGATGGC TCTAAAACTG TTCTTAGATC TCCACATATG AACTTGTCGG GGACTGCAGA ATCCTTAAAT ACAGTTTCTA TAACAGAATA TGAGGAGGAG AGTTTATTGA CCAGTTTCAA GCTTGATACT GGAGCTGAAG ATTCTTCAGG CTCCAGTCCC GCAACTTCTG CTATCCCATT CATCTCTGAG AACATATCCC AAGGGTATAT ATTTTCCTCC GAAAACCCAG AGACAATAAC ATATGATGTC CTTATACCAG AATCTGCTAG AAATGCTTCC GAAGATTCAA CTTCATCAGG TTCAGAAGAA TCACTAAAGG ATCCTTCTAT GGAGGGAAAT GTGTGGTTTC CTAGCTCTAC AGACATAACA GCACAGCCCG ATGTTGGATC AGGCAGAGAG AGCTTTCTCC 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CCCAACTGCA TCATTACTGC AGCCTACTCA TGCCCTCTCT GGTGATGGGG AATGGTCTGG AGCCTCTTCT GATAGTGAAT TTCTTTTACC TGACACAGAT GGGCTGACAG CCCTTAACAT TTCTTCACCT GTTTCTGTAG CTGAATTTAC ATATACAACA TCTGTGTTTG GTGATGATAA TAAGGCGCTT TCTAAAAGTG AAATAATATA TGGAAATGAG ACTGRACTGC ARATTCCTTC TTTCAATGAG ATGGTTTACC CTTCTGRAAG CACAGTCATG CCCAACATGT ATGATAATGT ARATAAGTTG AATGGTCTT TACAAGAAAC CTCTGTTTCC ATTTCTAGCA CCAAGGGCAT GTTTCCAGGG TCCCTTGCTC ATACCACCAC TAAGGTTTTT GATCATGAGA TTAGTCAAGT TCCAGAAAAT AACTTTTCAG TTCAACCTAC ACATACTGTC TCTCAAGCAT CTGGTGACAC TTCGCTTAAA CCTGTGCTTA GTGCAAACTC AGAGCCAGCA TCCTCTGACC CTGCTTCTAG TGAAATGTTA TCTCCTTCAA CTCAGCTCTT ATTTTATGAG ACCTCAGCTT CTTTTAGTAC TGAAGTATTG CTACAACCTT CCTTTCAGGC TTCTGATGTT GACACCTTGC TTAAAACTGT TCTTCCAGCT GTGCCCAGTG ATCCAATATT GGTTGAAACC CCCAAAGTTG ATAAAATTAG TTCTACAATG TTGCATCTCA TTGTATCAAA TTCTGCTTCA AGTGAAAACA TGCTGCACTC TACATCTGTA CCAGTTTTTG ATGTGTCGCC TACTTCTCAT ATGCACTCTG CTTCACTTCA AGGTTTGACC ATTTCCTATG CAAGTGAGAA ATATGAACCA GTTTTGTTAA AAAGTGAAAG TTCCCCACCAA 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GTGACTCAGA AATAACTCCT GGATTCCCAC AGTCCCCAAC ATCATCTGTT ACTAGGGAGA ACTCAGAAGT GTTCCACGTT TCAGAGGCAG AGGCCAGTAA TAGTAGCCAT GAGTCTCGTA TTGGTCTAGC TGAGGGGTTG GAATCCGAGA AGAAGGCAGT TATACCCCTT GTGATCGTGT CAGCCCTGAC TTTTATCTGT CTAGTEGITC TTGTGGGTAT TCTCATCTAC TGGAGGAAAT GCCTTCCAGAC TGCACACTTT TACTTAGAGG ACAGTACATC CCCTAGAGTT ATATCCACAC CTCCAACACC TATCTTTCCA ATTTCAGATG ATGTCGGAGC AATTCCAATA AAGCACTTTC CAAAGCATGT TGCAGATTTA CATGCAAGTA GTGGGTTTAC TGAAGAATTT GAGACACTGA AAGAGTTTTA CCAGGAAGTG CAGAGCTGTA CTGTTGACTT AGGTATTACA GCAGACAGCT CCAACCACCC AGACAACAAG CACAAGAATC GATACATAAA TATCGTTGCC TATGATCATA GCAGGGTTAA GCTAGCACAG

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		AAAAAAAA					
40							
		180 Protein	n sequence:				
	Protein Ac	cession #: 1	gos sedneuc	e			
			-		41	51	
45	Protein Acc	cession #: 1 11 }	Eos sequence 21 }	9 31 }	41	51 \	
45	1 MRILKRFLAC	11 } IQLLCVCRLD	21 } WANGYYRQQR	31 } KLVEEIGWSY	TGALNQKNWG	 KKYPTCNSPK	60
45	1 MRILKRFLAC QSPINIDEDL	11 } IQLLCVCRLD TQVNVNLKKL	21 WANGYYRQQR KFQGWDKTSL	31 } KLVEEIGWSY ENTFIHNTGK	 TGALNQKNWG TVEINLTNDY	 KKYPTCNSPK RVSGGVSEMV	120
45	1 MRILKRFLAC QSPINIDEDL FKASKITFHW	11 } IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS	21 WANGYYRQQR KFQGWDKTSL EHSLEGQKFP	31 { KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA	† TGALNQKNWG TVBINLTNDY DRFSSFEEAV	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS	120 180
	1 MRILKRFLAC QSPINIDEDL FKASKITFHW ILPEVGTBEN	11 IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV	21 WANGYYRQQR KFQGWDKTSL EHSLEGQKFP ESVSRFGKQA	31 { KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL	TGALNQKNWG TVBINLTNDY DRFSSFEEAV LPNSTDKYYI	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YNGSLTSPPC	120 180 240
45 50	1 MRILKRFLAC QSPINIDEDL FKASKITFHW ILPEVGTEEN TDTVDWIVFK	11 IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISESQL	21 WANGYYRQQR KFQGWDKTSL EHSLEGQKFP ESVSRFGKQA AVFCEVLTMQ	31 klveeigwsy Entfihntgk Lemqiycfda Aldpfillnl Qsgyvmlmdy	TGALNQKNWG TVBINLTNDY DRFSSPEEAV LPNSTDKYYI LQNNFREQQY	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVFSSY	120 180
	1 MRILKRFLAC QSPINIDEDL FKASKITFHW ILPEVGTESM TDTVDWIVFK TGKEEIHEAV	11	21 WANGYYRQQR KFQGWDKTSL EHSLEGQKFP ESVSRFGKQA AVFCEVLTMQ DPENYTSLLV	31 KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYVMLMDY TWERPRVVYD	TGALNQKNWG TVEINLTNDY DRFSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK	120 180 240 300
	1 MRILKRFLAC QSPINIDEDL FKAEKITFHEN ILFEVOTEEN TDIVDWIVFK TGKEELHEAV HEFLTDGYQD LIGTEEIIKE	11 IQLLCVCRLD TQVNVNLKKL GKCMMSSDG LDFKAIIDGV DTVSISESQL CSSEPENVQA LGAILMNLLP EEEGKDIEEG	21 WANGYYRQOR KEQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA	31 klvebigwsy Entrihntgk Lemqlycfda Alpprilint Qsgywnlmdy Twerpruvyd ictnglygky TNGIRKEPQ	TGALNQKNWG TVBINLTNDY DRFSSFEEAV LPNSTDKYJ LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTTTHYNRI	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN	120 180 240 300 360 420 480
50	1 MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEEIHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS	11	21 WANGYYRQQR KFQGWDKTSL EHSLEGQKFP ESVSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSQPVTKL	31 kLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTNGLYGKY TNQIRKKEPQ ATEKDISLTS	TGALNQKNWG TVBLINLTNDY DRFSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY SDQLIVDMPT ISTTTHYNRI QTVTELPPHT	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YMGSLTSPPC KFSRQVPSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTM VEGTSASLND	120 180 240 300 360 420 480 540
	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTBEN TDTVDWIVFK TGKEEIHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH	11	21 WANGYYRQOR KFQWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVMPGRDSA NSTSQPVTKL NTYSITEYEE	31 KLVEEIGWSY ENTPIHNTGK LEMGIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTNGLYGKY TNOIRKKEPQ ATEKDISLTS ESLITSFKLD	TGALNQKNWG TVBINLTNDY DRFSSFEEAV LPNSTDKYYI LQNNFREQQI TMIEKPAVLY SDQLIVDMPT ISTITHYNRI GTVTELPPHT TGAEDSSGSS	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDOTK DNPELDLPPE GTKYNEAKTN VEGTSASLND PATSALPPLS	120 180 240 300 360 420 480 540
50	1 MRILKRFLAC QSPINIDEDL FKASKITFHW ILPEVGTEEN TDTVDWIVFK TGKEEIHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS	11	21 WANGYYRQOR KFQSWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYULQIVA AIVNPGRDSA NSTSQPVTKL NTVSITEYEE VLIPESARNA	31 klveeigwsy entrihntek Lemqiycfda Aldprillinl Qsgywmlmdy TWEERPRVVYJ ICTNGLYGKY TNQIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSE	TGALNQKNWG TVBINLTNDY DRFSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY SDQLIVDMPT ISTTTHYNRI QTVTELPPHT TGAEDSGSS ESLKDPSMEG	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLFPE GTKYNEAKTN VEGTSASLMD PATSAIPPIS NVWFPSSTDI	120 180 240 300 360 420 480 540 600
50	1 MRILKRFLAC QSPINIDEDL FKAGKITFHW ILPFVGTBEN TDTVDWIVFK TGKEETHEAV HEFLTDGYQD LIGTEFIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR	11	21) WANGYYRQOR KFQSWDKTSL EHSLEGQKFP ESVSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVNPGRDSA NSTSQFVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT	31 klveeigwsy entrihntgk Lemqiycfda Aldprilini Qsgywmlmdy Tweeprvvyu ictnglygky Tngirkkepq Atekdislts eslitsfkld sedstssgse ksfsagpvms	TGALNQKNWG TVBINLTNDY DRFSSFEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTTHYNRI QTVTELPPHT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM	KKYPTCNSPK KKYPTCNSPK KKYGGVSEMV KGKGKLRALS YMGSLTSPE KPSRQVPSSY QQLDGEDQTK DNPELDLFPE GTKYNEAKTN VEGTSASLND PATSAIPFIS NVWFPSSTDI PHYSTFAYFP	120 180 240 300 360 420 480 540
50 55	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEELHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGT TEVTEHAFTP	11	21 WANGYYRQOR KFQWDKTSL EHSLESQKFP ESVSRFGKQA AVFCEVLIMQ DPENYTSLLV MMSYVLQIVA AIVMPGRDSA NSTSQFVTKL NTYSITEYBE VLIPESARNA IRVDESEKTT VNVVYSQTTQ	31 KLVEEIGWSY ENTPIHNTGK LEMGIYCFDA ALDPFILLNL QSGYVMLMDY TWERBRVVYD ICTNGLYGKY TNOIRKKEPQ ATEKDISLTS ESLLTSFKLD SEDSTSSGSE KSPSAGPVMS PVYMGETPLQ	TGALNQKNWG TVEINLTNDY DRFSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTITHYNRI TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YMGSLTSPPC QULDGEDOTK DMPELDLPPE GTKYNEAKTN PATSAIPPIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI	120 180 240 300 360 420 480 540 600 660 720
50	1 MRILKRFLAC QSPINIDEDL FKAEKITFHEN ILFEVOTEEN TDTVDWIVFK TGKEELHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEPS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTPHAFTP LNTTPAASSS ILPQVTSATE	11	21 WANGYYRQOR KEQSWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DEENYTSLLV MMSYVLQIVA AIVNPGRDSA NSTSQPVTKL MTVSITEYEE VLIPBSARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE	ALDPHILLING QSGYVMLMDY TMERPRVVYD ICTMGLYGKY TNOIRKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSE KSFSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVL	TGALNQKNWG TVBINLTNDY DRFSSFEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTTHYNRI QTVTELPPHT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STTHAASETL	KKYPTCNSPK KKYPTCNSPK KGKGKLRALS YMGSLTSPC KPSRQVPSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VEGTSASLND PATSAIPPIS NVWPPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ EFGSESGVLY	120 180 240 300 360 420 480 540 600 720 780 840 900
50 55	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEEIHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEPS GSKTVLRSPH ENISQGYIFS TAQPDVGSGT TEVTPHAFTP LNTTPRASSS ILPQVTSATE KTLMFSQVEP	11	21 WANGYYRQOR KFQGWDKTSI EHSLEGQKFP ESVSRFGKQA AVFCEVLIMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSQPVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL	ALDPFILLNL QSGYVMLMDY TWEERPRUYD ICTNGLYGKY TNOIRKKEPQ ATEKDISLTS ESLLTSFKLD SEDSTSSGSE KSFSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVL SDNEGSQHIF	TGALNQKNWG TVBINLTNDY DRFSSFERAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTITHYNRI QTVTELPPHT TGAEDSGSS ESLKDPSMEG QGPSTDLEM PSYSSEVFPL PFSSASFSSE STIHAASETL TVSYSSAIFV	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VECTSASLMD PATSAIPFIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG	120 180 240 300 360 480 540 660 720 780 900 960
50 55	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEELHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTPHAFTP LINTTPAASS ILFQVTSATE KTLMFSQVES SLFSGFSHIP	11	21 WANGYYRQOR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSQPVTKL ITVUESEKTT VNVVYSQTTQ PSYDVSFESI PVAGGDLLLE SSGPEPSYAL	ALDPFILLNL QSGYWMLMDY TWERPRVYYD ICTINGLYGKY TNQIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSE KSFEAGPVMS PYYNGETPLQ LSSYDGAPLL SDNEGSQHIF SGDGEWSGAS	TGALNQKNWG TVEINLTNDY DRFSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTITHYNRI QTVTELPPHT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STIHAASETL SDSEFILLPDT	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVPSSY QULDGEDOTK DNPELDLPPE GTKYNEAKTN VEGTSASLMD PATSAIPFIS NVWFPSSTDI PHYSTFAYFP VTPLILIDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG DGLTALNISS	120 180 240 300 360 480 540 660 720 780 840 900 960 1020
50 55	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEETHEAV HEFLITGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQQYIFS TAQPDVGSGR TEVTPHAFTP LNTTPRASSS ILFQVTSATE KTIMFSQVEP SLFSGPSHIP PVSVARETYT	11	21 WANGYYRQOR KFQWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVNPGRDSA NSTSQPYTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVYYSGTEY PVAGGDLLLE SSGPEPSYAL ASLLQPTHAL LSKSEIIYGN	ALDEFICION OF THE PROPERTY OF	TGALNQKNWG TVBINLTNDY DRFSSPEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT IGATEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL TVSYSSAFSSE STTHAASETL TVSYSSAIFV EMVYPSESTV	KKYPTCNSPK KKYPTCNSPK KVSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVFSSY DNPELDLPPE GTKYNEAKTN VEGTSASLND PATSALPPIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG DGLTALNISS MPMMYDNVMK	120 180 240 300 420 480 540 600 720 780 840 900 960 1020 1080
505560	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TOTVDWIVFK TGKEEIHEAV HEFLTDGYQD LIGTEFIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGE TEVTPHAFTP LNTTPRASSS ILFQVTSATE KTLMFSQVEP SLPSGPSHIP PVSVAFETYT LNASLGETSV	11	21 WANGYYRQOR KFQGWDKTSI EHSLEGQKFP ESVSRFGKQA AVFCEVLIMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSQPVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL ASLLOPTHAL LSKSEIIYGN GSLAHTTIKV	ALDEFINATION KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLEMGIYCFDA ALDPFILLNL QSGYVMLMDY ICTNGLYGKY TNOIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSE KSPSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVL SDNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE	TGALNQKNWG TVBINLTNDY DRFSSFEBAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTITHYNRI QTVTELPPHT TGAEDSGSS ESLKDPSMES QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STIHARSETL TVSYSSAIFV SDSEHLLPDT EMVYPSESTV NNFSVQPTHT	KKYPTCNSPK KKYPTCNSPK KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VECTSASLMD PATSAIPFLS NVWFPSSTD PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ EFGGESGVLY HDSVGVTYQG DGLTALNISS MPNMYDNVNK VSQASGDTSL	120 180 240 300 360 420 480 540 660 720 780 960 1020 1020 1140
50 55	MRILKRPLAC QSPINIDEDL FKASKITPHW ILPEVGTEEN TDTVDWILVFK TGKEELHEAV HEPLITGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIPS TAQPDVGSGR TEVTPHAFTP LNTTPAASS ILPQVTSATE KTLMFSQVEE SLFSGFSHIP PVSVARETYT LNASLQETSV KPVLSANSEP	11	WANGYYRQOR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVMPGRDSA NSTSOPVTKL NTVSITEYBE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL ASLLOPTHAL LSKSEIIYGN GSLAHTTTKV LSPSTQLLFY	XLVEEIGWSY KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVYYD ICTMGLYGKY TNQIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSE KSFSAGPVMS FVYNGETPLQ LSSYDGAPLL PSLAQYSDVLL SDNEGSQHIF SGDEWSGAS ETELQIPSFN FDHEISQVPE	TGALNQKNWG TVEINLTNDY DRYSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTITHYNRI TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STTHAASEIL TVSYSSAIPV SDSEPLLPDT EMVPSESTV LLQPSFQASD	KKYPTCNSPK RKYGGVSEMV KGKGKLRALS YNGSLTSPPC KGKGKLRALS YNGSLTSPPC QLDGEDOTK DNPELDLPPE GTKYNEAKTN PATSAIPPIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ EFGSESGVLY DBUTALNISS MENNYDNVKK VSQASGDTSL VDTLLKTVLE	120 180 240 300 420 480 540 600 720 780 840 900 960 1020 1080
505560	MRILKRFLAC QSPINIDEDL FKASKITPHW ILFEVGTEEN TDTVDWIVFK TGKEEIHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEPS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTBHAFTP LNTTPRASSS ILPQVTSATE KTLMFSQVEP SLFSGFSHIP PVSVAEFTI LNASLQETSV KPVLSANSEP AVPSDPILVE	11	WANGYYRQOR KFQGWDKTSI EHSLEGQKFP ESVSRFGKQA AVFCEVLITMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSOPVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL ASLLOPTHAL LSKSEIIYGN GSLAHTTTKV LSPSTQLLPY MLHLIVSNS	ALDEFIGNEY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLYFIDA ALDPFILLNL QSGYVMLMDY ICTNGLYGKY TNOIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSE KSFSAGPVMS PVYNGETFLQ LSSYDGAPLL PSLAQYSDVL SDNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV ESSAFFSTEV ESSAFFSTEV ELPGTANLEI	TGALNQKNWG TVBINLTNDY DRFSSFEBAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY SDQLIVDMPT ISTTTHYNRI QTVTELPPHT TGAEDSSGSS ESLKDPSMES QGPSVTDLEM PSYSSEVPPL PFSSASFSSE STTHAASETL TVSYSSAIFV SDSEPILLPDT EMVYPSESTV NNFSVQPTHT LLQPSFQASD VPVPDVSPTS NQAHPPKGRH	KKYPTCNSPK KKYPTCNSPK KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VECTSASLMD PATSAIPFIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG DGLTALNISS WPMNYDNVK VSQASGDTSL VDTLLKTVLF HMESASLQGL VFATFVLSID	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140 1260 1320
505560	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTBEN TDTVDWILVFK TGKEELHEAV HEFLTDGYQD LIGTEELIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIPS TAQPDVGSGR TEVTPHAFTP LINTTPAASSS ILFQVTSATE KTLMFSQVEP SLFSGFSHIP PVSVABETYT LNASLQETSV KPVLSANSEP AVPSDPILVE TISYASEKY	III IQLLCVCRLD TQVNVNLKKL GKCMMSSDGS LDFKAIIDGV DTVSISESQL CSSEPENVQA LGAILNNLLP EEECKOIEEG GKGDVPNTSL MALSGTAESL SENPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE DSALHATPVF SDKVPLHASL PSSDAMHAR IPKSSLITPT TSVFGDDNKA SISTKGMFP ASSDPASSEM TPKVDKISST PVLLKSESSE PVLLKSESSE PVLLKSESSE HSDEILTST	WANGYYRQOR KFQWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLIMQ DPENYTSLLV MMSYVLQIVA AIVMPGRDSA NSTSQPVTKL MTYSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SGGPEPYAL ASLLQPTHAL LSKSEIIYGN GSLAHTTTKV LSPSTQLLFY MLHLIVSNSA RVYPSLYSND KSSVTGKVFA	KLVEEIGWSY KLVEEIGWSY ENTPIHNTGK LEMQIYCFDA ALDPPILLNL QSGYWNLMDY TWERPRVVYD ICTNGLYGKY TNQIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSE KSFSAGPYMS FVYNGETPLQ LSSYDGAPLL PSLAQYSDVL SONEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSENMLHSTS ELFQTANLEI GIPTVASDTF	TGALNQKNWG TVBLINLTNDY DRYSSFERAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY SDQLIVDMPT ISTITHYNRI GYVTELPPHT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STIHAASEI TVSYSSAIFV SDSEPLLPDT EMVYPSESTV VRPSVQPTHT LLQPSFQASD VPVPVSPTS NQAHPPKGRH VSTDRSVPIG	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YMGSLTSPPC KFSRQVFSSY QQLDGEDOTK DMPELDLPPE GTKYNEAKTN PATSAIPPIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ DGLTALNISS MPMYDNVMY VSQASGDTSL VDTLLKTVLP HMEBASLQGL VFATPVLSID MCHVAITAVS	120 180 240 300 360 420 540 600 660 720 780 840 900 960 1020 1140 1200 1260 1320 1380
50556065	I MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEELHEAV HEFLTDGYOD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTPHAFTE LINTTPAASS ILFQVTSATE KTLMFSQVES SLFSGPSHIP PVSVAEFTYT LNASLQETSV KPVLSANSEP AVPSDPILVE TISYASEKYE EPLINTLINKE	II IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISESQL CSSEPENVQA LGAILNNLLP EEEGKDIEEG GKGDVPNTSL SEMPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE SDKVPLHASL PSSDAMMHASL PSSDAMHASL PSSDAMHSL TSVPGDDNKA SISSTKGMFP ASSDPASSEM TPKVDKISST PVLLKSESSH IHSDEILTST KLLPPSKATS	WANGYYRQOR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVNPGRDSA NSTSOPVTKL ITVSTSYPTEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL LSKSEIIYGN GSLAHTTTKV LSPSTQLLFY MLHLIVSNSA QVVPSLYSND KSSVTGKVFA ELSESAKSDA	ALDEFICATION KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTMGLYGKY TNQIRKKEPQ ATEXDISLTS ESLLITSFKLD SEDSTSSGSE KSFEAGPVMS FYNGETPLQ LSSYDGAPLL PSLAQYSDVL SDNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSEMMLHSTS ELFQTANLEII GIPTVASDTF GLVGGGEDGD	TGALNQKNWG TVEINLTNDY DRYSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTITHYNRI TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STIHAASETL TVSYSSAIPV SDSEPILLPDT EMVYPSESTV NNFSVQPTHI LQPSFQASD VPVPDVSPTS NQAHPPKGRH VSTDHSVPIG TDDDGDDDDD	KKYPTCNSPK KKYPTCNSPK KYSGGVSEMV KGKGKLRALS YNGSLTSPPC KFSRQVPSSY QULDGEDOTK DNPELDLPPE GTKYNEAKTN VEGTSASLMD PATSAIPPIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG DGLTALNISS MPMYDNVNK VSQASGDTSI WTTLKTVLF HMESASLQGL VFATFVLSID NGHVAITAVS DRGSDGLSIH	120 180 240 360 420 540 660 720 780 840 900 900 1080 1140 1200 1260 1380 1440
505560	I MRILKRFLAC QSPINIDEDL FKASKITFHW ILPEVGTEEN TDTVDWIVFK TGKEELHEAV HEFLITGYOD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQQYIFS TAQPDVGSGR TEVTEHAFTP LNTTPAASS ILPQVTSATE KTIMFSQVEP SLFSGPSHIP PVSVASETYT LNASLQETSV KPVLSANSEP AVPSDPILVE TISYASEKYE EPLINTLINKL PHRDGSVTST KCMSCSSYRE	II IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISESQL CSSEPENVQA LGAILMILP EEEGKDIEEG GKGDVPNTSL MNLSGTAESL SEMPETITYD ESPLQTNYTE SSRQQDLVST DSALHATPVF SDKVPLHASL PSSDAMMHAR IPKSSLITPT TSVFQDDNKA SISSTKGMFP ASSDPASSEM TPKVDKISST PVLLKSESSH IHSDEILTST KLLPPSKATS SQEXWMDSD	21 WANGYYRQOR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVNPGRDSA NSTSQPYTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVYYSGTG PVAGGDLLLE SSGPEPSYAL ASLLQPTHAL LSKSEIIYGN GSLAHTTTKV LSFSTQLLFU GSLAHTTTKV LSFSTQLLFU KSSVTGKVFA QVVPSLYSND KSSVTGKVFA ELSHSAKSDA THENSLMDQN	ALDEFICIONE KLVEEIGWSY ENTFIHNTGK ENTGINGTON ALDEFILLNI QSGYVMLMDY TWEERPKVVTO ICTNGLYGKY TNQIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSE KSFSAGPVMS PVYNGETFLG PSLAQYSDVL SSDNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSENMLHSTS ELFQTANLEI GIPTVASDTF GLYGGGEDGD NPISYSLSEN	TGALNQKNWG TVBINLTNDY DRFSSFEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTTHYNRI QTVTELPPHT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STTHAASETL TVSYSSAIPV SDSEPLLIPDT EMVYPSESTV NNFSVQPTHT LLQPSFQASS NQAHPPKGRH VSTDRSVPIG TDDDGDDDDD SEEDNRVTSV	KKYPTCNSPK KKYPTCNSPK KKYPTCNSPK KKYGGVSEMV KGKGKLRALS YNGSLTSPEV QQLDGEDQTK DNPELDLFPE GTKYNEAKTN VEGTSASLND PATSAIPFIS NVWFPSSTDI PHYSTFAYTP VTPLLLDNQI LFPHLHTVSQ DEGSESGVLY HDSVGVTYQG DGLTALNISS WPMMYDNVNK VSQASGDTSL VDTLLKTVLP HMESASLQGL VFATPVLSID NGRVAITAVS DRGSDGLSIH SSDSQTGMDR	120 180 240 300 360 420 540 600 720 780 840 900 960 1020 1140 1260 1320 1380 1480 1500
50556065	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTBEN TDTVDWILVFK TGKEELHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIPS TAQPDVGSGR TEVTPHAFTP LNTTPAASS ILPQVTSATE KTLMFSQVEP SLFSGPSHIP PVSVAEFTYT LNASLQETSV KAVSLOPILVE TISYASEKYE EPLNTLINKL PHRDGSVTST KCMSCSSYSE SPGKSPSANG	III IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCMMSSDGS LDFKAIIDGV DTVSISSQL CSSEPENVQA LGAILNNLLP EEEGKDIESG GKGDVPNTSL MMLSGTAESL SEMPETITYD ESPLQTNYTE SSRQQDLVST DSALHATPVF SDKVPLHASL PSSDAMMHAR IPKSSLITPT TSVFGDDNKA SISSTKGMFP ASSDPASSEM TPKVDKISST TVLLKSESSE IHSDEILTST KLLFPSKATS SQEKVMNDSD LSQKINNDGKE	WANGYYRQOR KFQWDKTSL EHSLESQKFP ESVSRFGKQA AVFCEVLIMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSQFVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SGGPRPSYAL ASLLQPTHAL LSKSEIIYGN GSLAHTTKV LSPSTQLLFY MLHLIVSNSA QVVPSLYSND KSSVTGKVFA ELSSSAKSDA THENSLMDQN ENDIQTGSAL	ALDERIGNSY KLVEEIGWSY ENTPIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTNGLYGKY TNQIRKKEPQ ATEKDISLTS ESLLTSFKLD SEDSTSSGSE KSPSAGPVMS PVYNGETFLQ LSSYDGAPLL PSLAQYSDVL SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSEMNLHSTS GLYGGEDGD NPISYSLSEN LPLSPESKAW	TGALNQKNWG TVBINLTNDY DRFSSFERAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPI GTTTHYNRI GTTTLPPHT TGAEDSSGSS ESLKDPSMEG QGPSTTDLEM PSYSSEVFPL PFSSASFSSE STTHAASETL TVSYSSAIPV SDSEHLLPDT EMVYPSESTV NNFSVQPTHT LLQPSPQASD VPVFDVSPTS NQAHPPKGRH VSTDHSVPIG TDDDGDDDDD SEEDNRVTSV AVLTEDEESG	KKYPTCNSPK KKYPTCNSPK KGKGKLRALS YNGSLTSPPC KGSGVSEMV KGKGKLRALS YNGSLTSPPC KPSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VECTSASLMD PATSAIPPIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ DGLTALNISS MPNMYDNVNK VSQASGDTSL VDTLLKTVLP HHBASLQCI VFATPVLSID MGHVALTAVS DRGSDGLSIH SCGGTSDSLM	120 180 240 300 360 420 480 540 600 720 780 900 960 1020 1080 1140 1200 1320 1380 1440 1500
50556065	I MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWILVFK TGKEELHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTPHAFTP LINTTPAASS ILFQVTSATE KTLMFSQVED SLFSGPSHIP PVSVABFTYT LNASLQETSV KPVLSANSEP AVPSDPILVE TISYASEKYE EPLNTLINKL PHRDGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDPSF	II IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISSQL CSSEPENVQA LGAILINNLLP EEEGKDIEEG GKGDVPNTSL SENPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTHYTO ESFLQTHYTO TSVPGDDNKA SISSTKGMFP TSVPGDNKA SISSTKGMFP TSVPGDNKA TSVPGDNKA TSVPGNKA TSVP	WANGYYRQOR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSQPVTKL ITVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSYDVSFESI PVAGGDLLLE SSGPEPSYAL LSKSEIIYGN GSLAHTTTKV MLHLIVSNSA QVVPSLYSND KSSVTGKVPA BLSHSAKSDA THENSLMDQN ENDIQTGSAI ILAAGDSEIT	XLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVYYD ICTNGLYGKY TNQIRKKEPQ ATEXDISLTS SEDSTSSGSE KSFSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVLL SDNEGSQHIF SGDGEWSGAS ETELQIPSPN FOHEISQYPE ETSASFSTEV SSENMLHSTS ELFQTANLEII GIPTVASDTF GLVGGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPTSS	TGALNQKNWG TVEINLTNDY DRFSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTITHYNRI TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STIHAASETIL TVSYSSAIPV SDSEPLLPDT EMVPSESTV VNFFSVQPTH LLQPSFQASD VPVFDVSPTS NQAHPPKGRI VSTDRSVPIG TDDDGDDDDD SEEDNRVTSV AVLTEDESG	KKYPTCNSPK KKYPTCNSPK KUSGGVSEMV KUSKUSEMV KUS	120 180 240 300 360 420 540 660 720 780 900 900 1080 1140 1200 1260 1380 1440 1500 1520
5055606570	MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTBEN TDTVDWILVFK TGKEELHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIPS TAQPDVGSGR TEVTPHAFTP LNTTPAASS ILFQVTSATE KTLMFSQVEP SLFSGPSHIP PVSVAEFTYT LNASLQETSV KAVSLOPILVE TISYASEKYE EPLNTLINKL PHRDGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDFSF HESRIGLAG VISTPLPIF	III IQLLCVCRLD IQLLCVCRLD IQLLCVCRLD IQVINVILKKL GKCMMSSDGS LDPKAIIDGV DTVSISSQL CSSEPENVQA LGAILNNLLP EERGKDIESG GKGDVPNTSL MMLSGTAESL SEMPETITYD ESPLQTNYTE SSRQQDLVST DSALHATPVF SDKVPLHASL PSSDAMMHAR IPKSSLITPT TSVFGDDNKA IPKSSLITPT TSVFGDDNKA SISSTKGMFP ASGDPASSEM TPKVDKISST FVLLKSESSEP IHSDEILTST KLLFPSKATS SQEKVMNDSD LSQKINDGKE ADTNEKDADG LEGKENDGKE ADTNEKDADG LEGEKKAVID	VANGYYRQOR WANGYYRQOR KFQGWDKTSL EHSLESQKFP ESVSRFGKQA AVFCEVLITMQ DPENYTSLLV NMSYVLQIVA AIVMPGRDSA NSTSQFVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLS SGGPRPSYAL ASLLQPTHAL LSKSEIIYGK GSLAHITTKV LSPSTQLLFY MLHLIVSNSA QVVPSLYSND KSSVTGKVFA ELSHSAKSDA THENSLMDQN ENDIQTGSAL ILAAGDSEIT LVIVSALTII	KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY ENTPIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTNGLYGKY TNQIRKKEPQ ATEKDISLTS ESLLTSFKLD SEDSTSSGSE KSPSAGPVMS PVYNGETFLQ LSSYDGAPLL PSLAQYSDVL SODGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSENNLHSTS ELFQTANLEI GIPTVASDTF GLVGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPISS CLVVLVGILI LHASSGFTEE	TGALNQKNWG TVBLINLTNDY DRFSSFERAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT TGAEDSGSS ESLKDPSMEG QCPSTDLEM PSYSSEVFPL PFSSASFSSE STHAASETL TVSYSSAIFV SDSEHLLPDT EMVYPSESTV NNFSVQPTHT LLQPSPQASD VPVFDVSPTS NQAHPPKGRH VSTDHSVPIG TDDDGDDDDD SEEDNRVTSV AVLTEDEBSG VTSENSSVFH YWRKCFQTAH FETLKEFYQE	KKYPTCNSPK KKYPTCNSPK KKYRTCNSPK KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VECTSASLND PATSAIPPIS NVWFPSSTID PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ DGLTALNISS MPNMYDNVNK VSQASGDTSL VDTLLKTVLP HHBASLQGL VFATPVLSID MGHVAITAVS DRGSDGLSIH VSSPAGNSS SCQCTSDSLN VSERBASNSS FYLEDSTSPR VQSCTVDLGI	120 180 240 300 360 420 660 660 720 780 900 960 1020 1080 1140 1200 1320 1380 1440 1560 1560 1620 1620 1740
50556065	MRILKRPLAC QSPINIDEDL FKASKITPHW ILPEVGTEEN TDTVDWILVFK TGKEELHEAV HEPLITGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIPS TAQPDVGSGR TEVTPHAFTP LINTTPAASS ILPQVTSATE KTLMFSQVEP SLPSGFSHIP PVSVARETYT LNASLQETSV KPVLSANSEP AVPSDPILVE TISYASEKYE EPLINTLINKL PHRDGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDFSF HESRIGLAEG VISTPPTPIF TADSSNHPDN	II IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISESQL CSSEPENVQA LGAILNNLLP EEEGKDIEEG GKEDVPNTS SENPETITYD ESFLQTNYTE SSRQQDLVST DSALHATPVF SDKVPLHASL PSSDAMMHAR IPKSSLITPT TSVFGDDNKA SISTKGMFP ASSDPASSEM TPKVDKISST PVLLKSESSH THENDELLTST KLLPPSKATS SQEXWMNDSD LSQKHNDGKE ADTHEKDADG LESEKKAVIP PISDDVGAIP KHKNRYINIV	WANGYYRQQR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVMPGRDSA NSTSOPVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL ASLLOPTHAL LSKSEIIYGN GSLAHTTTKV LSPSTQLLFY MLHLIVSNSA QVVPBLYSND KSSVTGKVFA ELSHSAKSDA THEMSLMDQN ENDIQTGSAL ILAAGDSEIT LVIVSALTFI IKHPPKHVAD AYDHSRVKLA	KLVEEIGWSY KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTMGLYGKY TNOIRKKEPQ ATZKDISLTS SEDSTSSGSE KSFSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVLL SDNEGSQHIF SGDEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSEMNLHSTS ELFQTANLEI GIPTVASDTF GLVGGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPTSS CLVVLVGILI LHASSGFTEE QLAEKDGKLT	TGALNQKNWG TVELNLTNDY DRYSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY SDQLIVDMPT ISTITHYNRI GYVTELPPHT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STIHAASEIL TVSYSSAIFV SDSEPLLPDT EMVYPSESTV VPVPDVSPTS NQAHPPKGH VSTDRSVPIG TDDDGDDDDD SEEDNRVTS VTSESSOV VTSENSEVFH YWRKCFQTAH FETLKEFYQE DYINANYVDG	KKYPTCNSPK KKYPTCNSPK KKYRTCNSPK KGKGKLRALS YMGSLTSPPC VGGLGEDOTK DNPELDLPPE GTKYNEAKTN PATSAIPPIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ BEGSESGVLY HDSVGVTYQG DGLTALNISS MPMNYDNVM VSQASGDTSL VDTLLKTVLP HMESASLQGL VFATPVLSID MGEVALTAVS DRGSDGLSIH SSDSQTGMDR EGGGTSDSLM VSEABASNSS FYLEDSTSPR VYBECTVDLGI YMRPKAYIAA	120 180 240 300 360 480 540 660 720 780 900 900 1080 1140 1200 1260 1320 1380 1440 1560 1620 1680
5055606570	I MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEELHEAV HEFLTDGYOD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTPHAFTI LINTTRASSS ILFQVTSATE KTLMFSQVED SLFSGPSHIP PVSVAEFTYT LNASLQETSV KPVLSANSEP AVPSDPILVE TISYASEKYE EPLINTLINKE EPLINTLINKE SPGKSPSANG ENETSTOFSF HESRIGLAEG VISTPPTPIF TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI TADSSNHPDI	II IQLLCVCRLD IQLLCVCRLD TQUNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISESQL CSSEPENVQA LGAILNNLLP EEEGKDIEEG GKGDVPNTSL SEMPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE SDKVPLHASL PSSDAMMHAS PSSDAMHASL PSSDAMHASL PSSDAMHASL PSSDAMHASL TSVPGDDNKA SISSTKGMFP ASSDPASSEM TPKVDKISST PVLLKSESSH IHSDEILTST KLLPPSKATS SQEKMNDSD LSQKINDGKE LSQKINDGKE ADTNERDADG LESEKKAVIP PISDDVGAIP KHKNRYINIV	VANGYYRQOR WANGYYRQOR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVNPGRDSA NSTSOPVTKL ITVSTSOPVTK ITVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL LSKSEIIYGN GSLAHTTTKV MLHLIVSNSA QVVPSLYSND KSSVTGKVFA ELSHSAKSDA THENSLMDQN ENDIQTGSAL LIAAGDSEIT LVIVSALTFI IKHFPKHVAD AYDHSRVKLA	ALPERISMSY KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTMGLYGKY TNQIRKKEPQ ATEXDISLTS ESLLITSPKLD SEDSTSSGSE KSFSAGPVMS FYNGETPLQ LSSYDGAPLL PSLAQYSDVL SDNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSENMLHSTS ELFQTANLEII GIPTVASDTF GLVGGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPTSS CLVVLVGILI LHASSGFTEE QLAEKDGKLT EKGRRKCDQY	TGALNQKNWG TGALNQKNWG TVBINLTNDY DRFSSPEAV LPNSTDKYYI LPNSTDKYYI TMIEKPAVLY SDQLIVDMPT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPLL PFSSASFSSE STTHAASETL TVSYSSAIPV SDSEPLLPDT EMVYPSESTV NNFSVQPTHT LLQPSFQASD NQAHPPKGRH VSTDRSVFIB VSTDRSVFIB VSTDRSVFIB VSTDRSVFIB VTSRSSEVFH YWKCFQTAH FETLKEFYQE DYINANYVDG WPADGSEEYG	KKYPTCNSPK KKYPTCNSPK KKYPTCNSPK KKKYPTCNSPK KKKGKLRALS YMGSLTSPC VMSCLTSPC QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VEGTSASLND PATSAIPPIS NVWPPSSTDI PHYSTFAYPP VTPLLLDNQI LFRHLHTVSQ BGLSGSGVLY HDSVGVTYQG DGLTALNISS MPMNYDNVMK VSQASGDTSL VDTLLKTVLP HMESASLQGL VFATPVLSID MCHVALTAVS BGGGTSDSLN VSERABASNSS FYLEDSTSPR VQSCTVDLGI YNRPKAYIAA NFLVTQKSVQ	120 180 240 300 360 420 600 720 780 840 900 900 1080 1140 1260 1380 1560 1560 1680 1740 1800 1860
5055606570	MRILKRFLAC QSPINIDEDL FKASKITPHW ILFEVGTEEN TDTVDWIVFK TGKEEIHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGE TEVTEHAFTP LNTTPRASSS ILFQVTSATE KTLMFSQVEP SLFSGPSHIP PVSVAFETYT LNASLQETSV KPVLSANSEP AVPSDPILVE EPLNTLINKL PHRDGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDFSF HESRIGLAEG VISTPPTPIF TADSSNHPDN QGPLKSTAEU VILAYYTVRNF	III IQLLCVCRLD IQLLCVCRLD IQLLCVCRLD IQLLCVCRLD IQVININKIL IQKCMMSSDGS LDPKAIIDGV DTVSISSQL CSSEPENVQA LGAILINILLP EERCKDIESG GKGDVPNTSL MMLSGTAESL SENPETITYD ESPLQTNYTE SSRQQDLVST DSALHATPVF SDKVPLHASL PSSDAMMHAR IPKSSLITPT TSVFGDDINA ASSDPASSEM TPKVDKISST FVLLKSESSH IHSDEILTST KLLFPSKATS SQEKWNDSD LSQKMNDSD LSGKMNDSD LSGKMNDSK ADTINENDADIG CHRINGENIN FWRMIWEHNV TURNIFIKKG	WANGYYRQOR KFQGWDKTSL EHSLESQKFP ESVSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSQFVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SGGEPPSYAL ASLLOPTHAL LSKSEIIYGK GSLAHTTTKV LSPSTQLLPY MLHLIVSNSA GVVPBLYSND KSSVTGKVFA ELSHSAKSDA THENSLMDQN ENDIQTGSAL ILAAGDSEIT LVIVSALTPI IKHFPKHVAD AYDHSRVKLA EVIVMITNLV SQKGRPSGRV	ALVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLYGFDA ALDPFILLNL QSGYVMLMDY ICTNGLYGKY TNOIRKKEPQ ATEKDISLTS ESLLTSFKLD SEDSTSSGSE KSPSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVL SONGCSQHIF SGDGEMSGAS ETELQIPSTN FDHEISQVPE ETSASFSTEV SSEMNLHSTTS GLVGGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPTSS CLVVLVGISL LHASSGPTEE QLAEKDGKLT EKGRRKCDQY VTQYHYTQWP	TGALNQKNWG TVBLINLTNDY DRFSSFEEAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY SDQLIVDMPT ISTTTHYNRI QTVTELPPHT TGAEDSSGSS ESLKDPSMES ESLKDPSMES FSTHAASETL TVSYSSAIFV SDSEFILLPDT TEMVYPSESTV NNFSVQPTHT LLQPSFQASD VPVPDVSPTS NQAHPPKGRH VSTDRSVPIG TDDGDDDDDD SEEDNRVTSV AVLTEDESSG VTSENSEVFE FYMKCGTAH FETLKEFYQE DYINANYVDG MYPADGSEEYG DMGVPEYSLE	KKYPTCNSPK KKYPTCNSPK KKYPTCNSPK KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VECTSASLND PATSAIPFIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG DGLTALNISS WPMNYDNVNK VSQASGDTSL VDTLLKTVLP HMHSASLQGL VFATFVLSID KGRVALTAVS DRGSDGLSIH SSDSQTGMDR SGQGTSDSLM VSEARASNSS FYLEDSTSPR VQSCTVDLGI YNRPKAYIAA	120 180 240 300 360 420 540 660 660 720 780 900 960 1020 1320 1380 1440 1500 1560 1620 1740 1800 1800 1920
5055606570	I MRILKRPLAC QSPINIDEDL FKASKITPHW ILPEVGTEEN TDTVDWIVFK TGKEELHEAV HEPLITGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIPS TAQPDVGSGR TEVTPHAFTP LINTTPAASS ILPQVTSATE KTLMFSQVES LIPQVTSATE KTLMFSQVES LIPQVTSATE KTLMFSQVES AVPSDPILVE TISYASEKYE PHRDGSVTST KCMSCSSYRE SPGKSPSANG SENETSTDFSF HESRIGLAEG VISTPPTPIF TADSSNHPDN QGPLKSTAED VLAYYTVRD	III IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCMMSSDGS LDFKAIIDGV DTVSISESQL CSSEPENVQA LGAILMNLLP EEEGKDIEEG GKGDVPNTS SENPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFRQQDLVST DSALHATPVF SDKVPLHASL PSSDAMMHAR IPKSSLITPT TSVFGDDNKA SISTKGMFP ASSDPASSEM TPKVDKISST PVLLKSESSH IHSDELITST KLLPPSKATS SQEXWMDSD LSQKHNDGKE ADTHENDANG LESEKKAVIP PISDDVGAIP KHKNRYINIV FWRMIWEHNV TLRNTKIKKG	VANGYYRQQR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVPCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVMPGRDSA NSTSOPVTKL MTYSITEYBE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL ASLLQPTHAL LSKSEIIYGN GSLAHTTTKV KLSPSTQLLFY MLHLIVSNSA QVVPSLYSND ELSHSAKSDA THENSLMDQN ENDIQTGSAL ILAAGDSEIT LVIVSALTFI IKHPPKHVAD AYDHSRVKLA EVIVMITNLV SQKGRPSGVL ETYIVLDSML	KLVEEIGWSY KLVEEIGWSY ENTFIHNTGK LEMGIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTMGLYGKY TNOIRKKEPQ ATEKDISLTS SEDSTSSGSE KSFSAGPVMS SUDSTSSGSE KSFSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVLL SDNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSEMNLHSTS ELFQTANLEI GIPTVASDTF GLVGGGEDGD NPISYSLSEN PGFPQSPTSS CLVVLVGILI LHASSGFTEE QLAEKOGKLT EKGRRKCDQY VTQYHYTQW OOIOREGTVN	TGALNQKNWG TVBLINLTNDY DRFSSFERAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY SDQLIVDMPT ISTITHYNRI GYVTELPPHT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STIHAASETL TVSYSSAIFV SDSEFLLPDT EMVYPSESTV VPVFDVSPTS NQAHPPKGH VSTDRSVPIG TDDDGDDDDD SEEDNRVTSV AVLITSDERSG VTSENSEVFH YWRKCFQTAH FETLKEFYQE DYINANYVDG WPADGSERYG DMGVPEYSLE IFGFLKHIRS	KKYPTCNSPK KKYPTCNSPK KKYRTCNSPK KGKGKLRALS YMGSLTSPPC KRSRQVFSSY QQLDGEDOTK DMPELDLPPE GTKYNEAKTN PATSAIPPIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ DGLTALNISS MPMYDNVM VSQASGDTSL VDTLLKTVLP HMESASLQGL VFATPVLSID MGHVALTAVS DRGSDGLSIH SGGGTSDSLN VSEABASNSS FYLEDSTSPR VQSCTVDLGI YMRPKAYIAA NFLUTQKSVQ VLTFVRKAAY QRMYLVQTEE	120 180 240 300 360 480 540 660 720 780 900 900 1080 1140 1200 1380 1440 1500 1680 1740 1860 1860 1980
505560657075	I MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEELHEAV HEFLTDGYOD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTPHAFTP LINTTPAASSS ILPQVTSATE KTLMFSQVES SLFSGPSHIP PVSVABFTYT LNASLQETSV KPVLSANSEP AVPSDPILVE TISYASEKYE EPLINTLINKL PHRDGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDPSF HESRIGLAEG VISTPPTPIF TADSSNHPDI QGPLKSTAED VLAYYTVRNF AKRHAVGPVU OVYFIHDTIV	II IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISSGL CSSEPENVQA LGAILINNLLP EEEGKDIEEG GKGDVPNTSL SENPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTHYTO ESFLQTNYTE TSVPGDDNKA SISTKGMFP ASSPEASSEM TPKVDKIST PULKESSLITPT TSVPGDDNKA SISTKGMFP ASSPEASSEM TPKVDKISST FULKESSLITPT TSVPGDDNKA SISTKGMFP ESFLGTNYTE ESFLGTNYTH	WANGYYRQOR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV MMSYVLQIVA AIVNPGRDSA NSTSOPVTKL ITVSUTSYES VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL LSKSEIIYGN GSLAHTTIKV MLHLIVSNSA QVVPSLYSND ENDIGTGSAL THENSLMDQN ENDIGTGSAL LVASATTPI IKHFPKHVAD AYDHSRVKLA EVIVMITNLV SQKGRPSGRV GTYIVLDSML LDSHIRAYVN	KLVEEIGWSY KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVVYD ICTNGLYGKY TNQIRKKEPQ ATEXDISLTS SEDSTSSGSE KSFEAGPVMS PYNGETPLQ LSSYDGAPLL PSLAQYSDVIL SDNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQYPE ETSASFSTEV SSENMLHSTS ELFQTANLEII GIPTVASDTF GLVGGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPTSS CLVVLVGILI LHASSGPTEE QLAEKDGKLT EKGRKCDQY VTQYHYTQWP QQIQHEGTVN ALLIPGPAGK	TGALNQKNWG TGALNQKNWG TVBINLTNDY DRFSSPEAV LPNSTDKYYI LPNSTDKYYI TMIEKPAVLY SDQLIVDMPT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STTHAASETL TVSYSSAIPV SDSEPLLPDT EMVYPSESTV NNFSVQPTHT LLQPSPQASD NQAHPPKGRH VSTDRSVFI VSTDRSVFI VSTDRSVFI YWRKCFQTAH FETLKEFYQE DYINANYVDG WPADGSEEYG DMGVPEYSLS TKLEKGFQLL	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YMGSLTSPC KPSRQVPSSY QQLDGEDQTK DNPELDLFPE GTKYMEAKTN VEGTSASLND PATSAIPFIS NVWFPSSTDI PHYSTFAYFP YTPLLLDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG DGLTALNISS MEMNYDNVMK VSQASGDTSL VDTLLKTVLP HMESASLQGL VFATPVLSID KGKUVALTAVS EGGGTSDSLN VSEREASNSS FYLEDSTSPR VQSCTVDLGI YMRFKAYIAA NFLVTQKSVQ VLTTVRKAAY QRNYLVQTEE SQSNIQQSDY	120 180 240 300 360 420 540 600 720 780 840 900 1080 1140 1260 1380 1560 1560 1680 1740 1800 1860 1920 1980
5055606570	I MRILKRFLAC QSPINIDEDL ILFEVGTEEN TOTVDWIVFK TGKEEIHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEPS GSKTVLRSPH ENISQGYIFS TAQPDVGSGE TEVTERAFTP LNTTPRASSS ILFQVTSATE KTLMFSQVEP SLPSGPSHIP PVSVARETYT LNASLGETSV KPVLSANSEP AVPSDPILVE EPLNTLINKL PHROGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDPSF HESRIGLAEG VISTPETPIF TADSSNHPDN QGPLKSTAED VLAYYTVRNF AKRHAVGPVV QYVFIHDTLV SAALKQCNRE	III IQLLCVCRLD IQLLCVCRLD IQLLCVCRLD IQULCVCRLD IQVANINKKL IQKCMMSSDGS LDPKAIIDGV DTVSISSQL LGSEPENVQA LGAILNNLLP EEEGKDIESG GKGDVPNTSL MMLSGTAESL SENPETITYD ESPLQTNYTE SSRQQDLVST DSALHATPVF SDKVPLHASL PSSDAMMHAR IPKSSLITPT TSVFGDDNKA IPKSSLITPT TSVFGDDNKA SISSTKGMFP ASSDPASSEM TPKUDKISST FVLLKSESSH LHSDEILTST KLLFPSKATS SQEKWNDSD LSQKWNDSD LSQKWNDSD LSQKWNDSD LSQKWNDSD LSGKWNDSD LSGKWN	WANGYYRQOR KFQGWDKTSL EHSLESQKFP ESVSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSQFVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL ASLLOPTHAL LSKSEIIYGN GSLAHTTTKV LSPSTQLLFY MLHLIVSNSQ KSSVTGKVPA BLSHSAKSDA THENSLMDQN ENDIQTGSAL ILAAGDSEIT ILVIVSALIPI IKHFPKHVAD AYDHSRVKLA EVIVMITNLV SQKGRPSGRV GTYIVLDSML LDSHIHAYVN ERSRVGISSL	ALLPEPAGK KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY ENTITHNTGK LEMGIYCFDA ALDPFILLNL QSGYVMLMDY ICTNGLYGKY TNOIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSGSB KSPSAGPVMS PYVMGETPLQ LSSYDGAPLL PSLAQYSDVL SONEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSERMLHSTI GIPTVASDTF GLVGGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPTS CLVVLVGISI LHASSGPTEE QLAEKDGKLT EKGRRKCDQY VTQYMYTQWF QQIQHEGTVN ALLIPGPAGK SGEGTDYINA	TGALNQKNWG TGALNQKNWG TVBINLTNDY DRFSSFEAV LPNSTDKYYI LQNNFREQQY TMIEKFAVLY SDQLIVDMPT ISTTHYNRI QTVTELPPHT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVPPL PFSSASFSS STTHAASETL TVSYSSAIPV SDSEPLLIPDT TEMVYPSESTV NNFSVQPTHT LLQPSFQASD VPVFDVSPTS NQAHPPKGRH VSTDRSVPIG TDDDGDDDDD TDDDGDDDDD SEEDNRVTSV AVLTSDEESG VTSENSEVFL FFTLKEFYQE DYINANYUG MPADGSEEYG DMGVPEYSLF IFGFLKHIRS TKLEKQFQLL SYIMGYYQSN	KKYPTCNSPK KKYPTCNSPK KKYPTCNSPK KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLFPE GTKYNEAKTN VECTSASLND PATSAIPFIS NVWFPSSTDI PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ BEGGSESGVLY HDSVGVTYQG DGLTALNISS WPMNYDNVNK VSQASGDTSL VDTLLKTVLF LMEHSASLQGL VFATFVLSID KGHVAITAVS DRGSDGLSIH SSDSQTGMDR 6CQGTSDSLN VSEAEASNSS FYLEDSTSPR VQSCTVDLGI YNRPKAYIAA NFLVTQKSVQ VLTFVRKAAY QRNYIVQTEE SQSNIQQSDY BEFITTQHPLL	120 180 240 300 360 420 540 660 720 780 900 960 1020 1320 1380 140 1500 1560 1560 1560 1680 1740 1860 1920 1980 2040 2100
505560657075	I MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTBEN TDTVDWIVFK TGKEELHEAV HEFLTDGYQD LIGTEELIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIPS TAQPDVGSGR TEVTPHAFTP LNTTPAASSS ILFQVTSATE KTLMFSQVEP SLFSGPSHIP PVSVAEFTYT LNASLQETSV KAVSLOPILVE TISYASEKYE EPLITTINKL PHRDGSVTST KCMSCSSYRE EPLITTINKL PHRDGSVTST KCMSCSSYRE EPLITTINKL PHRDGSVTST KCMSCSSYRE EPLITTINKL PHRDGSVTST KCMSCSSYRE TISYASEKYE EPLITTINKL PHRDGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDFSF HESRIGLAEG GVISTPPTPIF TADSSNHPDN QGPLKSTAED VLAYYTVRNF AKRHAVGPVV QYVFIHDTLV SAALKQCNRM	III IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCMMSSDGS LDFKAIIDGV DTVSISSQL CSSEPENVQA LGAILNNLLP EERGKDIESG GKGDVPNTSL MMLSGTAESL SENPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE DSALHATPVF SDKVPLHASL PSSDAMMHAR IPKSSLITPT TSVFGDDNKA SISSTKGMFP ASGDPASSEM TPKVDKISST PVLLKSESSH IHSDEILTST KLLFPSKATSS QEKVMNDSD LSQKINNDGKE ADTNEKDADG LEGEKKAVIP PISDDVGAIP KHKNRYINIV FWRMIWEHNV TTLRNTKIKKG VHCSAGVGRT EAILSKETEV KNTTSSIIFV WDHNAQLVVM	WANGYYRQOR KFQWDKTSL EHSLESQKFP ESVSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVMPGRDSA IRVDESEKT VNVYYSQTTQ PSVDVSFESI PVAGGDLLLS SGGPEPSYAL ASLLQPTHAL LSKSEIIYGK GSLAHTTKV LSPSTQLLFY MLHLIVSNSA QVVPSLYSND KSSVTGKVFA ELSHSAKSDA THENSLMDQN ENDIQTGSAL ILAAGDSEIT LVIVSALTFI LVIVSALTFI LVIVSALTFI LVIVSALTFI SQKGRPSGRV GTYIVLDSML LDSHIHAYVM ERSRVGISSL IPDGQMMAED	KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY ENTPIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWIMDY TWERPRVVYD ICTNGLYGKY TNQIRKKEPQ ATEKDISLTS ESLITSFKLD SEDSTSSGSE KSPSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVL SODGEWSGAS ETELQIPSFN SODGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSENMLHSTS GLVGGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPTSS CLVVLVGLIL LHASSGPTEE QLAEKDGKLT EKGRRKCDQY VTQYHYTQWP QQIQHEGTVN ALLIPGPAGK SGEGTDYINA EFVYWENKDE	TGALNQKNWG TVBINLTNDY DRFSSFERAV LPNSTDKYYI LQNNFREQQY TMIEKPAVLY SDQLIVDMPT ISTITHYNRI QTVTELPPHT TGAEDSGSS ESLKDPSMEG QCPSTDLEM PSYSSEVFPL PFSSASFSSE STHARASETL TVSYSSAIFV SDSEHLLPDT EMVYPSESTV NNFSVQPTHT LLQPSFQASD VPVFDVSPTS NQAHPPKGRH VSTDHSVPIG TDDDGDDDDD SEEDNRVTSV AVLTSDEBSG VTSENSEVFH YWRKCFQTAH FETLKEFYQE DYINAMYVDG WPADGSEEFIG DMGVPEYSLE IFGFLKHIRS TKLEKQFQLL SYIMGYYQSN PINCESFKVI	KKYPTCNSPK KKYPTCNSPK KKYRTCNSPK KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VECTSASLND PATSAIPPIS NVWFPSSTID PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ DGLTALNISS MPNMYDNVNK VSQASGDTSL VOTILKTVLP HMESASLQGL VFATPVLSID MGHVAITAVS DRGSDGLSIH VSEABASNSS FYLEDSTSPR VQSCTVDLGI YNRFKAYIAA NFLVTQKSVQ VLTTVRKAAY QRNYLVQTEE SQSNIQQSDY EPILTQHPLL LMAEEHKCLS	120 180 240 300 360 420 540 660 660 720 780 900 960 1020 1080 1140 1260 1560 1560 1560 1740 1800 1920 1980 2040 2160
505560657075	I MRILKRFLAC QSPINIDEDL FKASKITFHW ILFEVGTEEN TDTVDWIVFK TGKEELHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTPHAFTP LINTTPAASS ILFQVTSATE KTLMFSQVED PVSVABFTYT LNASLQETSV KPVLSANSEP AVPSDPILVE TISYASEKYE EPLNTLINKL PHRDGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDFSF HESRIGLAEG VISTPFTPIF TADSSNHPDN AKRHAVGPVV QVVFIHDTLV SAALKQCNRE HTIKDFWRILL HTIKDFWRILL HTIKDFWRILL SAALKQCNRE HTIKDFWRILL HTIKDFW	III IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISSQL CSSEPENVQA LGAILNNLLP EEGKDIEGC GKGDVPNTSL SENPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTLYT TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP ASSPRASSEM TPKVDKISST FVLLKSESSH LHSDEILTST KLLFPSKATS SQEKMNDSD LSGKMNDSD LSGKMNSSIPV WDHNAGLVV WDHNAGLVV ILEATODDYV	WANGYYRQQR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVMPGRDSA NSTSOPVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSYDVSFESI PVAGGDLLLE SSGPEPSYAL LSKSEIIYGN MLHLIVSNSA QVVPSLYSND KSSVTGKVPA BLSHSAKSDA THENSLMDQN ENDIQTGSAL LILAAGDSEIT LVIVSALTPI IKHFPKHVAL EVIVMITNLV SQKGRPSGRV LDSHTHAYVN ERSRVGISSL IPDGQMMAEU LDSHTHAYVN ERSRVGISSL IPDGQMMAEU LEVRHFQCPK	KLVEEIGWSY KLVEEIGWSY ENTFIHNTGK LEMQIYCFDA ALDPFILLNL QSGYWNLMDY TWERPRVYYD ICTNGLYGKY TNQIRKKEPQ ATEXDISLTS SEDSTSSGSE KSFSAGPVMS FSEAGPYMS FYVNGETPLQ LSSYDGAPLL PSLAQYSDVLL SDNEGSQHIF SGDGEMSGAS ETELQIPSFN FOHEISQVPE ETSASFSTEV SSENMLHSTS ELFQTANLEII GIPTVASDTF GLVGGEDGD NPISYSLSEN LPLSPESKAW PGFPQSPTSS CLVVLVGLLI LHASSGPTES QLAEKDGKLT EKGRRKCDQY VTQYHYTQWF QQIQHEGTVN ALLIPGPAGK SGEGTDYINA EFVYWPNKDE WPNPDSFISK	TGALNQKNWG TGALNQKNWG TVBINLTNDY DRFSSPEAV LPNSTDKYYI LPNSTDKYYI TMIEKPAVLY SDQLIVDMPT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STTHAASETL TVSYSSAIPV NNFSVQPTHT LLQPSPQASS NQAHPPKGRH VSTDRSVPG TDDDGDDDDD SEEDNRVTSV AVLTEDESSF VWRKCFQTAH FETLKEFYQE DYINANYVDG WPADGSEEYG DMGVPEYSLE TKLEKGFQLL SYIMGYYQSN FINCESFKVI TFELISVIKE	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YMGSLTSPEV KGKGKLRALS YMGSLTSPEV QQLDGEDQTK DNPELDLEPE GTKYMEAKTN VEGTSASLND PATSAIPPIS TOTAL TOTAL PHYSTFAYFP YTPLLLDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG DGLTALNISS MPMYDNVMK VSQASGDTSL VFATPVLSID NGGUSDSTL SSDSQTGMDR SGQGTSDSLM VSERASANSS FYLEDSTSPR VQECTVDLGI YMRPKAYIAA NFLVTQKSVQ VLTTVRKAAY QRNYLVQTEE SQSNIQSDY LMAEEHKCLS LMAEEHKCLS EANRRDGPMI	120 180 240 300 360 420 660 720 780 840 900 960 1020 1080 1140 1200 1260 1380 1560 1680 1740 1860 1980 2040 2160 2160 2220
50 55 60 65 70 75	I MRILKRFLAC QSPINIDEDL ILFEVGTEEN TDTVDWIVFK KTGKEELHEAV HEFLTDGYQD LIGTEEIIKE RSPTRGSEPS GSKTVLRSPH ENISQGYIFS TAQPDVGSGR TEVTERAFTP LINTTPRASSS ILFQVTSATE KTLMFSQVEP SLFSGPSHIP PVSVABFTIT LNASLQETSV KPVLSANSEP AVPSDPILVE EPLNTLINKL PHROGSVTST KCMSCSSYRE SPGKSPSANG ENETSTDFSF HESRIGLAEG VISTPPTPIF TADSSNEPDN QGPLKSTAED VLAYYTVRNF AKRHAVGPVV QYVFIHDTLV SAALKQCNRE HTIKDFNRMI NEEKLILQGD	III IQLLCVCRLD IQLLCVCRLD TQVNVNLKKL GKCNMSSDGS LDFKAIIDGV DTVSISSQL CSSEPENVQA LGAILNNLLP EEGKDIEGC GKGDVPNTSL SENPETITYD ESFLQTNYTE ESFLQTNYTE ESFLQTNYTE ESFLQTLYT TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP TSVFGDDNKA SISSTKGMFP ASSPRASSEM TPKVDKISST FVLLKSESSH LHSDEILTST KLLFPSKATS SQEKMNDSD LSGKMNDSD LSGKMNSSIPV WDHNAGLVV WDHNAGLVV ILEATODDYV	WANGYYRQOR KFQGWDKTS EHSLEGQKFP ESVSRFGKQA AVFCEVLTMQ DPENYTSLLV NMSYVLQIVA AIVNPGRDSA NSTSOPVTKL NTVSITEYEE VLIPESARNA IRVDESEKTT VNVYYSQTTQ PSVDVSFESI PVAGGDLLLE SSGPEPSYAL ASLLOPTHAL LSKSEIIYGN GSLAHTTTKV LSPSTQLLFY MLHLIVSNSA QVVPSLYSND KSSVTGKVFA ELSHSAKSDA THENSLMDQN ENDIQTGSAL ILAAGDSEII IKHPPKHVAD AYDHSRVKLA EVIVNITNLV SQKGRPSGRV GTYIVLDSML LDSHIHAYVN ERSRVGISSL IPDGQNMAED LEVRHPQCPK HQLEKENSVD	ALLPEJGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY ALDPFILLNL QSGYVMLMDY ICTNGLYGKY TNOIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSSSB KSFSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVL SSNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSERMLHSTS ELFQTANLEI GIPTVASDTF GLVGGEGEDG NPISYSLSEN LPLSPESKAW PGFPQSPTSS LPLSPESKAW PGFPQSPTSS LVVLVGILI LHASSGFTEE QLAEKDGKLT VTQYHYTQWP QQIQHEGTVN ALLIPGPAGK SGEGTDYINA EFVYWPNKDE WPNPDSPISK VYQVAKMINL	TGALNQKNWG TGALNQKNWG TVBINLTNDY DRFSSPEAV LPNSTDKYYI LPNSTDKYYI TMIEKPAVLY SDQLIVDMPT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STTHAASETL TVSYSSAIPV NNFSVQPTHT LLQPSPQASS NQAHPPKGRH VSTDRSVPG TDDDGDDDDD SEEDNRVTSV AVLTEDESSF VWRKCFQTAH FETLKEFYQE DYINANYVDG WPADGSEEYG DMGVPEYSLE TKLEKGFQLL SYIMGYYQSN FINCESFKVI TFELISVIKE	KKYPTCNSPK KKYPTCNSPK KKYRTCNSPK KGKGKLRALS YNGSLTSPPC KFSRQVFSSY QQLDGEDQTK DNPELDLPPE GTKYNEAKTN VECTSASLND PATSAIPPIS NVWFPSSTID PHYSTFAYFP VTPLLLDNQI LFRHLHTVSQ DGLTALNISS MPNMYDNVNK VSQASGDTSL VOTILKTVLP HMESASLQGL VFATPVLSID MGHVAITAVS DRGSDGLSIH VSEABASNSS FYLEDSTSPR VQSCTVDLGI YNRFKAYIAA NFLVTQKSVQ VLTTVRKAAY QRNYLVQTEE SQSNIQQSDY EPILTQHPLL LMAEEHKCLS	120 180 240 300 360 420 660 720 780 840 900 960 1020 1080 1140 1200 1260 1380 1560 1680 1740 1860 1980 2040 2160 2160 2220
505560657075	MRILKRPLAC QSPINIDEDL FKASKITFHW ILFEVGTBEN TDTVDWILVFK TGKEELHEAV HEPLITDGYQD LIGTEELIKE RSPTRGSEFS GSKTVLRSPH ENISQGYIPS TAQPDVGSGR TEVTPHAFTP LINTTPAASSS ILFQVTSATE KTLMFSQVEP SLFSGFSHIP PVSVABETYT LNASLQETSV KCMSCSSYBE EPLINTLINKL PHRDGSVTST KCMSCSSYBE SPGKSPSANG ENETSTDFSF HESRIGLAEG VISTPPTPIF TADSSHIPDN QGPLKSTAED VLAYYTVMI SAALKQCNRE HTIKDENRMI NEEKLIIQDF VHDEHGGVTA SLVSTRQEEN	III IQLLCVCRLD IQLLCVCRLD IQLLCVCRLD IQLLCVCRLD IQKCMMSSDGS LDPKAIIDGV DTVSISSQL LGSEPENVQA LGAILNNLLP EEEGKDIEEG GKGDVPNTSL MALSGTAESL SENPETITYD ESPLQTNYTE SSRQQDLVST DSALHATPVF SDKVPLHASL PSCLAMMHAR IPKSSLITPT TSVPGDDNKA SISTKGMFP ASSDPASSEM TPKVDKISST LTSTTGMFP ASSDPASSEM TPKVDKISST LHSDEILTST KLLFPSKATS LSQEKMNDSD LSQEKMNDSD LSQEKMNDSD LSQEKMNDSD LSQEKMNDSD LSGEKAVIP PISDDVGAIP KHCRYINIV FWRMIWEHNV TLRNTKIKKG VHCSAGVGRT EAILSKETEV WDHNAQLVVM ILEATQDDYV GTPCALTILM	WANGYYRQOR WANGYYRQOR KFQGWDKTSL EHSLEGQKFP ESYSRFGKQA AVPCEVLIMO DPENYTSLLV MMSYVLQIVA AIVMPGRDSA NSTSOPVTKL MTYSITEYEE VLIPESARNA IRVDESEKTT VNVVYSQTTQ PSVDVSFESI PVAGGDLLLE SGGPEPSYAL ASLLQPTHAL LSKSEIIYGN GSLAHTTTKV LSPSTQLLFY MLHLIVSNSA RQVVPSLYSND KSSVTGKVFA ELSHSAKSDA THENSLMDQN ENDIQTGSAL ILAAGDSEIT LVIVSALTFII IKHPPKBVAD AYDHSRVKLA EVIVNITNLV SQKGRPSGRV GTYIVLDSML LDSHIHAYVN ERSRVGISSI LPDGQNMAED LEVRHPQCPK HQLEKENSVU ALPDGNIAES	ALLPEJGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY KLVEEIGWSY ALDPFILLNL QSGYVMLMDY ICTNGLYGKY TNOIRKKEPQ ATEXDISLTS ESLLTSFKLD SEDSTSSSSB KSFSAGPVMS PVYNGETPLQ LSSYDGAPLL PSLAQYSDVL SSNEGSQHIF SGDGEWSGAS ETELQIPSFN FDHEISQVPE ETSASFSTEV SSERMLHSTS ELFQTANLEI GIPTVASDTF GLVGGEGEDG NPISYSLSEN LPLSPESKAW PGFPQSPTSS LPLSPESKAW PGFPQSPTSS LVVLVGILI LHASSGFTEE QLAEKDGKLT VTQYHYTQWP QQIQHEGTVN ALLIPGPAGK SGEGTDYINA EFVYWPNKDE WPNPDSPISK VYQVAKMINL	TGALNQKNWG TGALNQKNWG TVBINLTNDY DRFSSPEAV LPNSTDKYYI LPNSTDKYYI TMIEKPAVLY SDQLIVDMPT TGAEDSSGSS ESLKDPSMEG QGPSVTDLEM PSYSSEVFPL PFSSASFSSE STTHAASETL TVSYSSAIPV NNFSVQPTHT LLQPSPQASS NQAHPPKGRH VSTDRSVPG TDDDGDDDDD SEEDNRVTSV AVLTEDESSF VWRKCFQTAH FETLKEFYQE DYINANYVDG WPADGSEEYG DMGVPEYSLE TKLEKGFQLL SYIMGYYQSN FINCESFKVI TFELISVIKE	KKYPTCNSPK RVSGGVSEMV KGKGKLRALS YMGSLTSPEV KGKGKLRALS YMGSLTSPEV QQLDGEDQTK DNPELDLEPE GTKYMEAKTN VEGTSASLND PATSAIPPIS TOTAL TOTAL PHYSTFAYFP YTPLLLDNQI LFRHLHTVSQ EFGSESGVLY HDSVGVTYQG DGLTALNISS MPMYDNVMK VSQASGDTSL VFATPVLSID NGGUSDSTL SSDSQTGMDR SGQGTSDSLM VSERASANSS FYLEDSTSPR VQECTVDLGI YMRPKAYIAA NFLVTQKSVQ VLTTVRKAAY QRNYLVQTEE SQSNIQSDY LMAEEHKCLS LMAEEHKCLS EANRRDGPMI	120 180 240 300 360 420 660 720 780 840 900 960 1020 1080 1140 1200 1260 1380 1560 1680 1740 1860 1980 2040 2160 2160 2220

Seq ID NO: 181 DNA sequence Nucleic Acid Accession #: Eos sequence

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5	CACACATACG	CACGCACGAT	CTCACTTCGA	TCTATACACT	GGAGGATTAA	AACAAACAAA	60
		ATTTCCTTCG					120
		CCGCAGACCG					180
	CAGCTCCTCT	GTGTTTGCCG	CCTGGATTGG	GCTAATGGAT	ACTACAGACA	ACAGAGAAAA	240
10		AGATTGGCTG					300
10		CATGTAATAG					360
		TGAATCTTAA					420
		TTCATAACAC GAGTTTCAGA					480 540
	AAATGCAATA	TGTCATCTGA	TGGATCAGAG	CATAGTTTAG	AAGGACAAAA	ATTTCCACTT	600
15		TCTACTGCTT					660
		AGTTAAGAGC					720
		CGATTATTGA					780
		TCATACTGTT					840
20		TGACATCTCC					900
20		TCTCTGAAAG TCATGCTGAT					960 1020
		AGGTGTTTTC					1080
		CAGAAAATGT					1140
	TGGGAAAGAC	CTCGAGTCGT	TTATGATACC	ATGATTGAGA	AGTTTGCAGT	TTTGTACCAG	1200
25	CAGTTGGATG	GAGAGGACCA	AACCAAGCAT	GAATTTTTGA	CAGATGGCTA	TCAAGACTTG	1260
	GGTGCTATTC	TCAATAATTT	GCTACCCAAT	ATGAGTTATG	TTCTTCAGAT	AGTAGCCATA	1320
	TGCACTAATG	GCTTATATGG TTGATCTTTT	AAAATACAGC	BACCAACTGA	AACAAATAAT	CAACCACCAC	1380 1440
		AAGACATTGA					1500
30		GGAAAAAGGA					1560
••	ACGAAATACA	ATGAAGCCAA	GACTAACCGA	TCCCCAACAA	GAGGAAGTGA	ATTCTCTGGA	1620
	AAGGGTGATG	TTCCCAATAC	ATCTTTAAAT	TCCACTTCCC	AACCAGTCAC	TAAATTAGCC	1680
	ACAGAAAAAG	ATATTTCCTT	GACTTCTCAG	ACTGTGACTG	AACTGCCACC	TCACACTGTG	1740
25						TCCACATATG	
35		GGACTGCAGA CCAGTTTCAA					1860 1920
	CCAACTTCTC	CTATCCCATT	CATCTCTGAG	AACATATCCC	ARGGGTATAT	ATTTTCCTCC	1980
	GAAAACCCAG	AGACAATAAC	ATATGATGTC	CTTATACCAG	AATCTGCTAG	AAATGCTTCC	2040
	GAAGATTCAA	CTTCATCAGG	TTCAGAAGAA	TCACTAAAGG	ATCCTTCTAT	GGAGGGAAAT	2100
40	GTGTGGTTTC	CTAGCTCTAC	AGACATAACA	GCACAGCCCG	ATGTTGGATC	AGGCAGAGAG	2160
		AGACTAATTA					2220
	TCCTTTTCTG	CAGGCCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280 2340
		CCTTTGCCTA AGGATTTGGT					2400
45		CAGAGGCCAG					2460
		AGAAGAAGGC					2520
		TTCTTGTGGG					2580
	TTTTACTTAG	AGGACAGTAC	ATCCCCTAGA	GTTATATCCA	CACCTCCAAC	ACCTATCTTT	2640
50	CCAATTTCAG	ATGATGTCGG	AGCAATTCCA	ATAAAGCACT	TTCCAAAGCA	TGTTGCAGAT	2700 2760
50	CTCCACGCAA	GTAGTGGGTT GTACTGTTGA	CTTLCCTLTT	ACAGCAGACAC	GCTCCAACCA	CCCAGACAAC	2820
	AAGCACAAGA	ATCGATACAT	AAATATCGTT	GCCTATGATC	ATAGCAGGGT	TAAGCTAGCA	2880
		AAAAGGATGG					2940
	TACAACAGAC	CAAAAGCTTA	TATTGCTGCC	CAAGGCCCAC	TGAAATCCAC	AGCTGAAGAT	3000
55		TGATATGGGA					3060
		GGAGAAAATG					3120
		TCACTCAGAA ACACAAAAAT					3180 3240
		ATCACTACAC					3300
60		TTGTGAGAAA					3360
		GTGCTGGAGT					3420
		AACACGAAGG					3480
	CAAAGAAATT	ATTTGGTACA	AACTGAGGAG	CAATATGTCT	TCATTCATGA	TACACTGGTT	3540
65	GAGGCCATAC	TTAGTAAAGA	AACTGAGGTG	CIGGACAGIC	ATATTCATGC	CCAGCTCCTG	3600 3660
65	ACCCACTCA	ATATACACCA	CACTGACTAT	TCTGCAGCCC	TARAGCARTG	CAACAGGGAA	3720
	AAGAATCGAA	CTTCTTCTAT	CATCCCTGTG	GAAAGATCAA	GGGTTGGCAT	TTCATCCCTG	3780
	AGTGGAGAAG	GCACAGACTA	CATCAATGCC	TCCTATATCA	TGGGCTATTA	CCAGAGCAAT	3840
	GAATTCATCA	TTACCCAGCA	CCCTCTCCTT	CATACCATCA	AGGATTTCTG	GAGGATGATA	3900
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TGTGGGTATT CTCATCTACT GGAGGAAATG CTTCCAGACT GCACACTTTT ACTTAGAGGA CAGTACATCC CCTAGAGTTA TATCCACAC TCCAACACCT ATCTTTCCAA 2520 2580 2640 45 2700 TTTCAGATGA TGTCGGAGCA ATTCCAATAA AGCACTTTCC AAAGCATGTT GCAGATTTAC ATGCAAGTAG TGGGTTTACT GAAGAATTTG AGACACTGAA AGAGTTTTAC CAGGAAGTGC AGAGCTGTAC TGTTGACTTA GGTATTACAG CAGACAGCTC CAACCACCCA GACAACAAGC 2760 2820 ACAAGAATCG ATACATAAAT ATCGTTGCCT ATGATCATAG CAGGGTTAAG CTAGCACAGC 2880 TTGCTGAAAA GGATGGCAAA CTGACTGATT ATATCAATGC CAATTATGTT GATGGCTACA 2940 50 ACAGACCAAA AGCTTATATT GCTGCCCAAG GCCCACTGAA ATCCACAGCT GAAGATTTCT 3000 GGAGAATGAT ATGGGAACAT AATGTGGAAG TTATTGTCAT GATAACAAAC CTCGTGGAGA AAGGAAGGAG AAAATGTGAT CAGTACTGGC CTGCCGATGG GAGTGAGGAG TACGGGAACT 3060 3120 TTCTGGTCAC TCAGAAGAGT GTGCAAGTGC TTGCCTATTA TACTGTGAGG AATTTTACTC TAAGAAACAC AAAAATAAAA AAGGGCTCCC AGAAAGGAAG ACCCAGTGGA CGTGTGGTCA 3180 3240 55 CACAGTATCA CTACACGCAG TGGCCTGACA TGGGAGTACC AGAGTACTCC CTGCCAGTGC 3300 TGACCTTTGT GAGAAAGGCA GCCTATGCCA AGCGCCATGC AGTGGGGCCT GTTGTCGTCC 3360 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5160

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OO		CAMBA BRACKO	CONTRACTOR	דידי ע עבובאדיייידי	ተርርልሮልፎፕር	CTGTTGGGAT	4020
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		220 Protei		1	•		
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AACGAATTTC TGGCAAAATG GCACTGAATC ATCCATATTT TAATGATTTG GACAATCAGA 780 25 TTAAGAAGAT GTAGCTTTCT GACAAAAAGT TTCCATATGT TATGTCAACA GATAGTTGTG 900 960 30 Seq ID NO: 242 Protein sequence: Protein Accession #: NP 203698.1 31 51 35 MEDYTKIEKI GEGTYGVVYK GRHKTTGQVV AMKKIRLESE EEGVPSTAIR EISLLKELRH 60 PHIVSLQDVL MQDSRLYLIF EFLSMDLKKY LDSIPPGQYM DSSLVKVVTL WYRSPEVLLG 120 SARYSTPVDI WSIGTIFAEL ATKKPLFHGD SEIDQLFRIF RALGTPNNEV WPEVESLQDY 180 KNTFPKWKPG SLASHVKNLD ENGLDLLSKM LIYDPAKRIS GKMALNHPYF NDLDNQIKKM 40 Seq ID NO: 243 DNA sequence Nucleic Acid Accession #: AF101051.1 Coding sequence: 221-856 45 51 31 GAGCAACCTC AGCTTCTAGT ATCCAGACTC CAGCGCCGCC CCGGGCGCGG ACCCCAACCC 60 CGACCCAGAG CTTCTCCAGC GGCGGCGCAG CGAGCAGGGC TCCCCGCCTT AACTTCCTCC 120 GCGGGGCCCA GCCACCTTCG GGAGTCCGGG TTGCCCACCT GCAAACTCTC CGCCTTCTGC 180 50 ACCTGCCACC CCTGAGCCAG CGCGGGCGCC CGAGCGAGTC ATGGCCAACG CGGGGCTGCA GCTGTTGGGC TTCATTCTCG CCTTCCTGGG ATGGATCGGC GCCATCGTCA GCACTGCCCT 240 300 GCCCCAGTGG AGGATTTACT CCTATGCCGG CGACAACATC GTGACCGCCC AGGCCATGTA 360 CGAGGGGCTG TGGATGTCCT GCGTGTCGCA GAGCACCGGG CAGATCCAGT GCAAAGTCTT 420 TGACTCCTTG CTGAATCTGA GCAGCACATT GCAAGCAACC CGTGCCTTGA TGGTGGTTGG 480 CATCCTCCTG GGAGTGATAG CAATCTTTGT GGCCACCGTT GGCATGAAGT GTATGAAGTG 55 CTTGGAAGAC GATGAGGTGC AGAAGATGAG GATGGCTGTC ATTGGGGGTG CGATATTTCT 600 TCTTGCAGGT CTGGCTATTT TAGTTGCCAC AGCATGGTAT GGCAATAGAA TCGTTCAAGA 660 ATTCTATGAC CCTATGACCC CAGTCAATGC CAGGTACGAA TTTGGTCAGG CTCTCTTCAC 720 TGGCTGGGCT GCTGCTTCTC TCTGCCTTCT GGGAGGTGCC CTACTTTGCT GTTCCTGTCC 780 CCGAAAAACA ACCTCTTACC CAACACCAAG GCCCTATCCA AAACCTGCAC CTTCCAGCGG 60 840 GAAAGACTAC GTGTGACACA GAGGCAAAAG GAGAAAATCA TGTTGAAACA AACCGAAAAT GGACATTGAG ATACTATCAT TAACATTAGG ACCTTAGAAT TTTGGGTATT GTAATCTGAA 900 GTATGGTATT ACAAAACAAA CAAACAAACA AAAAACCCAT GTGTTAAAAT ACTCAGTGCT 1020 AAACATGGCT TAATCTTATT TTATCTTCTT TCCTCAATAT AGGAGGGAAG ATTTTACCAT
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	TGGGTGGATT	CTCNATCNAC	AGTAAACTTA	AGAGACCCCC	GATGCTCCCC	TGGTTTAACT	660
	MOUNT WOODING	ስ እ እ እ ጥጥ እ ጥር ጥ	CAGAGGGAAT	AAACATCTTT	TCCTTCTTCC	CTCTCCAGAA	720
20	CONCORDO COR	ስ ሞስ ሞሞስ <i>ከርያር</i> ር	CAGGAGTTGC	TTTGGGGATG	GCTGGAAGTG	CAATGTCTTC	780
20	OR BOTH CONTO	CONTRACTOR	TEGECATATT	TTTCTCCTTC	GCCCAGGTTG	TAATTGAAGC	840
	CA A TWIP CHIPTYCIC	TOCTOCOTAG	GTATGAATAA	CCCTGTTCAG	ATGTCAGAAG	TATATATIAI	900
	ACCACCACAC	COTOTOTO	GCCAACTGGC	AGGACTTTCT	CAAGGACAGA	AGAAACIGIG	960
	CCS CONTURS OF	CACCIACCACA	TCCACTACAT	CGGAGAAGGC	GCGAAGACAG	GCATCAAAGA	1020
25	A DOCOCACEA T	CAATTCCGAC	ATCGA CGGTG	GAACTGCAGC	ACTGTGGATA	ACACCTCTGT	1080
	THE THE PROPERTY OF THE PARTY O	CTCATCCAGA	TAGGCAGCCG	CGAGACGGCC	TTCACATACG	CCGTGAGCGC	1140
	3 CC3 CCCCTC	GTGAACGCCA	TGAGCCGGGC	GTGCCGCGAG	GGCGAGCTGT	CCACCTGCGG	1200
•	CONCLUS COCCCC	CCCCCCCCCCCC	CCAAGGACCT	GCCGCGGGAC	TGGCTCTGGG	GCGGCTGCGG	1260
	CONCRETE STATE	CACTATICCT	ACCGCTTTGC	CAAGGAGTTC	GTGGACGCCC	GCGAGCGGA	1320
30	COCCATOCAC	CCCAACCCCT	CCTACGAGAG	TGCTCGCATC	CTCATGAACC	TGCACAACAA	1380
	- CONTRACTOR CONTRACTOR	CCCACCACCC	TGTACAACCT	GGCTGATGTG	GCCTGCAAGT	GCCATGGGGT	1440
	GTCCGGCTCA	TGTAGCCTGA	AGACATGCTG	GCTGCAGCTG	GCAGACTTCC	GCAAGGTGGG	1500
	TGATGCCCTG	AAGGAGAAGT	ACGACAGCGC	GGCGGCCATG	CGGCTCAACA	GCCGGGGCAA	1560 1620
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	CHACAGAGGGGG	1474TCTTAC	DDAADACCACA	TAAAGAAAT	CATTTTCTT	TTCTCAAATA	2220
45	MCCCC N TO N TO N TO N	TOTAL NAME OF THE PARTY OF THE	· ACCTTCCACT	TGAAAGAGGG	TGGTAGAAA	CTATTCACAA	2280
43	THE PROPERTY OF THE PROPERTY O	* ATCACCAAA	TGAGTTGTAA	ATTCTCTGGT	GCAAGATAAA	AGGICTIGGG	2340
	*******		* ΔΔΔCCTCCCT	TCCCCAGCAG	GGCTGCTAGC	TIGCTITCIG	2400
	as awarman as a s	· አጥናአጥአአጥጥ	• ACBATGGBAG	GACAAGAATO	TCATATTCTC	: AAGGAAAAAA	2460
	COMMENTATION	¬ እጥርጥርጥር ፕ	' CTCCTCAAAT	ATTCCATTTC	CAGACAGAC	GICATATICI	2520
50	8 8 M 8 C CTC 8 C	ኮ ርአአአጥጥጥርርር	: CAGCAGGGAG	GAAAGTCCCC	AGAAATTAA	WANTITAWA	2580
	CONCERN & COCKE	~ NACATOTTC	TOTAL A COMPANY	TTATAAGAAT	TGGGATTCC	GATTIGIAAA	2640
	A A C A C C C C C C	ስ አጥርኔስጥተርግርፈር	ACACTAGATI	TTTTGTTTG	GGAGGTTGGC	TIGAACATAA	2700
	ATGAAATAT	C CTGTATTTTC	TTAGGGATAC	TTGGTTAGT	AATTATAATA	GTAGAAATAA	2760
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	ACACTGAGC	C CTCTCTGAT	CCTCCGTGTT	GTGATGTGA	r GCTGGCCAC	TTTCCAAACG	3000
	GCAGCTCCA	C IGGGICCCC	r TTGGTTGTAG	GACAGGAAA	P GAAACATIA	GAGCTCTGCT	3060
	TGGAAAACA	G TTCACTACT	r AGGGATTTT	GTTTCCTAA	A ACTITIALL	TGAGGAGCAG	3120
60	TAGTTTTCT	A TGTTTTAAT	ACAGAACTIC	GCTAATGGA	A LICACAGAGA	TGTTGCAGCG	3180
60	TATCACTGT	T ATGATCCTG	r GTTTAGATTA	CARCICAL	CITCICCIA	TGTACTGCAG GGGGAAATGT	3240
	GTGTACCTT.	A AAACTGTTC	CAGIGIACI	GAACAGIIG	ATTATATA A	TATATACAT	3300
	GGTTTAATG	G TGCCTGATA	T CICAMAGIC	TTCCACCCA	G TGATTTAGA	r TTACAGCTTA	3360
	ATATATAAA	T WINNAININ	r CTAGAGCATT	CTTGTCCTT	CACTGCAGTC	CAGTTGGGATT	3420
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	THE PROPERTY OF THE PROPERTY O	C THEOREM CAR	A GGGCATTACT	r TGTTCGTTA	T AGACATGGA	C GTTAAGAGAI	3660
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70	N N COCONTOC	A G G S G T T T T T T T T T T T T T T T T	т сасастаст	r attaattga	G TCCCTAAGG	A ATATTCAGCC	3/00
	CNCTNCNTN	ር አጥልሮርጥጥጥ	T TTTTTTT	r titititita	A TAAGGACAC	C TCTTTCCAAA	3040
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	A CA TOTOTO	T ATROCCCC	С ТТАССАССТ	r GGGCTTTCA	T ATCACCTCA	G CCAACTGTGG	3960
	CONCORDED A THE	መ አጥጥርር አጥል ነ	ጥ ርኔፕልፕሮርእር	A TCAGCCAAC	T GTGGCTCIT	T AATTTATTGC	4020
75	20022007200	# PC2C2#CCC	<i>ጦ ጥ</i> ፖልርጥፕሃርርል፣	S TEDATTETE	A GCAAAAGAT	C TIGAAAGCAA	4000
	AAAGCACTA	A TTAGTTTAA	A ATGTCACTT	T TTTGGTTTT	T ATTATACAA	A AACCATGAAG	4140
	ma conductivity	ጥ አጥጥጥርርጥልል	n ጥርልርልጥጥርጥ	T CCTTTTTAG	T GACTCAIGI	T TATGAAGAGA	4200
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80	GTCTTGCGI	G ATTTGTATA	T TTCACTGGT	TAAAAAAACA	M WOULDSWAN	g gcttattcca	-500
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MAGSAMSSKF FLVALAIFFS FAQVVIEANS WWSLGMNNPV QMSEVYIIGA QPLCSQLAGL
        SQGQKKLCHL YQDHMQYIGE GAKTGIKECQ YQFRHRRWNC STVDNTSVFG RVMQIGSRET
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        LADPRKVGDA LKEKYDSAAA MRLNSRGKLV QVNSRFNSPT TQDLVYIDPS PDYCVRNEST
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ICRPHSTEDP ETVDKIVQLV LHEKLQDAVG PPKVDPHSVK IKKINKTETD SYLNHCCGTR
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                                                                                               180
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                                                                                              1140
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288

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Seq ID NO: 285 DNA sequence Nucleic Acid Accession #: Eos sequence Coding sequence: 1-1746

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	1	AGCATTATCT	acomposition of	OTTOGGGGGGGGG	N N COOTTOCCC	TOCACOCTTO	60
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WO 02/086443

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WO 02/086443

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65		298 Prote: cession #: 1	Eos sequenc	e			
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WO 02/086443
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WO 02/086443

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.0	COMCOMCOMO	でででもだけできながっ	CCCCCCCCCCCC	GACGGGAGCT	GACACGGAGG	CGGIGGICIG	240
	ACTUACION CO.	CCCTCCTT CA	CCCCCCACTC	GGGCAAGCTG	AGCGCTGCCG	AGGCCCAGAA	300
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	5 mom 5 5 C5 CC	**************************************	<b>ምተር</b> ርተር ልተርር	TCATTAGGAI	TGAAAIGAI	TGITTCICIT	2520
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	TCATAGTCCA	CAGTTGATGO	AGCATCCIGA	TGCTTAAGG	ACTITICIT	GGGTGGCGCA TCTGTCTCTT	3300
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	000000000000000000000000000000000000000	* <b>*******</b> ****************************	・サインアンコンコンファ・・	CACCGATGG	CAGAGICAC	I AGAAGITACC	3600
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			- mannamana 22	י מרודים להרודים י	T GGTCTCCAU	T TITLAGITIG	3300
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	00 1 00 1 00 0	~ MCCCAMCCA	• ~~***********************************	TATTTTCAC	A GIGITUIGN	T TOCTOTONOM	4320
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	43 3 4 4 4 4 C C C C C C	יייייייייייייייייייייייייייייייייייייי	n carcecere	A AATGGGTGA	T AAAGAATU	A GTTCCTCAAA T GCACACCACT	4440
		~ ~~~~~~~~~~	~ *~~****	A CCAGACAGO	T CAUGITUL	ic wicigatodw	4500
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85			~ «አጥ/ማጥርርርር	C CTACAGTAG	T CCGTAAAC	M MIGCCCACCO	4000
		~ ~~~~~~~	* ALCOUNTED *	T CTGAGGGG	C CCCAGCIIV	C TCGGGCGTGG A CCTGCTAACT	4/40
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11

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WO 02/086443

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                                                                                                      660
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25	GTGAGAGCCC	AGATTCTTGC	AGAACCAGAA	TGGGTCATGC	AGCCATCCAT	AGATATCCAG	1320
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	CAAACAATAT	CCACCAAAGA CTGTGCAAAG	AGATCAGACT	GTCCTGGAAG	GGGGTCCATG	CCAGTTGAGC	1500
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	GAGAAAGACA	CAGTGACAAT	TGGCAAGAAC	CCAGGGGAGT	CGGTGACATT	GCCTTGCAAT	1800
0.5	GCTTTAGCAA	TACCCGAAGC	CCACCTTAGC	TGGATTCTTC	CAAACAGAAG	GATAATTAAT	1860
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	CATTTTACGG	TGGGAATCAC	AGTGACCAAG	AAAGGGTCTG	GCTTGCCATC	CAAAAGAGGC	2040
	AGACGCCCAG	GTGCAAAGGC	TCTTTCCAGA	GTCAGAGAAG	ACATCGTGGA	GGATGAAGGG	2100
40	GGCTCGGGCA	TGGGAGATGA	AGAGAACACT	TCAAGGAGAC	TTCTGCATCC	AAAGGACCAA	2160 2220
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	CCTCCCACAC	TGTTTGAATC	TAGACGAAGG	ATAAACATGG	CAAACAAACA	GATTAATCCG	2340
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			TACTGACCGA				5100
						TCCCAGTCCA	
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60			CTGGTGGGTT				8640
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	ATACTGTACA	TTTGATAATA	AAATAATATT	CTCCCAAAAA	AAAAA		
90		417 Protei					
80	Protein Acc	cession #: 1	NP_056234.1				
	1	11	21	31	41	51	
	ī	ī	ī	Ĭ	ī	1	
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85 ·	NLGFNSIOAL	SETSFAGLTK	LELLMIHGNE	IPSIPDGALR	DLSSLQVFKF	SYNKLRVITG	120
	QTLQGLSNLM	RLHIDHNKIE	FIHPQAFNGL	TSLRLLHLEG	NLLHQLHPST	FSTFTFLDYF	180 240
	KP2.LTKHPAP	VRNWAKLPBY	PMPKWWhrff	WHITMGMEMI	<b>プレーセルが出たり</b> は	WDAKSRGILK	240

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        PSGAVQRDQT VLEGGPCQLS CNVKASESPS IFWVLPDGSI LKAPMDDPDS KFSILSSGWL
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                                                                                       840
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                                                                                      1260
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25
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                                                                                      2160
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                                                                                      2400
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                                                                                      2520
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                                                                                        840
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СТСТАЛАЛА АССЛАЛАССС АЛАЛАЛАЛА ЛАЛАЛАЛАЛ Seg ID NO: 425 Protein seguence Protein Accession #: AAH10423 5 31 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE 60 QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA 120 10 DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS 240 VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL 300 GPPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL 360 FCLLVVVVVL MSRYHRRKAQ QMTQKYEBEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA 15 EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ 480 AMNHFVOENG TLRAKPTGNG IYINGRGHLV Seq ID NO: 426 DNA sequence Nucleic Acid Accession #: NM_003474.2 20 Coding sequence: 37..3036 51 CACTAACGCT CTTCCTAGTC CCCGGGCCAA CTCGGACAGT TTGCTCATTT ATTGCAACGG 60 25 TCAAGGCTGG CTTGTGCCAG AACGGCGCGC GCGCGACGCA CGCACACACA CGGGGGGAAA CTTTTTTAAA AATGAAAGGC TAGAAGAGCT CAGCGGCGGC GCGGGCCGTG CGCGAGGGCT 180 CCGGAGCTGA CTCGCCGAGG CAGGAAATCC CTCCGGTCGC GACGCCCGGC CCCGCTCGGC GCCCGCTGG GATGGTGCAG CGCTCGCCGC CGGGCCCGAG AGCTGCTGCA CTGAAGGCCG 240 GCGACGATGG CAGCGCGCCC GCTGCCCGTG TCCCCCGCCC GCGCCCTCCT GCTCGCCCTG 360 30 GCCGGTGCTC TGCTCGCGCC CTGCGAGGCC CGAGGGGTGA GCTTATGGAA CGAAGGAAGA GCTGATGAAG TTGTCAGTGC CTCTGTTCGG AGTGGGGACC TCTGGATCCC AGTGAAGAGC 420 480 TTCGACTCCA AGAATCATCC AGAAGTGCTG AATATTCGAC TACAACGGGA AAGCAAAGAA 540 CTGATCATAA ATCTGGAAAG AAATGAAGGT CTCATTGCCA GCAGTTTCAC GGAAACCCAC TATCTGCAAG ACGGTACTGA TGTCTCCCTC GCTCGAAATT ACACGGTAAT TCTGGGTCAC 600 660 35 TGTTACTACC ATGGACATGT ACGGGGATAT TCTGATTCAG CAGTCAGTCT CAGCACGTGT 720 TCTGGTCTCA GGGGACTTAT TGTGTTTGAA AATGAAAGCT ATGTCTTAGA ACCAATGAAA 780 AGTGCAACCA ACAGATACAA ACTCTTCCCA GCGAAGAAGC TGAAAAGCGT CCGGGGATCA
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0,5	CAGCTCATTI	. BIGHCHACHI	· TOUTHION	TGTGAGACCI	TTAGCATTGC	AGGCCAAACC	9540
	CAACCACTG	. WOODWOOD	. TICHCIGCI	AACCATATCT	GCTACCCACA	ACACCTCATT	9600
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WO 02/086443
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                                                                                         600
        ILCLIIEALF WKQIKKSQTS HTRRICMVNI ALSLLIADVW FIVGATVDTT VNPSGVCTAA
                                                                                         660
        VFFTHFFYLS LFFWMLMLGI LLAYRIILVF HHMAQHLMMA VGFCLGYGCP LIISVITIAV
                                                                                         720
        TOPSNTYKRK DYCWLNWSNG SKPLLAFVVP ALAIVAVNFV VVLLVLTKLW RPTVGERLSR
                                                                                         780
        DDKATIIRVG KSLLILTPLL GLTWGPGIGT IVDSQNLAWH VIFALLNAFQ GFFILCFGIL
                                                                                         840
50
        LDSKLRQLLF NKLSALSSWK QTEKQNSSDL SAKPKFSKPF NPLQNKGHYA FSHTGDSSDN
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        GGGCATGCAG CCATCGGGGA AAATCCATAG TGCAGATAAA GCAAGGAGGA AGAAGAAGGA
                                                                                          60
        CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAAGAAGG
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        CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTTGGT
                                                                                         180
        TTGGTTTGAA AGCATACAGT AAATATGATG TCTGTCCCTG GCAGTGTTGG CAGAGTAGGA
                                                                                         240
        AGGAGGAAGG GAGCAAGAG ATAATATCAT TITCTCTGTG CTCCAACTGT ACTTACATAT
GAGACTATIT CCCTCTCTGC TITTCAAACC TTACTGGAGT TGTTTTCCCT CATGAAAACC
                                                                                         300
65
        AAGAAAGGAA AGCTAGTTAG TCTTGTTCTG AGGTTGTTCA ATGTATACAT ATCTATATCT
                                                                                         420
        GTAGACAGAA TCCTTGGGAA TACAGTAATT GACATATATT CTGTTATTTG ATGCTTGAAA
                                                                                         480
        ARTCICCTCC ACTRACCAGT TTCCCTATAG ATTGCCACAA GCACATAATA AGAAACAATA
AATAAAATGT TCTCTTGACT TTGTTACTTA ACAATGCTGA GAAAACTTTA CAGCCTTCAT
                                                                                         600
        AAGGAAGTGA GGTCCAGGAA AATCTAGGAG ATATTTCTTA ACCAATCTAT AAAGGCATTA
                                                                                         660
        GTAATGACAG GATATTTCCT GAAAGTGTAA TTTCCCATTG AGGATTTGTT TITAATTTCT
GGATTCCTGG AGCCAATGAA GTTGGTGTAT GTTTATGAAA TATCAAGAGA CATAAGTTGG
70
                                                                                         720
        CAAGTGTTCA TATGCAAAAA CTTCTTGGAA TTTCTGAGTT CTCTGTGGCA ATATATGACA
                                                                                         840
        TCAGGATATG TCCAGTCTCA CACACCAGGA TATGTCCTTT CTAGCCTGTC TATCACATGC
                                                                                         900
        TAGGAGAACT ATTTAGGAAC AGAAAAAAAT GCCTGAAATG ATTTCTCATT TGAACTCATC
                                                                                         960
        CAAGCTTTCT CTAAATTTAA GCAAACTCCT GGTCATTTTC AGTTAGTACC TTTCCTTAAG
75
                                                                                        1020
        TTCAACCTTC AGGGCAAACC TCCGTGCCTC AGACGTTTAG CCATAGTCTG AAATTCTCTT
                                                                                        1080
        CCATAGATTG GTCCCCTGTA ACCCCGGTTT GTCTCAGCTT GTTATCCTGT TTTTTTCTTC
                                                                                        1140
         CCTCCATTCC CAGGATGAGC TTGTTGCTTC TGTCCTATGA GACATTAGAT TCCTTTTCTT
        TGGTACCCGA GTAAATCCAT CCTACTCCAA TAGAGGAAGG TCCATTTTG TCTTATAGCG
                                                                                        1260
80
         CTGGATGCAG ACTCAGCTGA GAAGACCATT ATTCATTTTT GGAATTCTTT ATCTCAGATA
                                                                                        1320
         TITECTICITE TITETTITE TICTATETIT GGATTITIAG TECATERACG CECCATTAGT
                                                                                        1380
        CTATTCCCCG ACTICAATCA GGGAACTTAT ACCTCTTAAA CTCATTCAGA GACTCAAAAC
                                                                                        1440
        ATATATATTO ATACAGGAGA CCTAAGAAGA GCATGTCTTG GGGGTTGAGG AAACAGGCAG
GTGAGAAATT TCCAGATTGG AAACACAGCT TCCTTTCTCC CATCCAGCCC CTACTTTCAG
CCTATGTGTT TCTGGCACCT TGTTGTAGAT AAATCTCCCT TGACTTTGTG ATGTGCTGAG
                                                                                        1500
                                                                                        1560
85
                                                                                        1620
         AAAACAAACT CACGGCTGGT GTTAAAAAGG GCCCATGACA ATACCAAGTG TTGGGGAGAA
                                                                                        1680
         TGTGGAGAAA TCAGAACTCT ATTCACGGTC GGTTGGAATG CACACTTGTG CAGAATTCTA
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	WO 02/0	186443					
	TGGAGAAGAG	TCTGGCATTT	CCTCAAAATG	TTAACCTGGA	TTTACCATAT	GACCCAGCGA	1800
	TTTCATTCAT	AGGTTTATAC	TCAAAAGAAA	TGAAGAAATA	TGCCATGCAA	AAAAATGTAC	1860
	ATGAAAGGTC	ACAACATCAT	TATTCATAAT	AGTAAAAGGA	TGGAAACAAC	ACAAATGTCC	1920
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5	AAAAGGAATG	ATGTACTGAT	CCATGCAATG	ATGTGGACAA	ACCATGAAAA	TAACACTAGA	2040
	TTAAAGAAGC	CAGTCACAAA	AGGACTTACT	GTATGATTCC	ATTTACCTGA	AATGTTTGGA	2160 2160
	ATAGGCAAAT	CCATAGAAAC	AGGAGGTAGA	TTCCTGGTTT	TOTAL DESCRIPTION OF THE PROPERTY OF THE PROPE	ACATCATGAT	2220
	AGAATGAAGT GATGATAGCA	ACAAGATTTC	TTTTGGAGGT	AGTGAAATTG	TIGIGGAAIG	CARTCAIGAI	2280
10	GATGATAGCA	ATATGTTAAT	MAIAIMAIMA	TCCSCSSSSC	ABACAGCCCC	CCACTCTGGT	2340
10	TOTCAGGGAG	ATATTGGATT	AAAAAAAAAA	GGACAACAAC	CCCTCTCCCT	GGCCACAGAC	2400
	ATTCTTCAGA	TTACAAGATA	TTCCAGGGGA	AACACTGGAA	TGAGTCTGAA	GCCAGGTGCT	2460
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15	CCTCTTCTCA	GTGTCAGCCT	GTTAACTCAA	TGTGTTAGTC	TGTTTTCATG	CTGCTGATAA	2640
	AAACATACCT	GAGACTGGCA	AGAAAAAGAG	GTTTAATTGG	GCTTAGAGTT	CCACGIGATT	2700 2760
	GGGGAGGCCT	CAGAATCACA AGAAGCAAAA	GTAGGAGGCA	AAAGTTATTC	CATCCCATCT	CCTCACCCTT	2820
	AAGATGAGGA	AGAAGCAAAA	CARGARACCC	ACCECCCCC	ATCATTCAAT	TACCTCTACC	2880
20	TCCCTCCCTC	CAATAACATG	TOTALAGAMA	GGTAGATACA	ATTCAAGTTG	AGATTTGGGT	2940
20	GGGAACACAG	CCAAACCATA	TCACTCAGCA	AGGCAGATAA	CTTTCTCACT	GAGCCTATGC	3000
	AACAGAAAAC	CATCTGGGAT	GGTTGTAAGG	GGCACAGGAA	GTGACTGGTA	GGATCACTGC	3060
	CARACCTCAG	CACTCAGGAG	AAGGCAATAG	AATCCTATTC	TCCATAGTAT	GCTATAAGAT	3120
~ ~	ACTGAAGTAC	ACTTCTTCAC	TATCTCTTTG	GACTTAGAAT	TAGCACTACA	TTCCTTGTTA	3180
25	TACAGAAAAA	TTACTAAGGA	AATTCATAGG	ATGACAAAAA	CTTTCAGAAC	TGAAAAACAG	3240
	GAAATGTAAG	CTTTTTAGTT	CTTTGGTATT	CGAAGTATGC	CTAAAAGACA	CACCECCACA	3300 3360
	CAAGAAAAGA	ATGGTGGGGT GGGATGGAGT	TTTTGTTTGT	TIGGITTIGI	TITIGITIA	A A CHTATTCT	3420
	AGAATACAAA	AGAAAGGCAC	CTACATCTAT	TTCDCDTCDG	CCGGTGACTG	CTGACTTGCA	3480
30	Telephoraphoraphoraphoraphoraphoraphoraphora	TTCCCTATAG	ATTAAAAAGG	AGGTACAATG	GTAGAACTGT	AATCCTGTCC	3540
50	ተተግየያተርልጥልል	ATTTTCATAT	TCATAAAGGT	GAGTGTTAGC	CCGCTTGTGA	AATCTGAAGT	3600
	TOACTAACTT	CABATACTAA	CCACAGAGGG	AAAGGCAGCA	AGAGGAGAGG	CATAAATTTA	3660
	CCATCTCACC	CTTCATTCCA	CAGACACACA	CAGCCTCTCT	GCCCACCTCT	GCTTCCTCTA	3720
0.5	GGAACACAGG	TAAGAGCTTC	AAGCCTCTCC	AGCTTAATAA	CATGAATTAT	TTTTGAGAAT	3780
35	AATAATGATA	CTGTGTTCTA	TATCATGCAT	CTCCTGCATT	CTGTCTGATT	ATATTTTACT	3840 3900
	TATTCTGCCA	GAGCAAAATT	AAAATACCTA	CCAACACACA	CCCACACTCC	CTTGCAGCCA	3960
	CTTAGTTCCA	AGTAAACCAA	CACCCACCITIA	TCTTAACAGC	TGGTTGGATG	TGATCCACAG	4020
	AGGTCTCCTG	TTAGCATTCA	TTGTAAAGCC	ATCCTACCTA	GCTCTAGTGT	AACCAGCAAT	4080
40	GRANGARAGA	TARAGAGGGT	CGATTACTTA	TTTACAATAG	TCTTTAAAAA	CGTAGTTTTG	4140
	<b>ጥል አርርርርምምርም</b>	AATTAGGACA	TTAATATATT	TAATATATGC	ACATTGTAGA	AAGATTGAAG	4200
	CGTTAAAAAT	AAGAGAAAAA	CTTTAAATGT	CAAAATCTCA	CAACCCAGAT	ATATCATTTC	4260 4320
	TTTAAGAAAA	TTGTACTACA	AAATACCATT	CCATTTATTA	AAGICATICI	GACAGGAATC TCAGTGAAGC	4380
45	TGATGCTTTT	CCAGGAGTTC	ATCTCTTCCA	ACAGTTCAGA	AAATCAAAAG	AGAACAACAT	4440
75	CTTCTATTCC	CCTATCAGCA	TCACATCAGC	ATTAGGGATG	GTCCTCTTAG	GAGCCAAAGA	4500
	CANCACTGCA	ATTAGANGA	GCAAGGTAGC	TATCAGCATC	ATTACGTTGT	CCTGTTGCAG	4560
	فالمالمال للململطة	GTTCCGTCGG	CTAGCACGCA	GATGGTAATA	GATGTGGTGG	TCTGATGGGT	4620
50	AGCACAGGGG	GCTGTGCAGG	AATTCCCATA	ACTGTGAGAC	CACTGACTTA	AACAGATCIT	4680 4740
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	CACAGAGAAC	TCCCTGAACA	CCTCATACTT	TANACCTGGA	ACTTCACAAA	AACTAAGAAA	4860
	አርርርርርልርጥጥ	TACCCAAAAT	CTTGGACACA	AAGATTGAGA	CATACAGAGT	GGGTTGGCAT	4920
	<b>ササビ及すびほごとと</b>	ATTATTATTA	TTCCTCATTT	CTGCGTTACT	AAAAGACAGI	CAGCACTGTA	4980
55	CCTCAGAGCA	TAGGTCTGGA	TCAGGATAGG	CTGGGTTCAG	ACTCCAGCTI	TGCTCTTCAC	5040
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	GCCTTGCCCA	TAAAAGTCAT	AATAAATGTT	ATTATTATTA	TAAAGTAGCT	ATAATTATAC ATTCAGAGGA	5220 5280
60	TAATCATAAT	AATGTGAAAA	AGTTTAATT	ATCATIGAGI	TATATATATAT	TGGTTTAGAG	5340
UU	ATAAGCACAA CCTTD ATACT	GCAAAATGCT	TTGCTGGAAG	GTAGAAAGTT	CTAGATTTAA	ACAGGCTTAG	5400
	CTTCAAAACT	TGGCACTTCT	AATTTATGTC	TCTATAAACA	GGGTTTTTTT	CCCCATTCTC	5460
	ጥርአርርሚጥጥርጥ	ጥሬፕሃሬጥሞሮልሞሮ	TGAATTGAAC	TAAAGACTTA	GAGTTACCCA	TGTAAAGTCC	5520
<i>CE</i>	ጥጥአርያርር አጥርያር	ATATIOTOTO	CACTCTTCTT	' ACGTGCAGAG	AATGACCAT	DAAADDADTA	5580
65	AGCCACAGAT	CAGTCAATGT	GTCCTACAAG	ATAATAGCAC	CAACAGGTAT	AACAGGGCTT	5640 5700
	CCTGGCATAA	TCTATTTAAA	ATATCCAACC	* TICAACATAC	TUGIATUCI	GATGACTGTT A AGCTAAACCT	5760
	AGAAGIGAAA	ACCARCARCE	ACA A A ATOTA	CTCCTAGAGI	GCGCTGCAT	TTTAGTTCAG	
	ARCAGRARAG	<b>ልተተናረርልርተልር</b>	GTTAGAGCAA	GAAGAATTTT	CTGGAAGAAG	; TCAAATATAA	5880
70	<b>プローアンシャンコン</b>	TTATIONALD	TGAGGTGAAA	TACACCAATT	ATCAGGGAA?	PAACATCAAAG	5940
	GTCCTCAATG	AGACTACCAG	CATTTAGGGA	CTGATCTAAC	AGAÇTTAGC	A TGGGTTTAGT	6000
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75	ATATGAGCTG	AAGATCGCCA	ACAAGCTCTT	CGGAGAAAAG	ACGTATCAA	TTTTACAGGT	6180 6240
75	AATTTCACCT	ANCONACCO	CATTICATTI	GCATCCTGAT	GTGGAGAGAGC	CTGAGTGGCC A TTTACTCAGA	
	ARATGGAAGA GEGCETERGC	TOCKTOTOCA	CAIGAGCCIC	CCACTGGAGT	GTCCCAGAC	CCAACGATAC	6360
	ATCACTGAAG	ATTTACHMENT !	CCCATAATCT	<b>TGTGATAAA</b>	GAGGAGGTT	3 TGTAATAGAG	6420
	TODOTABOAG	TAATAAGTAA	TAAGATACC	TCGATAAACT	GGCACTGAC	r cagtcacata	6480
80	CGATACATCT	TGGTGGGAAA	TGTATGACTA	ATGGGATATI	ATTGGAATG	G GCAGGCTTGG	6540
	GTGAGTTCCT	GAGAATAGTT	GAGGAAGTAG	CAGGAAATAI	TGAATGCAC	a ggatgaaaga	6600
	CAAAAACAAA	GATCAGAAAC	ATCATGGTT	AAATTACTGG	AGAGAAGTC	I GAGAAGCAAT	6660 6720
	GAATCTCCTT	CAGGGAAGCC	TGCTCTGCAC	ACCTCTTTC	TGTGCCICI	r ctgcttctgc c cacattcccc	6780
85	ተመተፈረገር ያብዛንን	ገል፡ንፐልጉልተግጉ ፤	ACCTGTATA	<b>LAAATATCCAT</b>	GGACAGGAG	A TACTGCATCT	6840
	ስጥንያንያ <i>ል</i> ግጥል	CONTRACTOR	TTACTGTTG	DAATAAADAT 1	TAAGTTTGG	T AATATATAGT	6900
	TACATAAATI	ACTOCTAATT	CCTACTTCT	CCTTCATATO	TCAAAGGAA	T ATTTAGATGC	6960

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	CATCAAGAAA		CC3 CTCTCC3	አጥርጥ አርጥር <b>አ</b> ጥ	TTTCCAAATC	CTCCAGAAGA	7020
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	GAACAGGTGT	ACCITIONON	ANCCIAIGCC	TODOROTOR	GAAGAGGGCA	CTCCAGATGA	7200
5	AGGATTTGTC	CARATCARA	TCARCACACC	CTACCCCACC	CAAGGAGGAA	ATCACAGGAA	7260
J	GCCAATTAGA	TOTALOGIA	TCTCCAGAGA	TATTTGCTTA	TGGCCCTGCA	TGACAATAGC	7320
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	AGACTCAAAT	TTTTATCATC	TAATTTATA	AGAAAACATT	AGAAAGCGTC	TCTCGTCTCC	7440
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10	CTGCCTGGAT	CACATCTGTA	GCCAATGTGT	TCTGCAGGGA	TTATCACAGC	TCTCTTCCCC	7560
10	እጥሮ እ አርርርር C እ	ANGAGOTTGA	CARAGTCTCC	ATTCTACAGA	CATCTTTCTT	ACCTCCCACC	7620
	TCTCATTACA	CCCCAAACTT	ACAGCAACTC	AACATGAGAG	TGAATAGGAA	GATACCCCCG	7680
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	CTAAAATGCA	ATCAGGGCCT	CCTTCCTCTG	AATGGGGACC	CCGTAGTTAA	AAAAAATAA	7800
15	ANGTAGGAAG	ACGAGGGAGG	GAGAAAGGAA	AGACACATGT	TGGAAGAGTA	GACAAAATCA	7860
10	ርምምክምርልርም	ATTCCAAATC	AGATGATTGG	AGACATTCAT	ACACAGAGAA	CGTGAACTCC	7920
	<b>ጥተርሞታልጥር አ</b>	CAAGAAGTGA	TGTCTCCATC	AAGGGTAACT	TTATACGACT	GGAGCCTTGA	7980
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25	ተጠረፈተማሌ ያለርነት	CACALALAM	GTTGTTTTAC	TCTTATAACT	TTATTTAGTT	AGGAATACCT	8460
	GAAAACTAT	TGTTTCTAAC	TCATGGAATT	CCTGGGTTAT	TTCTTAGAAG	AAGAAGGATG	8520
	<b>ባኒርጥፕኒርጥ</b> ልጥር	TCAATAATAT	TATCTTTTT	GTCTTGTGTT	TCACGTGTTA	TTTGTTGGAC	8580
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••	TTAATTTTGC	CTTGCTGGAG	GATGTACAGG	CCAAGGTCCT	GGAAATACCA	TACAAAGGCA	8700
30	AAGATCTAAG	CATGATTGTG	CTGCTGCCAA	atgaaatcga	TGGTCTGCAG	AAGGTAAGAA	8760
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	CAAGGTAAAA	GCTTATGACC	GAGTTGCCTC	AAAATGATGA	AAAATTCTAA	ATGAGGAATG	8880
	ATGACTCACC	TTCATATTAC	AAATATTTGA	GCATAGGGCC	TGACACAAAC	TGAAAGCTTA	8940 9000
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	MANAMATATO MANAMATATO	ACACTTCATT	GTGTACAAAA	TAATGTAATC	ATATTTTACA	TGTGTATCAT	9540
	ስርስርምምርም <b>ስ</b> ጥ	DCDTDCDTDT	GTACACATAT	ACATATACGT	AAAAACATGA	TTCTGTTTTT	9600
45	カクカサカクカザグサ	ΑΤΑΤΑΓΑΤΑΤ	ACACATATAA	CCCAATGTAT	TTATATATTC	AGGACTCATA	9660
	ጥልምንን ለጥጥጥ	TRADATABATA	ATCTCTATTA	AAGTGAACCT	TCTGTATTTC	ACATTTATIG	9720
				CROWCOWN AC	<b>CTCTATTAGA</b>	GATCGACAGT	9780
	CCAAAATAAC	GAATCTCCAC	ATAGTCAATT	CHILGIIANG	GIGINIINGN		3.00
	ምክረም/ርክሞልሞር	GAATCTCCAC AGTTTCTTTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ATAGCTTGAA	GAGAAACTCA	CTGCTGAGAA	9840
	TAGTCATATC	AGTTTCTTTT	TTCCATTTGT	ATAGCTTGAA GAGAGAGACA	GAGAAACTCA TGTGTCGATT	TACACTTACC	9840 9900
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50	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC	AGTTTCTTTT TGGACAAGTT ATGGAAGAGA AATGGGGATG CTACACAAGG	TTCCATTIGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA	ATAGCTTGAA GAGAGAGACA CAAGGACACG AGGCATGACC GGTCACTGAG ATCTCCTTCA	GAGAAACTCA TGTGTCGATT TTGAGAACCA TGGAGCCACG GAGGGAGTGG ACTAATGAAG	TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG	9840 9900 9960 10020 10080 10140
	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT	AGTTTCTTTT TGGACAAGTT ATGGAAGAGA AATGGGGATG CTACACAAGG GTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA	ATAGCTTGAA GAGAGAGACA CAAGGACACG AGGCATGACC GGTCACTGAG ATCTCCTTCA AAATAAGACC	GAGAAACTCA TGTGTCGATT TTGAGAACCA TGGAGCCACG GAGGGAGTGG ACTAATGAAG AACAGCATCC	TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG	9840 9900 9960 10020 10080 10140 10200
50 55	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT	AGTTTCTTTT TGGACAAGTT ATGGACAGAGA AATGGGGATG CTACACAAGG GTAGTAGTAGT TCCCTATTCT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT	ATAGCTTGAA GAGAGACAC CAAGGACACG AGGCATGACC GGTCACTGAG ATCTCCTTCA AAATAAGACC CTGTCACTCCC	GAGAAACTCA TGTGTCGATT TTGAGAACCA TGGAGCCACG GAGGGAGTGG ACTAATGAAG AACAGCATCC ATTTAGAAAAA	TACACTTACC TEGGAATEST GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA	9840 9900 9960 10020 10080 10140 10200 10260
	TAGTCATATC ATTGATGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA	AGTTTCTTTT TGGACAAGTT ATGGACAGA AATGGGATG CTACACAAGG GTAGTAGTAG TTCCTATTCT TCCCCATAGA	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTTGCAA	ATAGCTTGAA GAGAGAGACA CAAGGACACG AGGCATGACC GGTCACTGAG ATCTCCTTCA AAATAAGACC CTGTCACTCC CAACAGATTC	GAGAAACTCA TGTGTCGATT TTGAGAACCA TGGAGCCACG GAGGGAGTGG ACTAATGAAG AACAGCATCC ATTTAGAAAA TCTTGGCTCA	TACACTTACC TAGACATTACC TAGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTTCTTTT	9840 9900 9960 10020 10080 10140 10200 10260 10320
	TAGTCATATC ATTGATGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGTTCTTCA	AGTTTCTTTT TGGACAAGTT ATGGACAGGTA AATGGGGATG CTACACAAGG GTAGTAGTAGT TCCTATTCT TCCCCATAGA GGTAAACTGA TTIGATGATGA	TTCCATTIGI TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCA TTGCTGCACAT TAGTCATCAT	ATAGCTTGAA GAGAGACA CAAGGACACG AGGCATGACC GGTCACTGAG ATCTCCTTCA AAATAAGACC CTGTCACTCC CAACAGATTC CAACAGATTC	GAGAAACTCA TGTGCGATT TTGAGAACCA TGGAGCCACG GAGGGAGTGG ACTAATGAAG AACTAGAAAA TCTTGGCTCA ATGATAAAAA ATGATGAAAAA	TACACTTACC TAGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTTCTTTT TAGCATGCCT	9840 9900 9960 10020 10080 10140 10200 10260 10320 10380
	TAGTCATATC ATTGATGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTGTTCT CTATCTCATC	AGTTCTTTT TGGACAAGTT TAGGACAGAT AATGGGGATG CTACACAAGG GTAGTAGTAG TTCCTATTCT TCCCCATAGA GGTAAACTGA TTGATGATGATGATGAT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT TAGTCATCAT GCCCACATAT	ATAGCTTGAA GAGAGAGACA CAAGGACACG AGCATGACC GGTCACTGAG ATCTCCTTCA ANATAAGACC CTGTCACTCC CAACAGATTTC CAAGAATTTA AAATGTACTT	GAGARACTCA TGTGTCGATT TTGGAGACCA TGGAGCCACG GAGGGAGTGG ACTAATGAAG ACTAATGAAAA TCTTGGCTCA ATGATTAAAA TTCCTTCCAG	TACACTTACC TAGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATAGG TGTTCACCTA TATTTCTTTT TAGCATGCT AAAAATTTCC	9840 9900 9960 10020 10080 10140 10200 10260 10320 10380 10440
55	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGT TGGCACCGCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTATCTCATC TTCTCTCTTTT	AGTTTCTTTT TGGACAAGTT ATGGAAGAG AATGGGATG CTACACAAGG GTAGTAGTAG TTCCTATTCT TCCCCATAGA GGTAAACTGA TTGATGATGA CTCTTAATAA	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT GCCCACATAT TAGATGAA	ATAGCTTGAA GAGAGAGACA CAAGGACACG AGGCATGACC GGTCACTGAG ATCTCCTTCA AAATAAGACC CTGTCACTCC CAACAGATTC CAAGAATTTA AAATGTACTT TCATTTAATA	GAGARACTCA TGTGCGATT TTGGAGACCA TGGAGCCACG GAGGGAGTGG ACTAATGAAG AACAGCATCC ATTTAGAAAA TCTTGGCTCA ATGATTAAAAA TTCCTTCCAG CCGTGTCTTC	TACACTTACC TAGGAATGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTTCTTTT TAGCATGCCT AAAAATTTCC TAAAATTTGAA	9840 9900 9960 10020 10080 10140 10200 10320 10320 10380 10440 10500
	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TAATCACCCT CAGATTCTCA GAGGTGTTCT CTATCTCATC CTATCTCATC CTTCTCTCTTT CTTCAGGGAAA TATAAATCT	AGTTCTTTT TGGACAAGTT ATGGAAGAGA AATGGGGATG CTACACAAGG GTAGTAGTACT TCCCCATAGA GGTAAACTGA TTGATAGTAGATGA CTCTTAATAA AATGTCCAAG	TTCCATTTGT TGCAGACTTC CAGACCTCTC CAGACCTCTC CCTTTGTGGA TCCAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT GCCCACATAT ATAAGATGAA ATGTTAAAATTAAA TGTTTTAAAT	ATAGCTTGAA GAGAGACA GAGCATGAC AGGCATGAC GGTCACTGAG AAATAAGACC CTGTCACTCC CAACAGATTC CAACAGATTTA AAATGTACTT TCATTTAATA AAATGTACTT TCATTTAATA AAACGAACC	GAGARACTCA TGGAGCCAC TGGAGCCACG GAGGGAGTGG ACTAATGAAG ACTACTCACACAC ATTTAGAAAA TCTTGGCTCA ATGATAAAA TCCTTCCAG CAGTGTCTCAG AAATCATACT	TAGCATTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTCTTTT TAGCATGCCT AAAATTTGCA TTCTCTTCAATTCCA TTCTCTTCAATTCCA	9840 9900 9960 10020 10080 10140 10200 10320 10380 10440 10500 10560
55	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTATCTCATC CTTCTCTCTTT CTTGAGGAAA ATATAATCCA	AGTTCTTTT TGGACAAGTT ATGGAGAGA AATGGGGATG CTACACAAGG GTAGTAGTACT TCCCCATAGA GGTAAACTGA TTGATGATGA CTCTAATAAA AATGTCCAAG GTTTCTTAATAA CCTACAAGA	TTCCATTTGT TGCAGACTTT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TGCTGGCAA TAGTCATCAT ATAAGATCAT ATAAGATGAT ATAAGATGAA TGTTTTAAAT LCATTTTAATT	ATAGCTTGAA GAGAGAGACA GAGCATGACC AGGCATGACC GGTCACTGAG ATCTCCTTCA ANATAAGACC CAACAATTC CAACAATTTA ANATGTACTT TCATTTAATA GAACCAAACC GAATTTAAGACC GAATTTAAGACC GAATTTAAGACC GAATTTAAGACC GAATTTAAGACC GAATTTAAGACC GAATTTAAGAC	GAGARACTCA TGGAGCACT TTGGAGACCA TGGAGCCACG GAGGGAGTGG ACTANTGAACA ACTATTAGAAAA TCTTGGCTCA ATGATTAAAA TTCCTTCCAG CCGTGTCTTC AAATCATACT AAATCATACT GATACCTAAA	TACACTTACA TAGAATGAT GTCTCTAGT AGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTTCTTTT TAGCATGCCT AAAATTTCC TAAAATTTCA TCTTCTCAA TCCTTCTAA	9840 9900 9960 10020 10080 10140 10200 10320 10380 10440 10500 10560 10620
55	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTATCTCATC TCTCTCTCTT CTTGAGGAAA ATATAATTCT ATTTAGCAAC	AGTTTCTTTT TGGACAGGT ATGGAGAGA AATGGGATG CTACACAAG GTAGTAGTAGT TCCCCATAGA GGTAAACTGA TTGATGATGATGATGATGATGATGATGATGATGATGATGA	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ACATTACT TATAAGATGAA TGTTTTAAAT ACATTTCTTT TATAABACAC	ATAGCTTGAA AGAGGACAC AGGCATGACC AGGCATGAC ATCTCCTTCA ANATAAGACC CAACAGATTC CAAGAATTCA ANATGTACTT TCATTTAATA GAACCAAACC GAATTTCAAT ATTCAATA ATTCAATA ATTCAATA ATTCAATA ATTCAATA	GAGARACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT GGAGCGAGTGG ACTANTGAAG ACAGCATCC ATTTAGAAAA TCCTTCCAG CCGTGTCTTC AAATCATACT GATACCATAA AAATAATGAC	TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCATCG TGTTCACCTA TATTCTTTT TAGCATGCCT AAAAATTTCC TAAAATTTCA TCTCTTCAA TCTCTTTAA TCTCTTTAA TCTCTTTAA TCTTCTTTAA	9840 9900 9960 10020 10080 10140 10260 10320 10380 10440 10560 10660
55	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTATCTCATC TTCTCTCTTT CTTGAGGAAA ATATAATTCT ATTTAGCAAC GTTTCTAAACT TTTTTTAGCTAACT TTTTTTAGCTAACT TTTTTTAGCTTTAAATT TTTTTTTTTT	AGTTCTTTT TGGACAGGT ATGGAGAGA AATGGGGATG CTACACAGG GTAGTAGTAG TTCCTATTCT TCCCATAGA TTGATAGATAG TTGATAGATAG TTGATAGATA	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CATTTGTGGA TCCAATTAGT TTCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA ATAAGATGAA ATAAGATGAA TGTTTTAAAAT CCTCTAGAAAAG	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATCTCCTTCA AAATAAGACC CTGTCACTCC CAACAGATTC CAAGAATTTA AAATGTACTT TCATTTAATA GAACCAAACC GAATTTAGGT ATCATCAGTA	GAGARACTCA TGGAGCCAC TGGAGCCACG GAGGGAGTGG ACTANTGAAG ACAGCATCC ATTTAGAAAA TCTTGGCTCA ATGATTAAAA TTCCTTCCAG CCGTGTCTTC AAATCATACT GATACCTAAA CAGTTACACA CAGTTACACACA CAGTTACACACA	TACACTTACC TAGGAATGAT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATAGG TGTTCACCTT TAGCATGCCT AAAAATTTCC TAAAATTTCA TCTCTCTCAA TCCTTCTAA TCCTTCTTAA TTAGAAATCAT TAGAAAAGAT	9840 9900 9960 10020 10080 10140 10200 10320 10380 10440 10500 10560 10620 10680 10740
55 60	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TAATCACCCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTATCTCATC TTCTCTCTTT CTTGAGGAAA ATATAATTCT ATTTAGCAAC GTTTCTAACT TTTTTGCTTAA TTTTTGCTTAA	AGTTCTTTT TGGACAGGT ATGGAGAGA AATGGGGATG CTACACAAGG GTAGTAGTACT TCCCCATAGA GTAAACTGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC CCTGTTTTCT TCTGTATTC TTTTTTTTTT	TTCCATTTGT TGCAGACTTC CAGACCTCTC CAGACCTCTC CAGACTTATGGCA TCCAATTATC TCATAAGGCA TGCCATTAGT TTGCTGCAA TAGTCATCAT ATAAGATGAA ATATTTTAAA TGTTTTAAAT TATAAAACAC CTCTGGAAAG ATATTAAAA	ATAGCTTGAA GAGAGACA GAGCATGACC GGTCACTGAG ATCTCCTTCA ANATANGACC CAACAGATTC CAACAGATTTA ANATGTACTT TCATTTAATA AAATGTACTT GAACAACC GAATTTAGGT ATCATCATAATA GGCAAACTC GAAATTTAGTA GGCAAACTC GAAATTTAGTA ATGGGT ATCATCAATA GGCAAACTC GAAATTTAA	GAGARACTCA TGGAGCCAC TGGAGCCACG GAGGGAGTGG ACTAATGAAA ACTTGGCTCA ATTTAGAAAA TCTTGGCTCA CCGTGTCTT GATACCACA AAATCATACT GATACCTAAA AAATAATGAC CAGTTACCA AAATCATACA AAATTACACAC AACAGAGTAG	TACACTTACC TAGGAATGAT GTCTCTCAGT AGCTGCAGC AGTTCTGTTG TCTTCTATGG TCTTCACCTA TATTCTTTT TAGCATGCCT AAAATTTCC TAAAATTTCA TCCTTCTAA TCCTTCTAA TCCTTCTAA TCCTTCTAA TCCTTCTAA TAGAAAGAT TAGGAAAGAT TTCATGAATGAT TTCATGAATGAT TTCATGATGA	9840 9900 9960 10020 10080 10140 10200 10320 10380 10440 10500 10560 10680 10680 10740
55	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTTATCTCATC TCTCTCTCTTT CTTGAGGAAA ATATAATCT ATTTTGCAAC GTTTCTAAC AATTTAAGGAA	AGTTTCTTTT TGGACAGGT TATGGAGAGA AATGGGATG CTACACAAG GTAGTAGTAGT TCCTATTCT TCCCCATAGA GGTAAACTGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC CTTGGATTCT TATATTAATC CCTGTTTTCT CAAGCATAT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA TGTTTTAAAT ACATTTCTTT TATAAAACAC CTCTGGAAAG ATATATAAAG CTCTGGAAAG	ATAGCTTGAA AGAGGACAC GAGGACACG GGTCACTGAG ATCTCCTTCA ANATAAGACC CTAGTCACTCC CAACAGATTCA ANATGTACTT TCATTTAATA GAACCAAACC GAATTTAAGT TTCATTAAGT TTCATTAAGT GCAAGTGC GAAATTTAAGT AGCAAACC GAATTTAAGT GCAAGTGC GAAATTTAAGT GCAAGTGC GAAATTTAAGT GGCAAGTGC GAAATTAAAA AGGGAGCCTT	GAGARACTCA TGGAGCCAC TGGAGCCACG GAGGGGGGG ACTAATGAAG ACAGCATCC ATTTAGAAAA TCCTTCCAG CCGTGTCTTC AAATCATACA GATACCATAA AAATCATACA AAACAGAGTAG CAGTTACACA AACAGAGTAG GTAAACCACA	TACACTTACC TGGGAATGGT AGGTGCAGC AGTTCTGTTG TGTTCACGT TGTTCACGT TATTCTTTT TAGCATGCT AAAAATTTCT TAAAATTTCAAATTCC TAAAATTTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATATCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTC	9840 9900 9960 10020 10080 10140 10200 10260 10320 10380 10440 10500 10560 10680 10740 10800 10860
55 60	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGT TAATCACCT TAATCACCT CAGATTCTCA GAGGTGTTCT CTATCTCATC TTCTCTCTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTGCTTAAAT TTTTGCTTAAAT TTTTGGCTTAAAT TTTTGGCTTAAAT TTTTGGCTAAAT TTTTGGCTAAAT TTTTGGCTAAAT TTTTGGCTAAAT TTTTGGCTAAAT TTTTTGAGGAA GCCTGGAGTA	AGTTCTTTT TGGACAGGT ATGGAGAGA AATGGGGATG CTACACAGG GTAGTAGTAG TCCCATAGA AGGTAAACTGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC CCTGTTTCTT TATATAATC GAAGGCATAT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTAGT TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA ATAAGATGAA ATATTCTTT TATAAAAAT CCTCTGGAAAG ATATATAAAA CCCAGAAACAG ATATATAAAAC CCCAGAAACAG	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATTACCTTCA AAATAAGACC CAACAGATTC CAAGAATTTA AAATGTACTT GAACCAAACC GAATTTAGGT ATCATTAGGT ATCATCAGATTC GAAATTTAGGT ATCATCAGATT ATCATTAAGT ATCATTAAGT ATCAATA GGCAAGTGTC GAAATTTAAG GAGGGCCTT TTACAGGCTT	GAGARACTCA TGGAGCCAC TGGAGCCACG GAGGGAGTGG ACTANTGAAG ACAGCATCC ATTTAGAAAA TCTTGGCTCA ATGATTAAAA TTCCTTCCAG GCGTGTTCTCCAG GATACCTAAA AAATAATGAC CAGTTACACA AACAGAGTAG GTAAACCACA AACAGAGTAG TGATGTTGTTCACAG AACAGAGTAG TGATGGTTGTTACACA AACAGAGTAG TGATGGTTGTT	TACACTTACC TAGGAATGAT AACTTACC TAGGAATGAT AACTTACAGAT TATTATAGATTATATAGATTATATATATATATATA	9840 9900 9960 10020 10140 10200 10260 10320 10380 10440 10560 10620 10680 10740 10800 10860 10920
55 60	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGTGTTCT CTATCTCATC TTCTCTCTTT CTTGAGGAAA ATATAATTCT ATTTTAGCAAC GTTTCTAAAT TTTTGCTTAA ATTTTTGCTTAA ATTTTTGCTAAC GCCCCAGAGTAAA GCCTGGAGTA	AGTTTCTTTT TGGACAGGTT ATGGAGAGA AATGGGGATG CTACACAGGG GTAGTAGTAGT TCCCCATAGA GGTAAACTGA CTCTAATAA AATGTCCAAG GTTTTGACC CTAGAAACAC TTTGTGATTC TCTGTTTTC TATATTAATC GAAGGCATAT CTAAAAGGA CTAAAAGGA CTAAAAGGA TTAAAAGGA TATATAAATC TAAAAGGATAT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CATTAGGCA TCCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA ACATTTCTTT TATAAAATAAA	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG AATAAGACC CTGTCACTCC CAACAGATTC CAACAGATTT AAATTAATT TCATTTAATT TCATTTAATT GAACCAAACC GAATTTAGGT ATCATCATATA GGCAAGTGTC GAAATTTAATT GGCAAGTGTC GAAATTAAAT AGGGAGCCTT TTACAGGCTT TTACAGGCTT ATACAGGCTT ATACAGGCTT TTACAGGCTT ATACAGGCTT ATACAGCTT ATACAGGCTT ATACAGGCT ATACAGGCTT ATACAGGCT ATACAGAGT ATAC	GAGARACTCA TGGAGCCAC TGGAGCCACG GAGGAGTGG ACTAATGAAG ACAGCATCC ATTTAGAAAA TCTTGCATCA ATGATTAAAA TTCCTTCCAG CCGTGTCTTC AAATCATACT GATACCTAAA AAATAATGAC CAGTTACCACA AACAGAGTAG TGATGGTTGT TCTGGGTACC	TACACTTACC TGGGAATGGT GTCTCTCAGT AGCTGCAGC AGTTCTGTTG TCTTCTATGG TCTTCACTA TAGCATGCCT AAAAATTTCC TAAAATTTCA TTCCTTCTAA TTCCTTCTAA TTCTTCTTAA TTCTTCTTAA TTCTTCTTAA TTCTTCTTAA TTCATGATGA TTCATGATGA TAGGAAAGAT TTCATGATGA TAGGAACTTC TTGTCAAAGA TTTCATCAAGA CTGATATCAA	9840 9900 9960 10020 10080 10140 10200 10320 10380 10440 10500 10620 10620 10680 10740 10800 10860 10920 10980
55 60	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTATCTCATC TTCTCTCTTT CTTGAGGAAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTGCTTAA AATTTAGGAG AAATTTAGGAG CCTGGAGTAA CCTATTTATG GGGGCATAAA TGGATGGAG	AGTTCTTTT TGGACAGGT ATGGAGAGA AATGGGGATG CTACACAGG GTAGTAGTAGT TCCCCATAGA GGTAAACTGA ATTGTGATAG CTCTTAATAA AATGTCCAG GTTCTGACC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT CTAAAGGGAT ATTATCAAAG ATTATCAAAG CTAGAAGCAG CTAGAACAG CTAGAAGCAG CTAGAACAG CTA	TTCCATTTGT TGCAGACTTC CAGACCTCTC CAGACCTCTC CAGACTTAGGCA TCGAATTAGT TTGCTGGCA TAGTCATCAT ATAAGATAAT ATAAGATAAT ATATTCATTT TATAAAAAACAC CTCTGGAAAA ATATTTCTTT TATAAAACAC CTCTGGAAAA ATATTATAAAA CCTCTGGAAAA ATATATAAAA CCCAGAACAG AAGAACTCA CCACATCTAC CTGGTTACC	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATATAAGACC CTGTCACTCC CAACAGATTC CAACAGATTTA AAATGTACTT TCATTTAATA GAACCAAACC GAATTTAGGT ATCATCAATA GGCAAGTTT GAATTAGGT ATCATCAATA GAGGAGCCTT TTACAGGCTT TTACAGGCTT AAAATACAT AAATACAT ATATATAAAT	GAGAAACTCA TGGAGCCACG GAGGAGTAG ACCACACACACACACACACACACACACACACACACAC	TAGACTTACC TAGGAATGAT GTCTCTCAGT AGCTGCAGC AGTTCTGTTG TCTTCTATGG TCTTCACCTA TATTTCTTTT TAGCATGCCT AAAATTTCC TAAAATTTCA TCCTTCTAA TCCTTCTAA TCCTTCTAT ATAAAATCAT TAGGAAAGAT TTCATGATGAT TAGGAAAGAT TTCATGAAAGA TTTCAAAGAA TTTCAAAGAA TTTCAAAGAA TTTCAAAGAA TTAGAAAGAT	9840 9900 9960 10020 10140 10200 10320 10320 10380 10440 10560 10680 10740 10860 10860 10920 10980 11040
<ul><li>55</li><li>60</li><li>65</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTTCTCA GAGGTTCTCA TCTTCTCTTC	AGTTTCTTTT TGGACAGGT ATGGAGAGA AATGGGATG CTACACAAG GTAGTAGTAG TTCCTATTCT TCCCCATAGA GGTAAACTGA TTGATGATGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT CTAAAGGAT ATTATCATAT GAAAGGAACAC ATTATCATAT GAAAGGAACAC ATTATCATAT GAAAGAACAC ATTATCATAT GAAAGAACAC	TTCCATTTGT TGCAGATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA TGTTTTAAAAT ACATTTCTTT TATAAAACAC CTCTGGAAAG ATATATAAAAC CCCAGAACAG ATGATATAAAACTCA CCACATCTAG TGTGTTACC TGTGGTTACC	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATCTCCTTCA ANATAAGACC CAACAGATTTA ANATGTACT TCATTTAATA GAACCAAACC GAATTTAGAT TCATTTAATA GGCAAGTCC GAATTTAGT TTCATTAATA GGCAACCT TACACCT TTACAGCTT AAAATACAC ATATACAGCTT AAAATACAT ATATATAATA TCGGGAATT TTACAGGCTT TTACAGGCT TTACAG	GAGARACTCA TGGGGCCACG TGGGGCCACG GAGGGGGGGGG ACTANTGAAG ACAGCATCC ATTTAGAAAA TCTTGGCTCAG CCGTGTCCTG GATACCTAAA AAATAATGAC CAGTTACAAA ACAGAGTAG GTAAACCACA TGGTGCTGC TGGGCTACC TGGGCTACA AACAGAGTAG TTCTGGCTACA AACAGAGTAG TGATGGTTGT TCTGGCTACA AACAGAGTAG TGAGAAACCACA TGATGGTTGT TAGGAAACAA	TACACTTACC TGGGAATGGT AGCTGCAGT AAGCTGCAGT TGTTCATCT TGTTCATCT TATCATCT TAGCATGCT AAAAATTTC TAAAAATTTC TAAAAATTTCATATAA TTCTCTTAA TCCTTCTAA TCCTTCTAA TTAAAAATAT TAAGAAACAT TTCATGAGAA TTAGGAACAT TTCATGAGAA TTAGAGAATT TAATAGAGAAT TTAATAGAGAAT TAAAAGATAT TAAAAGATAT TAAAAGATAT TAAAAGATAT	9840 9900 9960 10020 10140 10260 10320 10380 10440 10560 10620 10680 10740 10860 10920 10980 11100
55 60	TAGTCATATC ATTGATGGAA TCGGTTCANA GAATATCTTC ATCTANAGTC TGCCACCGCT TAATCACCCT TAATCACCCT CAGATTCTCA CTATCTCATC CTTATCTCATC TCTCTCTTCT TCTTGAGGAAA ATATAATCT ATTTTAGCAAC GTTTCTAAAT TTTTGCTTAA TTTTTGCTTAA TTTTTAGGAG GCCTGGAGTA CCATTTTATG GGGGCATAAA TGGATGGAG GGGAGTAGAA AGAACACAT	AGTTTCTTTT TGGACAGGTT TAGGACAGGA AATGGGATG CTACACAGG GTAGTAGTAGT TCCCCATAGA GGTAAACTGA TTGATGATGA TTGATGATGA CTCTAATAA AATGTCCAAG GTTTCTGACC CTAGAAGACAC CTAGAAGACAC CTAGAAGACAC CTAGAAGACAC CAAGGCATAT CTAAAGGGAT ATTATCATAT AATACATAG ATGGAGAACAC ATGGAGAACAC ATGGAGACAC ATGAAGAACAC ATGGAGAACAC ATGGAGGAA ATGAAGAACAC ATGGAGGAA	TTCCATTTGT TGCAGACTTTG TGCAGACTTTC CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATTAGGCA TGCATTAGT TTGCTGGCAA TAGTCATCAT ATAGATGAT ATAGATGAA ATATTTTTAAAT ACATTTCTT TATAAAACAC CTCTGGAAAG ATATTATAAAG CCCAGAACAG AAGAACTCAG CACATCTAG CACATCTAG CGACATTCTG AGAAAGAGCC GACCTATCTG GGTTTAAATT	ATAGCTTGAA AGAGGACAC GGTCACTGAG AGCATGAC ANATAAGACC CTACTCC CTACTCAC CTACTCAC CAACAGATTC CAACAGATTC AAATGTACTT TCATTTAATA GAACCAAACC GAATTTAGGT ATACATCAAACAC GAAATTAAG GCAAGTGC TTACAGGCTT TACAGGCTT AAAATACATC ATATATAAAT TGGGGGAATT ACTGGATGAT ACTGGATGAT ACTGGATGAT ACTGGATGAT ACTGGATGAT	GAGAAACTCA TGGAGCCACG TGGAGCCACG ACTAATGAAG ACTAATGAAG ACTAATGAAAA TCCTTCGCAG CCGTGTCTTC AAATCATACA AAATCATACA AAATCATACA GATACCTAAA AAATCATACA TGGTTACACA AACAGAGTAG TGTAGGTACACA AACAGAGTAG TGATGGTTGT TCTGGCTACC TGGATACACA AACAGAGTAA AATTAAGGTA ATTAAGGAAAATCA ATTAAGGAAAATCA ATTAAAGGTA AAATCAAGGTAA	TACACTTACC TGGGAATGGT AAGCTGCACGA AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTTCTTTT TAGCATGCCT TAAATTTCCATATATATTCCATATATATATTCATTTCAAATTTCAATTCAATTCATATATATATATATATATATATATATATATATATATATAT	9840 9900 9960 10020 10140 10200 10320 10320 10380 10440 10500 10680 10740 10860 10860 10920 10980 11100 11160 11220
<ul><li>55</li><li>60</li><li>65</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TAATCACCT TAATCACCT CAGATTCTCA GAGGGTTCTCA TCTTCTCTTC	AGTTTCTTTT TGGACAGGT ATGGAGAGA AATGGGATG CTACACAAG GTAGTAGTAG TTCCTATTCT TCCCCATAGA GGTAAACTGA TTGATGATGAC CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT CTAAAGGGAT ATTACATAT GAAAGAACAG ATTGCAAG ATTACATAT CAAAGGGAT ATTACATAT CAAAGGATTCCT AAGACTTTGCT AAGACTTTCCT AAGACTTTCCT AAGACTTTCCT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CCTTTGTGGA TCGAATTAGT TTGCTGGCAA TAGTCATCAT TAGTCATCAT ACACTTATT TATAAATGAAT TATATTCTTT TATAAAACAC CTCTGGAAAG ATATATAAAA CCTCTGGAAAG CCAGAACAG AAGAAACTCA CCACATCTAG TGTGGTTACC GAAAAGGCC GACCTATCTG GTTTAAATTG GTTTAAATTG	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATCTCCTTCA ANATAAGACC CTGTCACTCC CAACAGATTTA ANATGTACT TCATTTATA GAACCAAACC GAATTTAGAT GCAAGATTAGGT TATCATCATCA GAAATTAAGA GGCAAGCTT TTACAGCTT AAAATAAAAT	GAGARACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGAGAGCACTCC ATTAGAAA TCTTTGGCTCA ATGATTAAAA TCTTCTTCCAG CCGTTTCTCCAG CCGTTTCTCCAG CCGTTCTTC AAATCATACT AAATCATACT AAACCAGAGTAG TTAGAAACACA TGATGGTTGT TCTGGCTACG TAGGAAATCA ATTAAGGAA TGGAAGAATA ATTTAAGGAA TAGATCTCAG TAGGAGAATA TGGAAGAATA TAAATCTCAG	TACACTTACC TGGGAATGGT AGGTGCAGG AGTTCTGTTG TGTTCATCGT TGTTCATCGT TATTCTTTT TAGCATGCT AAAATTTCT TAGCATGCT TATTCTTTAT TAGCATGCT TAGAATTTCAT TAGAATTTCAT TTCTTTAT TAGAAACTT TAGGAAAGAT TTCATGAAGA TTGATCAAAGA TTAGAGTAT TAATAGTTAC TAATGAGTAT TAATAGTTAC CTCTTTTAATAT AAACAGAATA	9840 9900 9960 10020 10140 10260 10320 10380 10440 10560 10620 10680 10740 10860 10920 10980 11100 11160 11280
<ul><li>55</li><li>60</li><li>65</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTT TAATCACCT TAATCACCT CAGATTCTCA GAGGTGTTCT CTATCTCATC TTCTCTCTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTGCTTAA TTTTTGCTTAA TTTTTAGTAA GCCTGGAGTA AATTTTAGAGA GCCTGGAGTAA TGGATGGAA TGGATGGAA AGAAAGACAT GAGAGAAAAA TCAAATGGAT	AGTTCTTTT TGGACAGGT ATGGAGAGA AATGGGGATG CTACACAGG GTAGTAGTAG TTCCTATTCT TCCCCATAGA AGTTCATAGAG CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC CCTGTTTCT TATATTAATC GAAGGCATAT CTAAAGGGAT ATTATCATAT GAAGGCATAT CTAAAGGGAT ATTATCATAT GAAGACTTCG TGGAGAACAC TTGGAGTGCT AAGACTTTGG TTGCCTGGCA CTCTGATTTGT CTCTGCCTGCCA CTCTGATATTTTT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTAGT TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA ATATTCTTT TATAAAACAC CCTCTGGAAAG ATATATAAACAC CCCAGAAACAG AGAAACTCA CCACATCTAG TGTGGTTACC AGAAAGAGCC GACCTATCTG GTTTAAATTT GGCACTTGAA	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATTACCTTCA AAATAAGACC CTGTCACTCC CAACAGATTC CAAGAATTTA AAATGTACTT TCATTTAATA GAACCAAACC GAATTTAGGT ATCATCAG GAAATTAGAT TTACAGCCT TTACAGCCT TACAGGACCT TTACAGGATCC ATATATAAAT CGGGAAGTGTC GAAATTAAAT TGGGGAATT TGGGGGAATT TGGGGGATGGA GTACTTGATG GATATTATAAT CATGATGAG GTACTTGATG GATATTATA	GAGARACTCA TGGAGCCAC TGGAGCCAC GAGGGAGTGG ACTANTGAAG ACAGCATCC ATTTAGAAAA ATCCTTCCAG GCGGTCTTC AAATCATACT GATACCTAAA AAATAATGAC CAGTTACCACA ACAGAGTAG TTCTGGCTACC ATGATACACACA AACAGAGTAG TAAACCACA ATGATACACACA ATGATACACACA ATTAGGAAATAA ATTTAGGAAATA TGGAAACAATA ATTAAGGTA TTTAGGATCA	TACACTTACC TAGGAATGAT AGCTGCAGT AGCTGCAGT AGCTGCAGT TATTCTTTT TAGCATGCT TAGCATGCCT AAAAATTTCC TAAAATTTCA TCCTTCTAA TCCTTCTAA TCCTTCTAA TCATGATGA TTCATGATGA TTCATGATGA TTCATGATGA TTAGGAACTTC TTGTCAAGA CTGATATCAA TTAGAGTATT TAATAGTTAC TAGAGTATT TAATAGTTAC CTTTTAATAT AAACAGAATAT ATACAGATATA TTAGAGATATA TAACAGAATAT TTTGGATAAAA TTTGGATAAAA TTAGAGTATT TAATAGTTAC TCTTTTTAATAT AAACAGAATAT TTTGGATAAAA	9840 9900 9960 10020 10140 10200 10320 10380 10440 10500 10560 10620 10680 10740 10800 10980 11040 11160 11220 11280 11340
<ul><li>55</li><li>60</li><li>65</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGTGTTCT CTATCTCATC TTCTCTCTTT CTTGAGGAAA ATATAATTCT ATTTTAGCAAC GTTTCTAAAT TTTTTGCTTAA GCCTGGAGTA ACTTTAGGAA AGGATGGAA GGGGCATAAA TGGATCGAG GGGAGTGGAA AGAAAAAA TCAAATGGAT TGAATGGAT TGAATGGAT TGAATGGAT TGAATGGAT TGAATGGAT TGAATGGAT TGAATTGAAG TGAATTGAAG TGAATTGAAG TGAATTGAAG TGAATTGAAG	AGTTTCTTTT TTGGACAGGTT ATGGAGAGA AATGGGGATG CTACACAGGG GTAGTAGTAGT TCCCCATAGA GGTAAACTGA CTCTAATAA AATGTCCAAG GTTTTGACC CTAGAAACAC TTTGGACT CCTGTTTTC TATATTAATC GAAGGCATAT CTAAAGGGAT ATTACATAG ATTGGACAG ATGGAGAACAG TTGAAACAC TTAAATTAATC GAAGGCATAT CTAAAGTACT AAGACTTTGG TTGCCTGGCA CTTGCCTGCCA CTTGCACT TTGCCTGCCA CTTGCACT CTTGC	TTCCATTTGT TGCAGACTT CAGACCTCTC CAGACCTCTC CAGACCTCTC CAGACCTCTC CATTAGGCA TCCAATTAGT TTGCTGGCAA TAGTCATCAT GCCCACATAT ATAAGATGAA ACATTTCTT TATAAAACAA ACATTTCTT TATAAAACTCAA ACAAACACA CACAACTCAG TGTGGTAAC TGTGGTAAC TGTGGTTACC AGAAAGAGCC GACCTATTG GGCACTTGAA GTGTTAAATTT GGCACTTGAA GTGTTAAATTT GGCACTTGAA GTGTAATTT GGCACTTGAA GTGTAATTTAAATTT GGCACTTGAA GTGTAATTTAA	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATTACCTTCA AAATAAGACC CAACAGATTC CAACAGATTT CAATTTAATT TCATTTAATT TCATTTAGT ATATTAGT ATCATCACAATA GGCAAGCCT GAAAATTAAAT GAGGGGGAATT TTACAGGTT TTACAGGTT TTACAGGTT TTACAGGTT TACAGGATT AAAATACATC ATATATAAAT ACTGGATGGA GTACTTGATG GATATTAGT ATATATAGT ATATATAGT ATATATAGT ATATATAGT GATACTTGATGG GATATTAGT ATATATAGT ATATATAGT GATACTAGG GATATTAGGC GATATTAGT ATATATAGT ATATATAGT GATACTAGGA GATATTAGGA GATATTAGGA GATACTAGGA GATATTAGGA GATACTAGGA GATATTAGGA GATACTAGGA GATACTAGA	GAGARACTCA TGGAGCCAC TGGAGCCAC GAGGAGTAG ACTAATGAAA ACAGCATCC ATTTAGAAAA TCCTTGCCTCA ATTACATCAC AATTAACA AAATAATGAC CAGTTACCACA AACAGAGTAG GTAAACCACA TGGATCACACA AACAGAGTAG TTCTGGCTACA AACAGATAA AATTAAGAA ATTTAGGAAA ATTTAAGAAA ATTAAGGTA AATTAAGGTA AATTAAGGTA ATTTAAGGTAC TGAAACTACAC ATTTAAGGTAC ATTTAGAGTA ATTAAGGTA ATTAAGGTA ATTAAGGTA AATTAAGGTA AATTAAGGTA AATTAAGGTA AATTAAGGTA ATTAAGATA AATTAAGGTA TTAAGATTA AATTAAGGTA AGAAAGGATA	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC TCTTCTATGG TCTTCTATTG TCTTCTTTT TAGCATGCT AAAATTTCA TTCTCTCAA TCCTTCTATA TTAGAAAGAT TTCATGATGAAAGAT TTCATGATGAAAGAT TTCATGAAAGAT TTCATGAAAGAT TTAGAAAGAT TTAGAATATCAA TTAGAGTATT TAATAGTTAC CTTTTAATAT TAAAACAGAATA AAAGTTAGAAAA ATTGGGATAAA	9840 9900 10020 10080 10140 10200 10320 10380 10440 10550 10620 10620 10620 10680 10740 10800 10980 11040 11100 11120 11220 11280 11340
<ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTGTTCTCATC CTATCTCATC TCTCTCTTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTAA AGTTTAAAT GGGCATAAA TGGATGGAG AGGAGAAAAA AGAAGACAT GAGAGAAAAA TCAAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGATAGAA TCAATGGAT TCAATGGAT TAATGGATAT TAATGGATAT	AGTTTCTTTT TGGACAGGT ATGGAGAGA AATGGGATG CTACACAGG GTAGTAGTAGT TCCCCATAGA GGTAAACGA TTGATGATGA TTGATGATGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT CTAAAGAGAT ATTATATAAT GAAAGAACAG ATGGAGAGAA CTAGATGCT AAGACTTTGG TTGCTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTCTCTCT CTAAATTTGCT CTCTCTCT CTCTCTCT CTCTCTCT CTCTCTCT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA TGTTTTAAAT ACATTTCTTT TATAAAACAC CTCTGGAAAA ATATATAAAG CCCACATCTAG AGAAAACTCA CGCCTATCTG GTTTAAATTT GGCACTTGGAAAG GTGATATCTG GTGATATCA GGAAAATTAA CGCAATATCA GGAAAAATTAA CGCAAAAATTAA CTTGAAAGTC CCAAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAGTA	ATAGCTTGAA AGAGGACAC GAGGATGACC GGTCACTGAG ATCTCCTTCA ANATANGACC CTATCACTCC CAACAGATTC CAACAGATTCT TCATTTAATA GAACCAAACC GAATTTAGGT TACATCAATA GGCAAGTGTC GAAAATTAAGAT TTACATCAATA GAGGACCTT TTACAGGATT AAAATACATC ATATAAAT TGGGGGAATT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAAAT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATAC GATACTAGGAT TTACAGCATG TTACAGCAT	GAGAAACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT ATTAGAAA ATCATAGAAA TCCTTCCAG CCGTGTCTTC AAATCATACA AAATAATGAC CAGTTACCAA AACAGAGTAG TTAGGAACACA TGATGGATGTT TCTGGCTACG ATTAGGAAAT ATTAGGAAAT ATTAAGGAA TGAAAGATAG TAAAAGATAG TAAAGAATAA TGAAAGAATAA TGAAAGAATA	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTCTTTT TAGCATGCT TAAAATTTCA TCTCTTCAAAA TCCTTCTTAT TAGAAAATTCA TTCATGAAGA TTCATGAAGA TTCATGAAGA TTAGAGAATTCA TTAATAGATACA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGTTAC AAACGAATA TTGGGATAAAA AAGTTAGAAA AAGTTAGAAA	9840 9900 10020 10080 10140 10260 10380 10440 10560 10560 10680 10740 10860 10980 10980 11040 11160 11120 11280 11340 11460
<ul><li>55</li><li>60</li><li>65</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTGTTCTCATC CTATCTCATC TCTCTCTTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTAA AGTTTAAAT GGGCATAAA TGGATGGAG AGGAGAAAAA AGAAGACAT GAGAGAAAAA TCAAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGATAGAA TCAATGGAT TCAATGGAT TAATGGATAT TAATGGATAT	AGTTTCTTTT TGGACAGGT ATGGAGAGA AATGGGATG CTACACAGG GTAGTAGTAGT TCCCCATAGA GGTAAACGA TTGATGATGA TTGATGATGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT CTAAAGAGAT ATTATATAAT GAAAGAACAG ATGGAGAGAA CTAGATGCT AAGACTTTGG TTGCTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTCTCTCT CTAAATTTGCT CTCTCTCT CTCTCTCT CTCTCTCT CTCTCTCT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA TGTTTTAAAT ACATTTCTTT TATAAAACAC CTCTGGAAAA ATATATAAAG CCCACATCTAG AGAAAACTCA CGCCTATCTG GTTTAAATTT GGCACTTGGAAAG GTGATATCTG GTGATATCA GGAAAATTAA CGCAATATCA GGAAAAATTAA CGCAAAAATTAA CTTGAAAGTC CCAAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAGTA	ATAGCTTGAA AGAGGACAC GAGGATGACC GGTCACTGAG ATCTCCTTCA ANATANGACC CTATCACTCC CAACAGATTC CAACAGATTCT TCATTTAATA GAACCAAACC GAATTTAGGT TACATCAATA GGCAAGTGTC GAAAATTAAGAT TTACATCAATA GAGGACCTT TTACAGGATT AAAATACATC ATATAAAT TGGGGGAATT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAAAT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATAC GATACTAGGAT TTACAGCATG TTACAGCAT	GAGAAACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT ATTAGAAA ATCATAGAAA TCCTTCCAG CCGTGTCTTC AAATCATACA AAATAATGAC CAGTTACCAA AACAGAGTAG TTAGGAACACA TGATGGATGTT TCTGGCTACG ATTAGGAAAT ATTAGGAAAT ATTAAGGAA TGAAAGATAG TAAAAGATAG TAAAGAATAA TGAAAGAATAA TGAAAGAATA	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTCTTTT TAGCATGCT TAAAATTTCA TCTCTTCAAAA TCCTTCTTAT TAGAAAATTCA TTCATGAAGA TTCATGAAGA TTCATGAAGA TTAGAGAATTCA TTAATAGATACA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGTTAC AAACGAATA TTGGGATAAAA AAGTTAGAAA AAGTTAGAAA	9840 9900 9960 10020 10140 10200 10320 10380 10440 105500 10560 10620 10680 10740 10860 10920 10980 11100 11160 1120 11280 11340 11400 11460
<ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTGTTCTCATC CTATCTCATC TCTCTCTTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTAA AGTTTAAAT GGGCATAAA TGGATGGAG AGGAGAAAAA AGAAGACAT GAGAGAAAAA TCAAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGATAGAA TCAATGGAT TCAATGGAT TAATGGATAT TAATGGATAT	AGTTTCTTTT TGGACAGGT ATGGAGAGA AATGGGATG CTACACAGG GTAGTAGTAGT TCCCCATAGA GGTAAACGA TTGATGATGA TTGATGATGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT CTAAAGAGAT ATTATATAAT GAAAGAACAG ATGGAGAGAA CTAGATGCT AAGACTTTGG TTGCTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTCTCTCT CTAAATTTGCT CTCTCTCT CTCTCTCT CTCTCTCT CTCTCTCT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA TGTTTTAAAT ACATTTCTTT TATAAAACAC CTCTGGAAAA ATATATAAAG CCCACATCTAG AGAAAACTCA CGCCTATCTG GTTTAAATTT GGCACTTGGAAAG GTGATATCTG GTGATATCA GGAAAATTAA CGCAATATCA GGAAAAATTAA CGCAAAAATTAA CTTGAAAGTC CCAAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAGTA	ATAGCTTGAA AGAGGACAC GAGGATGACC GGTCACTGAG ATCTCCTTCA ANATANGACC CTATCACTCC CAACAGATTC CAACAGATTCT TCATTTAATA GAACCAAACC GAATTTAGGT TACATCAATA GGCAAGTGTC GAAAATTAAGAT TTACATCAATA GAGGACCTT TTACAGGATT AAAATACATC ATATAAAT TGGGGGAATT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAAAT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATAC GATACTAGGAT TTACAGCATG TTACAGCAT	GAGAAACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT ATTAGAAA ATCATAGAAA TCCTTCCAG CCGTGTCTTC AAATCATACA AAATAATGAC CAGTTACCAA AACAGAGTAG TTAGGAACACA TGATGGATGTT TCTGGCTACG ATTAGGAAAT ATTAGGAAAT ATTAAGGAA TGAAAGATAG TAAAAGATAG TAAAGAATAA TGAAAGAATAA TGAAAGAATA	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC TCTTCTATGG TCTTCTATTG TCTTCTTTT TAGCATGCT AAAATTTCA TTCTCTCAA TCCTTCTATA TTAGAAAGAT TTCATGATGAAAGAT TTCATGATGAAAGAT TTCATGAAAGAT TTCATGAAAGAT TTAGAAAGAT TTAGAATATCAA TTAGAGTATT TAATAGTTAC CTTTTAATAT TAAAACAGAATA AAAGTTAGAAAA ATTGGGATAAA	9840 9900 9960 10020 10140 10200 10320 10380 10440 105500 10560 10620 10680 10740 10860 10920 10980 11100 11160 1120 11280 11340 11400 11460
<ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGGTTCTCA CTATCTCATC TCTCTCTCTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTATA AATTTAAGGA GCCTGGAGTA CGATCTGAA TGGATGGAG GGGAGTAGAA AGAAGACAT GAGAGAAAAA TCGAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT TCAATGGAT AAGAGAAAAA TCAATGGAT TCAATTTTATT	AGTTTCTTTT TGGACAGGT ATGGAGAGA AATGGGATG CTACACAGG GTAGTAGTAGT TCCCCATAGA GGTAAACGA TTGATGATGA TTGATGATGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT CTAAAGAGAT ATTATATAAT GAAAGAACAG ATGGAGAGAA CTAGATGCT AAGACTTTGG TTGCTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTCTCTCT CTAAATTTGCT CTCTCTCT CTCTCTCT CTCTCTCT CTCTCTCT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA TGTTTTAAAT ACATTTCTTT TATAAAACAC CTCTGGAAAA ATATATAAAG CCCACATCTAG AGAAAACTCA CGCCTATCTG GTTTAAATTT GGCACTTGGAAAG GTGATATCTG GTGATATCA GGAAAATTAA CGCAATATCA GGAAAAATTAA CGCAAAAATTAA CTTGAAAGTC CCAAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAATTAA CCTTGAAAGTA	ATAGCTTGAA AGAGGACAC GAGGATGACC GGTCACTGAG ATCTCCTTCA ANATANGACC CTATCACTCC CAACAGATTC CAACAGATTCT TCATTTAATA GAACCAAACC GAATTTAGGT TACATCAATA GGCAAGTGTC GAAAATTAAGAT TTACATCAATA GAGGACCTT TTACAGGATT AAAATACATC ATATAAAT TGGGGGAATT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAAAT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATAC GATACTAGGAT TTACAGCATG TTACAGCAT	GAGAAACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT ATTAGAAA ATCATAGAAA TCCTTCCAG CCGTGTCTTC AAATCATACA AAATAATGAC CAGTTACCAA AACAGAGTAG TTAGGAACACA TGATGGATGTT TCTGGCTACG ATTAGGAAAT ATTAGGAAAT ATTAAGGAA TGAAAGATAG TAAAAGATAG TAAAGAATAA TGAAAGAATAA TGAAAGAATA	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTCTTTT TAGCATGCT TAAAATTTCA TCTCTTCAAAA TCCTTCTTAT TAGAAAATTCA TTCATGAAGA TTCATGAAGA TTCATGAAGA TTAGAGAATTCA TTAATAGATACA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGTTAC AAACGAATA TTGGGATAAAA AAGTTAGAAA AAGTTAGAAA	9840 9900 9960 10020 10140 10200 10320 10380 10440 105500 10560 10620 10680 10740 10860 10920 10980 11100 11160 1120 11280 11340 11400 11460
<ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTATCTCATC TTCTCTCTTT CTTTGAGGAAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTGCTTAA TTTTTGCTTAA TTTTTGCTTAA GCCTGGAGTA AGATTCTCAG GGGGCATAAA TGGATGCGAG GGGAGTAGAA TGGATGCGAG TGAAAGAACAT TGAAATGGAT TGAAATGGAT TGAAATGGAT TAAATTGATTAAT TAAATTGATT AAAGAAGAAT CATTTTTATT TCCC	AGTTTCTTTT TGGACAGGT ATGGAGAGA AATGGGATG CTACACAGG GTAGTAGTAGT TCCCCATAGA GGTAAACGA TTGATGATGA TTGATGATGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT CTAAAGAGAT ATTATATAAT GAAAGAACAG ATGGAGAGAA CTAGATGCT AAGACTTTGG TTGCTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTAAATTTGCT CTCTCTCT CTAAATTTGCT CTCTCTCT CTCTCTCT CTCTCTCT CTCTCTCT	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CAGACCTCTC CAGACTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA ATATTCTTT TATAAAACAA ATATTCTTT TATAAAACA ATATTAAAA CCCAGAACAG AAGAACTCA TGTGGTTACC AGAAAAGACC GACCTATCTG GTTTAAATT GGCACTTGAA GTGATATTCA GTGATATTCA GCAAAAAATAA CCTTGAAAGTA TTGCATTTCT TATAAATTCA TGTGTTTAAATTT AGCACTTGAAGTA TTGCATTTCA TTGCATATTCA TTGCATTTCA TTGCATTCA TTGCATTCA TTGCATTCA TTGCATTCA TTGCATTCA TTGCATTCA TTGCATTTCA TTGCATTCA TTGCATTTCA TTGCATTCA TTGCATTCA TTGCATTTCA TTGCATTTCA TTGCATTCA TTGCATTCA TTGCATTCA TTGCATTCA TTGCATTTCA TTGCATTCA TTGCAT	ATAGCTTGAA AGAGGACAC GAGGATGACC GGTCACTGAG ATCTCCTTCA ANATANGACC CTATCACTCC CAACAGATTC CAACAGATTCT TCATTTAATA GAACCAAACC GAATTTAGGT TACATCAATA GGCAAGTGTC GAAAATTAAGAT TTACATCAATA GAGGACCTT TTACAGGATT AAAATACATC ATATAAAT TGGGGGAATT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAAAT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATAC GATACTAGGAT TTACAGCATG TTACAGCAT	GAGAAACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT ATTAGAAA ATCATAGAAA TCCTTCCAG CCGTGTCTTC AAATCATACA AAATAATGAC CAGTTACCAA AACAGAGTAG TTAGGAACACA TGATGGATGTT TCTGGCTACG ATTAGGAAAT ATTAGGAAAT ATTAAGGAA TGAAAGATAG TAAAAGATAG TAAAGAATAA TGAAAGAATAA TGAAAGAATA	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTCTTTT TAGCATGCT TAAAATTTCA TCTCTTCAAAA TCCTTCTTAT TAGAAAATTCA TTCATGAAGA TTCATGAAGA TTCATGAAGA TTAGAGAATTCA TTAATAGATACA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGTTAC AAACGAATA TTGGGATAAAA AAGTTAGAAA AAGTTAGAAA	9840 9900 9960 10020 10140 10200 10320 10380 10440 105500 10560 10620 10680 10740 10860 10920 10980 11100 11160 1120 11280 11340 11400 11460
<ul><li>55</li><li>60</li><li>65</li><li>70</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTTCTCT CTATCTCATC TCTCTCTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTA AATTTATGG GCGCATAAA TGGATGGAA AGAAGACAT GAGAGAAAAA TCAAATGGAT TCATCTGAAC TATGGTAGTA AAGAAGAAT TCATCTGAAC TATGGTAGTT AAAGAAGAAT CATTTTTATT TCCC Seq ID NO:	AGTTCTTTT TGGACAGGT TAGGAAGAGA AATGGGGATG CTACACAGGG GTAGTAGTAGT TCCCCATAGA GGTAAACTGA CTCTAATAA AATGTCCAG GTTTGTGACC CTAGAAACAC CTTGTGTTTCT TATATTAATC GAAGGCATAT GAAGGCATAT GAAGGACAC ATTGCAGAGAACAC ATTGCAGAGACAC TTTGTGTTTCT TATATTAATC GAAGGCATAT GAAGGCATAT GAAGGCATAT GAAGGCATAT GAAGGCATAT GAAGGCATAT GAAGGCATAT GAAGAACAG TTGCCTGGCA CTCTAAATTGA TTGCCTGCAC CTCTAAATTGAT CTAGATTGCT GTAGCTTAAAAT CTAGAATTGA CTAGAATTGA TTCCAGAAAG	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CAGACTCTC TCATTAGGCA TCGAATTAGT TTGCTGGCAA TAGTCATCAT TAGTCATCAT ACAATTACT TATAAAATAA TGTTTTAAAT ACATTTCTTT TATAAAACAC CTCTGGAAAG ACACACTCTAG TGTGTTACC AGAAAACTCA GCCTATCTG GTTTAAATT GGCACTTGAA TGGTATCC GAAAAATAA CCTTGAAGTA TGGCATTTCC TGGAAATTAC TGGCATTTCA TGGCACTTGAA TTAGCTTTCT TGGCATTTCA TTAGCTTTCT TGGCATTTCT TGGCATTTCA TAGCTTTCT TTAGCTTTCT TTAGCTT	ATAGCTTGAA AGAGGACAC GAGGATGACC GGTCACTGAG ATCTCCTTCA ANATANGACC CTATCACTCC CAACAGATTC CAACAGATTCT TCATTTAATA GAACCAAACC GAATTTAGGT TACATCAATA GGCAAGTGTC GAAAATTAAGAT TTACATCAATA GAGGACCTT TTACAGGATT AAAATACATC ATATAAAT TGGGGGAATT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAAAT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATAC GATACTAGGAT TTACAGCATG TTACAGCAT	GAGAAACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT ATTAGAAA ATCATAGAAA TCCTTCCAG CCGTGTCTTC AAATCATACA AAATAATGAC CAGTTACCAA AACAGAGTAG TTAGGAACACA TGATGGATGTT TCTGGCTACG ATTAGGAAAT ATTAGGAAAT ATTAAGGAA TGAAAGATAG TAAAAGATAG TAAAGAATAA TGAAAGAATAA TGAAAGAATA	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTCTTTT TAGCATGCT TAAAATTTCA TCTCTTCAAAA TCCTTCTTAT TAGAAAATTCA TTCATGAAGA TTCATGAAGA TTCATGAAGA TTAGAGAATTCA TTAATAGATACA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGTTAC AAACGAATA TTGGGATAAAA AAGTTAGAAA AAGTTAGAAA	9840 9900 9960 10020 10140 10200 10320 10380 10440 105500 10560 10620 10680 10740 10860 10920 10980 11100 11160 1120 11280 11340 11400 11460
<ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTTCTCT CTATCTCATC TCTCTCTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTA AATTTATGG GCGCATAAA TGGATGGAA AGAAGACAT GAGAGAAAAA TCAAATGGAT TCATCTGAAC TATGGTAGTA AAGAAGAAT TCATCTGAAC TATGGTAGTT AAAGAAGAAT CATTTTTATT TCCC Seq ID NO:	AGTTTCTTTT TGGACAGGT TAGGAAGAGA AATGGGATG CTACACAAG GTAGTAGTAGT TCCCCATAGA GGTAAAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTTGTGATTC TATATTAAT GAAGGCATAT CTAAATAA AATGTCAAG ATGAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAAGTTGCT AAGACTTGCT AAGACTTGCG CTCTAAATTT GTAGCTAAAAT CTAGAATTGA CTAGAATTGA TTCCAGAAAC	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CATTGTGGA TCGAATTAGT TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA ATATTCTTT TATAAAACAC CTCTGGAAA ATATATAAAC CCCAGAACAG AAGAACTCA CCACCATCTAG TGTGGTTACC AGAAAGAGCC GACCTATCTG GTTTAAATT GGCACTTGAA CTGATATTCATT TATAAATTC TGTGTTTCT TTTAAATTC TGTGTTTCT TTTAAATTC TGTGTTTAATTC TGTCTTTAATTC TGTCTTTCT TTTAAATTC TGTCTTTCT TTTAAATTC TGCATTTCT TTTAAATTC TGCATTTCT TTTAAATTC TGCATTTCT TTTAAATTC TTTTAATTC TGCATTTCT TTTTTTCT TTTTTTCT TTTTTTCT TTTTTTCT TTTTTT	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATTACCTTCA AAATAAGACC CTGTCACTCC CAACAGATTC CAAGAATTTA AAATGTACTT GAACCAAACC GAATTTAGT TCATTTAATA GAGCAGGGCCTT TTACAGGCTT TAAATACACC ATATATAAAT TGGGATGGA GTACTTGATG GATATTAGTC ATATATAAAT TGGGGGATTC GATATTAGTC GATATTAGTC ATATATAAAT TGGGGGATTC TACTGGATGGA GTACTTGATG GATATTAGTC TATAAAATAC GATACTTGATG GATATTAGTC TAGGGTTCCA	GAGAAACTCA TGGAGCCAC TGGAGCCAC TGGAGCCAC GAGGAGTGG ACTAATGAAG ACTAATGAAA ATCTTGGCTCA ATGATAAAA TTCCTTCCAG CCGTGTCTTC GATACCTAAA AAATCATACT GATACCTAAA AAATCATACT TTGGCTACA TGGAGAATA TGGAGAATA TTGGAAGAATA AATTAAGGTA AATTAAGGTA TAAATCTCAG TTAAAGGTA TAAATCTCAG TTAAAGGTA TAAATCTCAG TTAAAGGTA TGAAAGAATC TTAAAGGTA TGAAAGAATC TTAAATCTCAG TTAAAAGGTA TGAAAGGATC TGTAAAGGATC	CTGCTGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCACCTA TATTTCTTTT TAGCATGCCT TAAATTTCCTTT TAGCATGCT TAAATTTCATTT TAGCATGCT TATTCTTTATGA TCCTTCTATA TCCTTCTATA TCCTTCTATA TCCTTCTATA TATAAATCAT TAGGAAACAT TTCATGATGA TTCATGATGA TTGCAAAGA TTGCAAAGA TTAGAAACATT TAATAGTTAC TCTTTTATATAT TAAACAGAATA TTGGGATAACA AAGTTAGAA AAGTTAGAAG AGGAATTCT CATAGAATAC CATAGATTCT	9840 9900 9960 10020 10140 10200 10320 10380 10440 105500 10560 10620 10680 10740 10860 10920 10980 11100 11160 1120 11280 11340 11400 11460
<ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTTCTCT CTATCTCATC TCTCTCTTT CTTGAGGAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTA AATTTATGG GCGCATAAA TGGATGGAA AGAAGACAT GAGAGAAAAA TCAAATGGAT TCATCTGAAC TATGGTAGTA AAGAAGAAT TCATCTGAAC TATGGTAGTT AAAGAAGAAT CATTTTTATT TCCC Seq ID NO:	AGTTTCTTTT TGGACAGGT TAGGAAGAGA AATGGGATG CTACACAAG GTAGTAGTAGT TCCCCATAGA GGTAAAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTTGTGATTC TATATTAAT GAAGGCATAT CTAAATAA AATGTCAAG ATGAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAGAACAC CTAAGTTGCT AAGACTTGCT AAGACTTGCG CTCTAAATTT GTAGCTAAAAT CTAGAATTGA CTAGAATTGA TTCCAGAAAC	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CAGACTCTC TCATTAGGCA TCGAATTAGT TTGCTGGCAA TAGTCATCAT TAGTCATCAT ACAATTACT TATAAAATAA TGTTTTAAAT ACATTTCTTT TATAAAACAC CTCTGGAAAG ACACACTCTAG TGTGTTACC AGAAAACTCA GCCTATCTG GTTTAAATT GGCACTTGAA TGGTATCC GAAAAATAA CCTTGAAGTA TGGCATTTCC TGGAAATTAC TGGCATTTCA TGGCACTTGAA TTAGCTTTCT TGGCATTTCA TTAGCTTTCT TGGCATTTCT TGGCATTTCA TAGCTTTCT TTAGCTTTCT TTAGCTT	ATAGCTTGAA AGAGGACAC GAGGATGACC GGTCACTGAG ATCTCCTTCA ANATANGACC CTATCACTCC CAACAGATTC CAACAGATTCT TCATTTAATA GAACCAAACC GAATTTAGGT TACATCAATA GGCAAGTGTC GAAAATTAAGAT TTACATCAATA GAGGACCTT TTACAGGATT AAAATACATC ATATAAAT TGGGGGAATT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAAAT ACTGGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATA CATCGATGGA GTATCTTGATG GATATTAGTC ATATAAATAC GATACTAGGAT TTACAGCATG TTACAGCAT	GAGAAACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT ATTAGAAA ATCATAGAAA TCCTTCCAG CCGTGTCTTC AAATCATACA AAATAATGAC CAGTTACCAA AACAGAGTAG TTAGGAACACA TGATGGATGTT TCTGGCTACG ATTAGGAAAT ATTAGGAAAT ATTAAGGAA TGAAAGATAG TAAAAGATAG TAAAGAATAA TGAAAGAATAA TGAAAGAATA	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATTCTTTT TAGCATGCT TAAAATTTCA TCTCTTCAAAA TCCTTCTTAT TAGAAAATTCA TTCATGAAGA TTCATGAAGA TTCATGAAGA TTAGAGAATTCA TTAATAGATACA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGATA TTAGAGTATT TAATAGTTAC AAACGAATA TTGGGATAAAA AAGTTAGAAA AAGTTAGAAA	9840 9900 9960 10020 10140 10200 10320 10380 10440 105500 10560 10620 10680 10740 10860 10920 10980 11100 11160 1120 11280 11340 11400 11460
<ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTTCTCA TCACCCT CAGATTCTCA GAGGTGTTCT CTATCACCT CTATCTCATC TTCTCTCTT CTTGACGAAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTAAAT TTTTTGATTATAG GCCTGGAGTA CTATTTATAG GGGCATAAA TCGAATGGAT TGAATCGAT TGAATCGAT TGAATCGAT TGAATCGAT TAGAATCGAT TAGAATCGAT TCAAATTGAT TCCC Seq ID NO: Protein Ac	AGTTCTTTT TGGACAGTT ATGGAGAGA AATGGGGATG CTACCAAGG GTAGTAGTAG TTCCTATTCT TCCCCATAGA AATGTCCAAGG CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC TTTGTGATTC TATATAATAC GAAGGCATAT CTAAAGGGAT ATTATCATAT GAAGGCATAT ATTATCATAT GAAGGCATAT CTAAAGGGAT ATTATCATAT GAAGGCATAT TCTACAGAAACAC TTGCTTGGCA CTGCTAAATTGC TTGCCTGGCA ACTCTAAATTGC TTGCCTGGCA CTCTAAATTGC TTGCCTGGCA TTCCAGAAAG CTCTAAATTGC TTGCTGCGCA TTCCAGAAAG TTCCAGAAAAG TTCCAGAAAAG TTCCAGAAAAG TTCCAGAAAAG TTCCAGAAAAAG TTCCAGAAAAG TTCCAGAAAAAG TTCCAGA	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTAGT TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA ATAGTTATAT ACATTTCTTT TATAAAAAC ACATTACTT TATAAAACAC ACATCATAC ACCACAATCAC GCCACAATCAC GCCACAACAG GAGAAACTCA CCACAATCTAG GGCACTTAGC GGACTTATCT GGCACTTGAA TGTGTTTAAATT GGCACTTGAA TTAAAATAT CCTTGAAGTA TTAAATTC TGTTAAATTC GCAAAAATAA CCTTGAAGTA TAGCTTTCT  D Bequence BAB21525.1	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATATAAGACC CTGTCACTCA AAATAAGACC CAACAGATTC CAAGAATTTA AAATTTAATT GAACCAAACC GAAATTTAGT ATCATTAATA GGCAAGTGTC GAAATTTAGT TTACATA GAGGACCTT TTACAGCAT TAGCATGAC GAAATTAAAT CGCAAGTGTC GAAATTAAAT CGCAGCTT ATATATAATA CGATTGATGA GATATTAGGT ATATATAATA CATGGATGGA GTACTTGATG GATATTAGGT TACTGGATGGA TACTAGGGT TACTGATGGA TACTAGGGT TACTGGATGGA GTACTTGATG GATACTAGGG TATCAGCATG TAGGGTTCCA	GAGARACTCA TGGAGCCACT TGGAGCCACT TGGAGCCACT TGGAGCCACT GAGGGAGTGG ACTANTGAAG ACACGATCA ATGATTAGAAA ATCTTCCACA GATACCTACA AAATAATGAC CAGTTACACA AACAGAGTAG TCTGGCTACC ATGATACACA AACAGAGTAG TTTAGGAAA ATTAAGGTA TTTAGGAAA ATTAAGGTA TTAAGGTAC TAGGAAATCA TTAAGCTAC TAGAAACACTA TTAAGGTAC TTAAAACTCCC TAGAAACACTA TTAAGGTAC TTAAACTCCC TAGAAACACTA TTAAACTCCC TTAAACTCCCC TTAAACCCCC TTATTACCCCC TTATTACCCCC TTATTACCCCC TTATTACCCCC	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AGCTGCAGC TGTTCACTT TAGCATGCCT AAAAATTTCC TAAAAATTTCA TCTCTCTAAA TCCTTCTAAA TCCTTCTAAA TCATGAAGAA TTAAAATCAT TAAGAACTTC TTGTCAAGA CTGATATCAA TTAAAATCAT TAAAATCAT TAAAATCAT TAAAATCAT TAAAATCAT TAAAAATCAA TTACAGTATA AAACAGAATT AAACAGAATT ATTGGATAAA AAGTTAGAT AAACAGAATT CCTTTTAATAT AAACAGAATC CTTTTAATAT AAACAGAATC CTTTTAATAT AAACAGAATT CATAGATTCT  51	9840 9900 9960 10020 10140 10200 10320 10380 10440 10500 10560 10680 10680 10740 10800 10980 11040 11160 11220 11280 11340 11400 11450 11520
<ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li><li>80</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT TAATCACCCT CAGATTCTCA GAGGTGTTCT CTTGTCTCATC TTTTTACCACC GTTTCTAAAT TTTTTGCTAAA TTTTTAGCAAC GCTGGAGTA CCATTTTATG GGGCATAAA TGGATGCGAG GGGAGTAGAA TGATCCGAG GGGAGTAGAA TGATCCGAG TATGGTAGT TAAGGAA TCGATGCGAG TAATGGTAGT TCAAATTGATA TCATTTTATT TCCC Seq ID NO: Protein Ac	AGTITCTITI TGGACAGGT TAGGAAGAGA AATGGGATG CTACACAGG GTAGTAGTAGT TCCCCATTAGA GGTAAACTGA TTGATGATGA TTGATGATGA TTGATGATGA CTCTTAATAA AATGTCCAAG GTTTCTGACC CTAGAAACAC CTAGAAACAC CTAGAAACAC CAGAACAC CTCTAAATTT GAAGCTTGCT GTAGCTTAAAT TTCCAGAAAC CTCTAAATTT GTAGCTTAAAC CTCTAAATTT CAGAAACC CTCTAAATTT CTCCAGAAACC CTCTAAACTT CTCAGAAACC CTCTAAACTT CTCAGAAACC CTCTAAACT CTCAGAACC CTCTAAACC CTCTAACC CTCTACACC CTCTAACC CTC	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCACATAT TTGCTGGCAA TAGTCATAT ATAAGATTAAT ATAAGATGAA TGTTTTAAAT ACATTTCTTT TATAAAAACAC CTCTGGAAAG AGAAACTCAG CCACATCTAG TGTGTTAACT CACATTCAG TGTGTTACC AGAAAGAGC GACCTATCTG GTGTTAAATT GCACTTGAAG CTTGAAGATA TAGCTTTTCT  DEQUENCE BAB21525.1  KSKENNIFYS	ATAGCTTGAA AGAGGAGACAC GGTCACTGAG AGGCATGACC GGTCACTGAG ANATAAGACC CTGTCACTCC CAACAGATTC CAAGAATTTA AAATGTACTT TCATTTAATA GGCAAGACC GAATTTAAGT TTCATCAATA GGCAAGCCTT TTACAGGCTT TTACAGGCTT TTACAGGCTT AAAATTAAAT TCGGGGGAATT ACTGGATGGG GATATTAAAT TCGGGGGAATT ACTGGATGGA GTACTTGATC GATATTAAAT TACATCATCA GATACTAGTC ATATAAAT CTGGATGGA GTACTTGATC ATATAAATACT CATGGATGGA GTACTTGATC TAGGGTTCCA  31	GAGARACTCA TGGAGCCACT TGAGACCACT TGAGACCACT TGAGACCACT TGAGACCACT TGAGACCACT ATTAGAAAA TCTTTGGCTCA ATGATTAAAA TTCCTTCCAG CCGTGTCTTC AAATCATACT AAATCATACT AAATCATACT AAATCATACT TGATACCACA ACACAGATAG TTAGGAACACA ATTTAGGAAA TTGAAGATAG TAGAACAATA TTAAGATCACA ATTTAGGAACA TTAAATCTCAG TTAAAACATCACACT TATTTACTCC  41  VILIGAKDNTX	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCACCA AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATATTCTTTT TAGCATGCT AAAAATTTCC TAAAATTTCC TAAAATTTCATTA TCCTTCTATA TCCTTCTATA TCCTTCTATA TCCTTCTATA TATAAATCAT TAGGAAAGAT TTCATGATGA CTGATATCAA TTGCAAAGA CTGATATCAA TTAGAGTATT TAATAGTTAC TTGTCAAAGA CTGTTTTCT TTGTCAAAGA CTGTTTTCT TTGTCAAAGA CTGTTTTCT CTTTTAATAT AAACAGAATA TTGGGATAAA AAGTTAGAAG AGGAATTGGT CATAGATTCT	9840 9900 9960 10020 10080 10140 10200 10320 10380 10440 10500 10620 10680 10680 10920 10860 11040 11160 11220 11280 11340 11460 11520
<ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTC TGCCACCGCT TAATCACCCT CAGATTCTCA GAGGGTTCTCT CTTGAGGAAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTAA AATTTAAGAA CCATTTATAG GGGGCATAAA TGGATGGAA AGAAAGACAT GAGAGAAAAA TCAAATGGAT TAGATCAAG TAGATCAGAG TAGGATAAT CATTTTTATT TCCC  Seq ID NO: Protein AC  I MNSLSEANTK OUTENTTEKA	AGTTTCTTTT TGGACAGGTT ATGGACAGGA AATGGGATG CTACACAGG GTAGTAGTAGT TCCCCATAGA GGTAAACTGA TTGATGATGAC TTGATGATGAC CTAGAACAC CTAGAAACAC TTTGTGATTC TATATTAAT GAAGGCATAT CTAAATAAC GAAGGCATAT CTAAAGGGAT ATTACATAT GAAAGACTTGCT AAGACTTTGC TGCCTGGCA CTCCAGAAACAC CTAGAATTGC TGCCTGGCA CTCTAAATTT GTAGCTTAAATT GTAGCTTAAATT GTAGCTTAAATT GTAGATTGCA TTCCAGAAAC 465 Protei Ce88ion #:  11	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTATC TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT TATAAGATAAT TATAAATTAT TATAAAACAC CCTCTGGAAAG ATATTATAAA CCTCTGGAAAG ACAATCTAG CCACATCTAG ACAAAACTCA GCACATCTAG TGTGTTTACC GAAAAAGGCC GACCTTTAAATTT GGCACTTGAAATTA TAGCTTTTAATTATAAT TAGCTTTTAATTTT TATAAAATTA CACATTCTG TTTAAATTT GGAAATTAA CCTTGAAGTA TAGCTTTTCT  I BEQUENCE BAB21525.1	ATAGCTTGAA GAGAGACA CAAGGACAC GGTCACTGAG ATCTCCTTCA ANATAAGACC CAACAGATTC CAAGAATTA ANATGTACTT TCATTTAATA GAACCAAACC GAATTTAGGT GAAAATTAAGA GGCAAGCTT TTACAATA GAGAGCCTT TTACAGCTT AAAATTAAGAT ATATAAAT ACTGGATGGA GTATTTAGT ATATATAAAT ACTGGATGGA GTATTTAGT ATATATAAAT ACTGGATGGA GTATTTAGT ATATAAAT ACTGGATGGA GTATTTAGTC ATATAAAT ACTGGATGGA TTAGGGTTCCA  31   PISITSALGM PISITSALGM EFNKSTDAYE	GAGARACTCA TGGAGCCACT TTGAGAACCA TGGAGCCACT GGAGCCACT ATGATAGAA ACAGCATCC ATTTAGAAA TCTTCGCTCA ATGATAAAA TCTTCCAC CAGTTACTACA CAGTTACCAA AAATAATGAC CAGTTACACA AAACAACATGTAG GTAAACCACA TGATGGTACT ATTTAGGAAA TGATGAGAATCA ATTTAGGAAA TGAAAGCACA TTTAGGAAACCA ATTTAAGGAA TTAAGGTAG TTTAGGAAACCA TTTAGGAAACCA TTTAGGAAACCA TTTAGGAAACCA TTTAGGAACA TTTAGGACA TTTAGCACC  41	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCAGC TGTTCACCTA TATTCTTTT TAGCATGCT TAAAATTTCC TAAAATTTCATTAT TAGCATGCAT TCTCTTATA TCCTTCTATA TCCTTCTAT TAGAAATTTCA TTAGAAACAT TTCATGAAGA TTCATGAAGA TTCATGAAGA TTGAATAAA TAGGAACTTC TGTCAAAGA TTAGAGTAT TAAAAGTTACAA AAGTTAGAGTA TGGGATATA TAGAGTAT CTTTTATTC CTTTTATTC AAACAGAATA TGGGATACA AAGTTAGAGA CGGAATTGAT CATAGATTAT CATAGATTAT TGGAATTAT TAAACAGAATA TGGGATACA AAGTTAGAAG CGGAATTGAT CATAGATTCT	9840 9900 9960 10020 10140 10260 10320 10380 10490 10560 10620 10620 10680 10740 10860 10980 11160 11160 11120 11280 11340 11400 11520
<ul><li>55</li><li>60</li><li>65</li><li>70</li><li>75</li><li>80</li></ul>	TAGTCATATC ATTGATGGAA TCGGTTCAAA GAATATCTTC ATCTAAAGTTCTC TGCCACCGCT TAATCACCT CAGATTCTCA GAGGTGTTCTCA GAGGTGTTCTCA TCTTCATCTTC TTTGAGGAAA ATATAATTCT ATTTAGCAAC GTTTCTAAAT TTTTTGCTTAAAT TTTTTTAGGAGA GCCTGGAGTA CCATTTTATG GGGGCATAAA TGGATGGAA TGAAATGGAT TGATCTGAAG TAGATTGAAC TAGATGGAT TAGATGGAT TAGATGGAT TAGATGGAT TAGATGGAT CATTTTTATT TCCC Seq ID NO: Protein Ac  NNSLSEANTK QVTENTTEKA QVTENTTEKA	AGTTCTTTT TGGACAGTT ATGGAGAGA AATGGGGATG CTACACAAGG GTAGTAGTATCT TCCCCATAGA AATGTCTATCT TCCCATAGA AATGTCCAAG GTTTCTGATCA CTGTATATAA AATGTCCAAG GTTTCTGATCC CTAGAAACAC TTTGTGATTC TATATTAATC GAAGGCATAT TATATCATAT GAAAGGAT ATTATCATAT GAAAGTTGCT AGACTTTGG TTGCCTGGCA ATGCAGAAAC CTAGAATTGA TTCCAGAAAG CTAGATTGG TTGCCTGGCA AGCTTTGG TTGCTTGGCAAAC CTAGAATTGA TTCCAGAAAG CTAGAATTGA TTCCAGAAAG TTCCAGAAAAG TTCCAGAAAAG TTCCAGAAAG TTCCAGAAAG TTCCAGAAAAG TTCCAGAAAAG TTCCAGAAAAG TTCCAGAAAAG TTCCAGAAAAAAAAAA	TTCCATTTGT TGCAGAATAT GCTATGACCT CAGACCTCTC CCTTTGTGGA TCGAATTAGT TCATAAGGCA TGCAATTAGT TTGCTGGCAA TAGTCATCAT ATAAGATGAA ATAGTCATCAT ATAAGATGAA ATATTCTTT TATAAAACAC CCCAGAACAG ATATATAAAC CCCAGAACAG GCCACTATCTG GGCATTTAG GGCACTTGA GGCACTTGA TGTGTTTACA GCACTTTCA GGCACTTTCA GGCACTTTCC TGTGAAATAA CCTTGAAGTA TAGCTTTCT  D BEQUENCE BAB21525.1  KSKENNIFYS VHAPFOKLINSK	ATAGCTTGAA GAGAGAGACA CAAGGACAC GGTCACTGAG ATATAAGAC CTGTCACTCA AAATAAGAC CAAGAATTTA AAATGTACTT CAAGAATTTAATA GAACCAAACC GAAATTTAGAT ATATATAATA GAGCAGCCTT TTACATA GAGCAGCCTT AAAATTAGAT TACAGCATC GAAAATTAGAT TACAGCATT GAAAATTAGAT TACAGCATT AAAATACAC GAAATTAAAT TACAGCATT AAAATACAC GATATTAAAT TACTGATGAG GTACTTGATG GATATTAAAT GATCATCAGCATG TACGGGTTCCA	GAGARACTCA TGGAGCCACT TTGAGAACCA TGGAGCCACG GAGGGAGTGG ACTAATGAAG ACACACACACA ATGATTAGAAA ATCTTCCTCCAG GATACCTAAA AAATAATGAC CAGTTACACA AACAGAGTAG TTCTGGCTACG TAGGAAACCACA TGATGGTTACCACA AACAGAGTAG TTCTGGCTACG TAGGAAATCA ATTAAGGTA ATTAAGGTA ATTAAGGTA TAATCTCAG TTTAGAACACA TTGAGAACACA TTATACTCCC  41    VLLGAKDNTR LKIANKLFGE	TIGCIGAGA TACACTTACC TGGGAATGGT GTCTCTCAGT AAGCTGCACCA AGTTCTGTTG TCTTCTATGG TGTTCACCTA TATATTCTTTT TAGCATGCT AAAAATTTCC TAAAATTTCC TAAAATTTCATTA TCCTTCTATA TCCTTCTATA TCCTTCTATA TCCTTCTATA TATAAATCAT TAGGAAAGAT TTCATGATGA CTGATATCAA TTGCAAAGA CTGATATCAA TTAGAGTATT TAATAGTTAC TTGTCAAAGA CTGTTTTCT TTGTCAAAGA CTGTTTTCT TTGTCAAAGA CTGTTTTCT CTTTTAATAT AAACAGAATA TTGGGATAAA AAGTTAGAAG AGGAATTGGT CATAGATTCT	9840 9900 9960 10020 10140 10200 10320 10380 10440 10500 10560 10680 10680 10740 10800 10980 11040 11150 1120 1120 11400 11400 11520

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TMGMVNIFNG DADLSGMTWS HGLSVSKVLH KAFVEVTEEG VEAAAATAVV VVELSSPSTN 360 EEFCCNHPFL FFIRQNKTNS ILFYGRFSSP 5 Seq ID NO: 466 DNA sequence Nucleic Acid Accession #: NM_001910.1 Coding sequence: 50..1240 10 GGAGAGAAGA AAGGAGGGG CAAGGGAGAA GCTGCTGGTC GGACTCACAA TGAAAACGCT CCTTCTTTTG CTGCTGGTGC TCCTGGAGCT GGGAGAGGCC CAAGGATCCC TTCACAGGGT 120 GCCCCTCAGG AGGCATCCGT CCCTCAAGAA GAAGCTGCGG GCACGGAGCC AGCTCTCTGA 180 GTTCTGGAAA TCCCATAATT TGGACATGAT CCAGTTCACC GAGTCCTGCT CAATGGACCA 240 GAGTGCCAAG GAACCCCTCA TCAACTACTT GGATATGGAA TACTTCGGCA CTATCTCCAT TGGCTCCCCA CCACAGAACT TCACTGTCAT CTTCGACACT GGCTCCTCCA ACCTCTGGGT 15 360 CCCCTCTGTG TACTGCACTA GCCCAGCCTG CAAGACGCAC AGCAGGTTCC AGCCTTCCCA GTCCAGCACA TACAGCCAGC CAGGTCAATC TTTCTCCATT CAGTATGGAA CCGGGAGCTT GTCCGGGATC ATTGGAGCCG ACCAAGTCTC TGTGGAAGGA CTAACCGTGG TTGGCCAGCA 420 480 540 20 GTTTGGAGAA AGTGTCACAG AGCCAGGCCA GACCTTTGTG GATGCAGAGT TTGATGGAAT 600 TCTGGGCCTG GGATACCCCT CCTTGGCTGT GGGAGGAGTG ACTCCAGTAT TTGACAACAT GATGGCTCAG AACCTGGTGG ACTTGCCGAT GTTTTCTGTC TACATGAGCA GTAACCCAGA 660 720 AGGTGGTGCG GGGAGCGAGC TGATTTTTGG AGGCTACGAC CACTCCCATT TCTCTGGGAG 780 CCTGAATTGG GTCCCAGTCA CCAAGCAAGC TTACTGGCAG ATTGCACTGG ATAACATCA GGTGGGAGGC ACTGTTATGT TCTGCTCCGA GGGCTGCCAG GCCATTGTGG ACACAGGGAC 840 25 900 TTCCCTCATC ACTGGCCCTT CCGACAAGAT TAAGCAGCTG CAAAACGCCA TTGGGGCAGC 960 CCCCGTGGAT GGAGAATATG CTGTGGAGTG TGCCAACCTT AACGTCATGC CGGATGTCACCTTCACCATT AACGGAGTCC CCTATACCCT CAGCCCAACT GCCTACACCC TACTGGACTT 1020 1080 CGTGGATGGA ATGCAGTTCT GCAGCAGTGG CTTTCAAGGA CTTGACATCC ACCCTCCAGC 30 TGGGCCCCTC TGGATCCTGG GGGATGTCTT CATTCGACAG TTTTACTCAG TCTTTGACCG 1200 TGGGAATAAC CGTGTGGGAC TGGCCCCAGC AGTCCCCTAA GGAGGGGCCT TGTGTCTGTG 1260 CCTGCCTGTC TGACAGACCT TGAATATGTT AGGCTGGGGC ATTCTTTACA CCTACAAAAA GTTATTTTCC AGAGAATGTA GCTGTTTCCA GGGTTGCAAC TTGAATTAAG ACCAAACAGA 1320 ACATGAGAAT ACACACACA ACACACATAT ACACACACA ACACTTCACA CATACACACC 1440 35 ACTCCCACCA CCGTCATGAT GGAGGAATTA CGTTATACAT TCATATTTTG TATTGATTTT TGATTATGAA AATCAAAAAT TTTCACATTT GATTATGAAA ATCTCCAAAC ATATGCACAA 1500 1560 GCAGAGATCA TGGTATAATA AATCCCTTTG CAACTCCACT CAGCCCTGAC AACCCATCCA 1620 CACAGGGCCA GGCCTGTTTA TCTACACTGC TGCCCACTCC TCTCTCCAGC TCCACATGCT GTACCTGGAT CATTCTGAAG CAAATTCCGA GCATTACATC ATTTTGTCCA TAAATATTTC 1680 1740 40 1800 TAACATCCTT AAATATACAA TCGGAATTCA AGCATCTCCC ATTGTCCCAC AAATGTTTGG CTGTTTTTGT AGTTGGATTG TTTGTATTAG GATTCAAGCA AGGCCCATAT ATTGCATTTA 1860 1920 TTTGAAATGT CTGTAAGTCT CTTTCCATCT ACAGAGTTTA GCACATTTGA ACGTTGCIGG TTGAAATCCC GAGGTGTCAT TTGACATGGT TCTCTGAACT TATCTTTCCT ATAAAATGGT 1980 AGTTAGATCT GGAGGTCTGA TTTTGTGGCA AAAATACTTC CTAGGTGGTG CTGGGTACTT 2040 45 CTTGTTGCAT CCTGTCAGGA GGCAGATAAT GCTGGTGCCT CTCTATTGGT AATGTTAAGA 2100 CTGCTGGGTG GGTTTGGAGT TCTTGGCTTT AATCATTCAT TACAAAGTTC AGCATTTT Seq ID NO: 467 Protein sequence Protein Accession #: NP_001901.1 50 51 31 41 MKTLLLLLLV LLELGEAGGS LHRVPLRRHP SLKKKLRARS QLSEFWKSHN LDMIQFTESC SMDQSAKEPL INYLDMEYFG TISIGSPPQN FTVIFDTGSS NLWVPSVYCT SPACKTHSRF 120 55 QPSQSSTYSQ PGQSFSIQYG TGSLSGIIGA DQVSVEGLTV VGQQFGESVT EPGQTFVDAE 180 PDGILGLGYP SLAVGGVTPV FDNMMAQNLV DLPMFSVYMS SNPEGGAGSE LIFGGYDHSH 240 PSGSLNWVPV TKOAYWQIAL DNIQVGGTVM FCSEGCQAIV DTGTSLITGP SDKIKQLQNA 300 IGAAPVDGHY AVECANLINVM PDVTFTINGV PYTLSPTAYT LLDFVDGMQF CSSGFQGLDI 360 HPPAGPLWIL GDVFIRQFYS VFDRGNNRVG LAPAVP 60 Seq ID NO: 468 DNA sequence Nucleic Acid Accession #: NM_018058.1 Coding sequence: 319..1575 65 TACGCGCTGC GGGACCGGCA GGGGAACGCC ATCGGGGTCA CAGCCTGCGA CATCGACGGG GACGGCCGGG AGGAGATCTA CTTCCTCAAC ACCAATAATG CCTTCTCGGG GGTGGCCACG 120 TACACCGACA AGTIGITICAA GITCCGCAAT AACCGGIGGG AAGACATCCI GAGCGATGAG GICAACGIGG CCCGIGGIGI GGCCAGCCIC TITGCCGGAC GCICTGIGGC CIGIGIGGAC 180 70 AGAAAGGGCT CTGGACGCTA CTCTATCTAC ATTGCCAATT ACGCCTACGG TAATGTGGGC 300 CCTGATGCCC TCATTGAAAT GGACCCTGAG GCCAGTGACC TCTCCCGGGG CATTCTGGCG 360 CTCAGAGATE TEGCTGCTGA GGCTGGGGTC AGCAAATATA CAGGGGGCCG AGGCGTCAGC
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	couring sequ	ichicu. IIII					
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PCT/US02/12476

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                                                                                                                               720
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GACARAAGGA AACAGACACA GARAGAGGTT ACTGTGCTGC TAGAACATCA GAAGAAGGTA TCGAAGACAA GACACACTAG AGAAACTGTT CTCAGGCGTG CCAAGAGGAG ATGGGCACCT 20 420 480 ATTCCTTGCT CTATGCAGA GAATTCCTTG GGCCCTTTCC CATTGTTTCT TCAACAAGTT GAATCTGATG CAGCACAGAA CTATACTGTC TTCTACTCAA TAAGTGGACG TGGAGTTGAT 540 600 AAAGAACCTT TAAATTTGTT TTATATAGAA AGAGACACTG GAAATCTATT TTGCACTCGG 660 AAAGAACCHI IAAATIATI IAAATIATATA GAATTAATTA CTTATGGGTC AACTGCAGAT GGATATTCAG CAGATCTGCC CCTCCCACTA CCCATCAGGG TAGAGGATGA AAATGACAAC 25 780 CACCCTGTTT TCACAGAAGC AATTTATAAT TTTGAAGTTT TGGAAAGTAG TAGACCTGGT ACTACAGTGG GGGTGGTTTG TGCCACAGAC AGAGATGAAC CGGACACAAT GCATACGCGC 840 CTGAAATACA GCATTTTGCA GCAGACACCA AGGTCACCTG GGCTCTTTTC TGTGCATCCC 960 30 1020 AGCACAGGCG TAATCACCAC AGTCTCTCAT TATTTGGACA GAGAGGTTGT AGACAAGTAC TCATTGATAA TGAAAGTACA AGACATGGAT GGCCAGTTTT TTGGATTGAT AGGCACATCA ACTTGTATCA TAACAGTAAC AGATTCAAAT GATAATGCAC CCACTTTCAG ACAAAATGCT TATGAAGCAT TTGTAGAGGA AAATGCATTC AATGTGGAAA TCTTACGAAT ACCTATAGAA 1080 1140 1200 GATAAGGATT 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	COLINIDADO	GKCNMSSDGS	PROTECUADD	T.EMOTYCEDA	DRESSEERAV	KCKCKLRALS	180
10	TIPERCTURN	LDFKAIIDGV	FEVERECKON	ALDDETI.I.MI.	I.PNSTDKVYI	YNGSLTSPPC	240
10	TDFEVGIEEN	DTVSISESQL	AUDCESSTAMO	OCCVVMT.MDV	LONNEBEOOA	KESROVESSY	300
	TOIVOMIVER	CSSEPENVQA	U.T.TOTVICAGA	AMED DERMAN	TMIEKEAVLY	OOLDGEDOTK	360
	TGREEIREAV	LGAILNNLLP	DEEN I I SULV	TOTNOTVORV	CDOLTIMATE	DMBELDIABLE	420
	HEFETDGYQD	TOAT DANGER	MUSIARAIAN	MICINGUIGKI	TOTOTOT	CTKYNEAKTN	480
15	LIGTERLIKE	BEEGKDIREG	ALVNPGRUSA	INVIRALED	TOTITIONT	VECTOROLIN	540
13	RSPTRGSEFS	GKGDVPNTSL	NSTSQPVIKL	ATERDISEIS	MUNEDOCCCO GIAIFHEERI	DATCATOUTC	600
	GSKTVLRSPH	MNLSGTAESL	MINSTIFFE	ESLLISFRED	TGAEDSSGSS	MANDECORDI	660
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	esukupsmed	DAMESONDI	720
	TAQPDVGSGR	ESFLOTNYTE	INVDESERTI	KSFSAGPVMS	QGPSVIDLEM	PRIDIPALEE	780
20		SSRQQDLVST					
20	LNTTPAASSS	DSALHATPVF	PSVDVSFESI	LSSYDGAPLL	PFSSASFSSE	LFRHLHTVSQ	840
	ILPQVTSATE	SDKVPLHASL	PVAGGDLLLE	PSLAQYSDVL	STTHAASETL	REGRESGATA	900
	KTLMFSQVEP	PSSDAMMHAR	SSGPEPSYAL	SDNEGSQHIF	TVSYSSAIPV	HDSVGVTYQG	960
	SLFSGPSHIP	IPKSSLITPT	ASLLQPTHAL	SGDGEWSGAS	SDSEFLLPDT	DGLTALNISS	1020
0.5	PVSVAEFTYT	TSVFGDDNKA	LSKSEIIYGN	ETELQIPSFN	EMVYPSESTV	MPNMYDNVNK	1080
25	LNASLQETSV	SISSTKGMFP	GSLAHTTTKV	FDHEISQVPE	nnfsvqptht	VSQASGDTSL	1140
	KPVLSANSEP	ASSDPASSEM	LSPSTQLLFY	etsasfstev	LLQPSFQASD	VDTLLKTVLP	1200
	AVPSDPILVE	TPKVDKISST	MLHLIVSNSA	SSENMLHSTS	VPVFDVSPTS	HMHSASLQGL	1260
	TISYASEKYE	PVLLKSESSH	QVVPSLYSND	BLFQTANLEI	NQAHPPKGRH	VFATPVLSID	1320
	EPLNTLINKL	IHSDEILTST	KSSVTGKVFA	GIPTVASDTP	VSTDHSVPIG	NGHVAITAVS	1380
30	PHRDGSVTST	KLLFPSKATS	ELSHSAKSDA	GLVGGGEDGD	TDDDGDDDDD	DRGSDGLSIH	1440
	KCMSCSSYRE	SQEKVMNDSD	THENSLMDQN	NPISYSLSEN	SEEDNRVTSV	SSDSQTGMDR	1500
	SPGKSPSANG	LSQKHNDGKE	ENDIQTGSAL	LPLSPESKAW	AVLTSDEESG	SGQGTSDSLN	1560
	ENETSTOFSF	ADTNEKDADG	ILAAGDSEIT	PGFPQSPTSS	VTSENSEVFH	VSEABASNSS	1620
	HESRIGLAEG	LESEKKAVIP	LVIVSALTFI	CLVVLVGILI	YWRKCFQTAH	FYLEDSTSPR	1680
35	VISTPPTPIF	PISDDVGAIP	IKHPPKHVAD	LHASSGFTEE	PETLKEFYQE	VQSCTVDLGI	1740
	TADSSNHPDN	KHKNRYINIV	AYDHSRVKLA	QLAEKDGKLT	DYINANYVDG	YNRPKAYIAA	1800
	OGPLKSTAED	FWRMIWEHNV	EVIVMITNLV	EKGRRKCDQY	WPADGSEEYG	nflutoksvo	1860
	VLAYYTVRNF	TLRNTKIKKG	SQKGRPSGRV	VTQYHYTQWP	DMGVPEYSLP	VLTFVRKAAY	1920
	AKRHAVGPVV	VHCSAGVGRT	GTYIVLDSML	QQIQHEGTVN	IFGFLKHIRS	QRNYLVQTEE	1980
40	OYVFIHDTLV	EAILSKETEV	LDSHIHAYVN	ALLIPGPAGK	TKLEKQFQLL	SQSNIQQSDY	2040
	SAALKOCNRE	KNRTSSIIPV	ERSRVGISSL	SGEGTDYINA	SYIMGYYQSN	EFIITQHPLL	2100
	HTIKDFWRMI	WDHNAQLVVM	IPDGQNMAED	EFVYWPNKDE	PINCESFKVT	LMAEEHKCLS	2160
	NEEKLIIODF	ILEATQDDYV	LEVRHPQCPK	WPNPDSPISK	TFELISVIKE	EAANRDGPMI	2220
	VHDEHGGVTA	GTFCALTTLM	HOLEKENSVD	VYQVAKMINL	MRPGVFADIE	QYQFLYKVIL	2280
45							
45		PSTSLDSNGA 574 DNA sec		TESTA			
	Seq ID NO: Nucleic Ac		quence n #: Eos se				
50	Seq ID NO: Nucleic Ac Coding seq	574 DNA sec id Accession Lence: 148-	quence n #: Eos se		41	51	
	Seq ID NO: Nucleic Ac Coding seq 1	574 DNA secid Accession mence: 148-4	quence n #: Eos se 4518 21 	quence 31	1	1	
	Seq ID NO: Nucleic Ac Coding seq 1	574 DNA secid Accession mence: 148-4	quence n #: Eos se 4518 21 	quence 31	1	1	60
50	Seq ID NO: Nucleic Ac Coding seq 1   CACACATACG	574 DNA secid Accession uence: 148-4	quence n #: Eos se 4518 21	quence  31   TCTATACACT	   GGAGGATTAA	 AACAAACAAA	60 120
50	Seq ID NO: Nucleic Ac Coding seq 1   CACACATACG CAAAAAAAAC	574 DNA secid Accession uence: 148-4  11    CACGCACGAT ATTTCCTTCG	quence n #: Eos sec 4518  21   CTCACTTCGA	quence  31    TCTATACACT CTCTCCACTC	 GGAGGATTAA TGAGAAGCAG	AACAAACAAA AGGAGCCGCA	
	Seq ID NO: Nucleic Ac Coding seq 1   CACACATACG CAAAAAAAAC CGGCAAGGGG	574 DNA secid Accession uence: 146-	quence n #: Eos sec 4518 21   CTCACTTCGA CTCCCCCTCC	quence  31   TCTATACACT CCCACTC CGAATCCTAA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT	AACAAACAAA AGGAGCCGCA CGCTTGCATT	120
50	Seq ID NO: Nucleic Ac Coding seq 1   CACACATACG CAAAAAAAAC CGGCGAGGGG CAGCTCCTCT	574 DNA set id Accession uence: 146  11   CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG	quence n #: Eos sec 4518 21   CTCACTTCGA CTCCCCCTCC TCTGGAAATG	quence  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA	120 180
50	Seq ID NO: Nucleic Ac Coding seq 1   CACACATACG CAAAAAAAA CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG	574 DNA secid Accession tence: 148	quence n #: Eos sec 4518  21   CTCACTTCGA CTCGCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA	quence  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT GCTAATGGAT TCTCCTATCA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA	120 180 240
50 55	Seq ID NO: Nucleic Ac Coding seq 1   CACACATACG CAAAAAAAA CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG	574 DNA secid Accession tence: 148	quence n #: Eos sec 4518  21   CTCACTTCGA CTCGCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA	quence  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT GCTAATGGAT TCTCCTATCA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA	120 180 240 300
50 55	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG	574 DNA secid Accession uence: 146 11	quence n #: Eos sec 4518  21   CTCACTTCGA CTCCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA	Juence  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT GCAGCACTGA TCTCCTATCA TTTCAGGGTT	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA	120 180 240 300 360
50	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CGAGGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA AGTCACATTGAGGG GTCAGGTGGGG	574 DNA secid Accession tence: 146	quence n #: Eos sec 4518  21   CTCACTTCGA CTCGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACTA AATGGTATTA	Juence  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGA TGACTACCGT TCACTGGGGA	120 180 240 300 360 420
50 55	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CGAGGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA AGTCACATTGAGGG GTCAGGTGGGG	574 DNA secid Accession tence: 146	quence n #: Eos sec 4518  21   CTCACTTCGA CTCGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGAAAACTA AATGGTATTA	Juence  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA	GGAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGA TGACTACCGT TCACTGGGGA	120 180 240 300 360 420 480
50 55	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CARARARARA CGGCGAGGGG CAGCTCCTC CTTGTTGAAG RARATATCCAR ACACTATACG ACACTATACG GTCAGCGGG ARATACCATA GTCAGCGGAG ARATGCARTA AGAGTACATA	574 DNA secid Accession uence: 146  11    CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGCCTG AGATTGCTGA TGAATATAG TGAATATAG TGAATATACAC GAGTTTCAGA TCTCATCTGA TCTCATCTGA TCTCATCTGA TCTCATCTGA TCTCATCTGA TCTCATCTGA	quence n #: Eos sec 4518  21	quence  31  TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT CTCCTATCA TTTCCAGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG	GGAGGATTAA TGAGAAGCAG AGCATTTCCT ACTACAGACA ATCAAAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAA GTTTTGAGGA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT	120 180 240 300 360 420 480 540 600
50 55 60	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAGCAGAGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGGGGGAGGTGAGGGATCAAT GAGATGCAATA GAGATGCAATA GGAAAGGGA	574 DNA secid Accession tence: 146-146-146-146-146-146-146-146-146-146-	quence n #: Eos sec 4518  21   CTCACTTCGA CTCCCCCTCC TCTGGAAATG GCTCATACA CCCAAAACAA TGGGAAAACA AATGGTGTTT TGGATCAGAG TTTATCCACT	Juence  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTRATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTCAG CATTTTCAG TTTTCAGTTT	GAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCANANAN ATATTGATGA GGGATANACC ATCTCACTAA AGATAACTTT AAGGACANAA GTTTTGAGGA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAA AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG	120 180 240 300 360 420 480 540
50 55 60	Seq ID NO: Nucleic Ac Coding seq  Coding seq  CACACATACG CAAAAAAAA CGGCGAAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAACTTAATG AACACATTCA GTCAGCGGAG AAATGCAAT GAGATGCAAAA GAGATGCAAAA GAGATGCAAAA	574 DNA secid Accession dence: 148	quence n #: Eos sec 4518  21   CTCACTTCGA CTCTGGAAATG CCTGGATTGG GTCCTATACA GAACTTAACA TGGGAAACA AATGGTGTTT TGGATCAGAG TGATCGGAC TTTATCCATT	TUENCE  31    TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTCAA TTGTTTTAGG	GGAGGATTAA TGAGAAGCAG AGCATTTCCT ACTACAGACA ATCARARARA ATATTGATGA AGGATAAACT ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTCGGCACAGA GTTTTGAGGA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAA AGATCTTACCA ATCATTGGAA TCACTGGGAA ATCATCACT TCACTGGGAA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT	120 180 240 300 360 420 480 540 600
50 55	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAAC CGGCGAGGGG CAGCTCCTC CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGCGGAG AAATGCAATA GGGAAAGGGA GGATTCAAAG GTTAGAATCAAAT	574 DNA secid Accession uence: 146	quence n #: Eos sec 4518  21	Juence  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAA TTGTTTGAG AGTGTTAGTCAA CCAAACTCAA	GGAGGATTAA TGAGAAGCAG AGCATTTCCT ACTACAGACA ATCANANAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTGGGAACGAAA GTTTTGGGAA GTTTTGGGAA CTCACAAGAACAAGTA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACCGT TCACTGGGG ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC	120 180 240 300 360 420 480 540 600 660 720
50 55 60	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAGACAGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGGGGGAGGGATCCACT GTCAGGGGGG AAATGCAAT GAGATCAAT AAGATCAAT AAGATCAAT AAGATCAAT TAGATCAAT AATGCATCAAT AATGCATCAAT AATGCATCAAT AATGCATCAAT AATGCATCAAT AATGCATCAAT	574 DNA secid Accession dence: 146	quence n #: Eos sec 4518  21   CTCACTTCGA CTCGCCCTCC TCTGGAAATG GTCCTATACA CCCAAAACAA TGGGAAACAA TGGGAAACAT TGGATCAGAG TTATACAGAC TTTATCCATT TGGATCGAC GAACCTTCTG GAACCTTCTG TCCCTGCACA	JUENCE  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTRATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTCAA TTTTTGAGG AGTGTTAGTC AGTGTTAGTC AGTGTTAGTC AGTGTTAGTC CCAAACTAGT	GAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCANANAN ATATTGATGA GGGATANACC ATCTCACTAA AGATAACTTT AAGGACANAA GTTTTGAGGA GTTTTGAGGA GTTTTGGGAA GTTTTGGGAA ACTGGATTGT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCATTGGA TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTTACATTTAAAGAT	120 180 240 300 360 420 480 540 660 720 780
50 55 60	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAGACAGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCA GTCAGGGGGAGGGATCCACT GTCAGGGGGG AAATGCAAT GAGATCAAT AAGATCAAT AAGATCAAT AAGATCAAT TAGATCAAT AATGCATCAAT AATGCATCAAT AATGCATCAAT AATGCATCAAT AATGCATCAAT AATGCATCAAT	574 DNA secid Accession dence: 146	quence n #: Eos sec 4518  21   CTCACTTCGA CTCGCCCTCC TCTGGAAATG GTCCTATACA CCCAAAACAA TGGGAAACAA TGGGAAACAT TGGATCAGAG TTATACAGAC TTTATCCATT TGGATCGAC GAACCTTCTG GAACCTTCTG TCCCTGCACA	JUENCE  31   TCTATACACT CTCTCCACTC CGAATCCTAA GCTRATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTCAA TTTTTGAGG AGTGTTAGTC AGTGTTAGTC AGTGTTAGTC AGTGTTAGTC CCAAACTAGT	GAGGATTAA TGAGAAGCAG AGCGTTTCCT ACTACAGACA ATCANANAN ATATTGATGA GGGATANACC ATCTCACTAA AGATAACTTT AAGGACANAA GTTTTGAGGA GTTTTGAGGA GTTTTGGGAA GTTTTGGGAA ACTGGATTGT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCATTGGA TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTTACATTTAAAGAT	120 180 240 300 360 420 480 540 600 660 720 780 840
50 55 60 65	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTCAA GTCAGCGGAG AAATGCAATA GAGATCCAAT GAGATCCAAT GAGATCCAAT AATGGCTCAT AATGGCTCAT AACAGTTAGGCA AATGGCTCAT AACAGTTAGGCA	574 DNA secid Accession dence: 146-11   CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGCTTA TGAATACAC TGAGTTCAGA TCTACTGGATTCAGA TCTACTGGATTAAGAGC CGATTATTGA TCATACAGT TCATACAGT TCATACAGT TCATACTGTT TGACATCTCC TCTCTGAAAG	quence n #: Eos sec 4518  21   CTCACTTCGA CTCGCATTCGA CTCGGATAGG GCCTATAGA GAAACTTAAA TGGGAAACAA TGGGATCGGA TTTATCCATT TGGATCAGAG GAACCTTCTG GACCTCCTGCACA CCCAGTTGGC	Juence  31   TCTATACACT CCGAATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTCAG TTTTCAGG TTTTTCAGG ATTTTCAG AGTTTTCAG AGTTTTGAG AGTTTTGAG AGTTTTGAG GATACTCAA GACACAGTTG GTTTTTTTTGTG	GAGGATTAA TGAGAAGCAG AGGTTTCCT ACTACAGACA ATCANANAN ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAA GTTTTGAGGA GTTTTGAGGA GTTTTGGGAA GTTTTGGGAA ACTGGATTGT AAGTTGT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATTGGAA ATCATCGGT TCACTGGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTACATTTACACTATAAAGAA TAATCAACAA	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60 65	Seq ID NO: Nucleic Ac Coding seq  CACACATACE CACACATACE CAGCIAGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAACTTAATG AACACATTCA GTCAGCGGAA GAGATCCAAA GAGATCCAAA GAGATCCAAA GAGATCCAAA CAGTTACAAA TTAGAACCATAAA TTAGATCCAT AATGGCTCAT ACAGTTATG	574 DNA secid Accession dence: 148	Quence n #: Eos sec 4518  21   CTCACTTCGA CTCCCCCTCC TCTGGAATGG GTCCTATACA GAACTTAAA TGGGAAACA AATGGTGTTT TGGATCAGAG TGATCGGAC TTATCCAT TGGATCAGAG TGAGTCGGAC TCCCTGCACA CCAGTTGGCT GGACTTGCTG	TUENCE  31    TCTATACACT CTCTCCACTC CGAATCCTAA GCTAATGGAT TCTCTATCA TCTCTATCA TCTCCTATCA TCTCCAGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CGATTTTCAG GGCACACTAGT GGCACACTAGT GGCACACTTAGT CCAAACTCAA GACACAGTTG CAAAACAATT	GGAGGATTAA TGAGAAGCAG AGCATTTCCT ACTACAGACA ATCAGACAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAGAA CTTGAGAAA CTTGAGAAA ACTTGAGAA ACTTGAGAA ACTTGAGAA ACTTGAATTA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TCACTGGGAA ATCATCACT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAAGTACAAG	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60	Seq ID NO: Nucleic Ac Coding seq  Coding seq  CARARARA  CAGCARTACG CAGCAGGGG CAGCTCCTCT CTTGTTGAAG ARATATCCAA CAAGTARATG AACACATTCA ACACATTCA GAGATGCAATA GAGATGCAATA GAAAAGGGA GGATTCAAAG TTAGATCCAT AATGGCTCAT ACAGTTAGCA TCTGGTTATG TCTCTGAGA CGTTCTAGAA	574 DNA secid Accession dence: 146-111   CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGCTTA TCATAACAC TGAGTTTCATAACAC TGAGTTCATATGATTAAGAGC CGATTATTGA TCATACTGTT TGACATCTC TTTGACATCTC TCTTGAAGAC TCTTGAAGAC TCATGAAGAC TCATGAAGAC TCATGAAAGAC TCATGAAAGAC TCATGAAAGAC TCATGAAAGAC TCAGAAATGT AGGTGTTTTC CAGAAAATGT	quence n #: Eos sec 4518  21	TUENCE  31   TCTATACACT CCGAATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTCAG AGTTTTCAGG AGTTTTCAGG AGTTTTCAGG AGTTTTGAGG AGACACTTA GACACACTTG GCAAACCAATT GGAAAGAACAATT GGAAAGAACA	GAGGATTAA TGAGAAGAA ATATTGATGA AGGATAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAA ATTTTGAGGA GTTTTGAGGA ATTGAGAAAA CTGACAAGTA ACTGGATTGT AAGTTCTTAC AAGTTCTTAC AAGTTCTTAC AAGTTCTTAC AAGTTCTTAC AAGTTCTTAC AAGTTCATGA AAGTTCATGA AAGATCATGA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATTGGAA ATTCCACTT AGCAGTCAAA AGAAAATTTC GCAGGCTGCT TTACATTTAAAGAT AATGCAACAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTTACAA ACAGTTACAA	120 180 240 300 360 420 480 540 660 720 780 840 900
50 55 60 65	Seq ID NO: Nucleic Ac Coding seq  Coding seq  CACACATACG CAAAAAAAA CGGCGAGGGG CAGCTCCTCTTGTTGAGG AAATATCCAA CAACTTAATG AACACATTCA GTAGCGGAA GAAAAGGGA AAATGCAATA GAGATGCAATA AGAGTTACAT AATGCTCAT AATGCTCAT ACAGTTAGAC TTCGTTATG TTCTCTAGAAC AGTTCAGAAAA AGTTCAGAAAA	574 DNA secid Accession dence: 148 11   CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGATA TCATAACAC GAGTTTAAG TCTACTGAT AGTTAAGAGC CGATTATGA TCATACTGT TGACATCTCT TGACATCTCT AGTTATGAT TCATACTGTT TGACATCTCT AGGTGTTTCCAGAAAGT TCATACTGAT AGGTGTTTCCAGAAAGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAGTGT	Quence n #: Eos ser 4518  21   CTCACTTCGA CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA AAAGATTAAA TGGGAAACA AATGGTGTT TGGATCGGAC TTTATCCATT TGGATCGGAC GACCTTCTG GCACTACAC GCACTTGCC GGACTACTTA CTCATACACT TCAGGCTGAC TTAGGATTAC	TUENCE  31    TCTATACACT CCGATCCACTC CCGATCCTACA GCTAATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAGG AGTTTTCAG GACACAGTTG GCAAACTCAA GACACAGTTG CCAAACAATT GGAAAGGAAC CCAGAGAATT ATGATTAGAG CCAGAGAATT ATGATTAGAGA	GGAGGATTAA TGAGAAGCAG AGCATTCCT ACTACAGACA ATCARAAAAA ATATTGATGA AGGATAAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAAAA CTTGGACAGA CTGACAGAA CTGACAAGTA ACTGATTCTTAC ACTGATTATA ACTTGATTAC ACTGATTATAC ACTGATTACAGA AGATTCATGA ATACCAGCCT AGGTTTGAGGA ATACCAGCT AGTTTTGAGGA ATACCAGCT AGTTTTGAGGA ATACCAGCT AGTTTTGAGGA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAA ATCATTGGAA TCACTGGGAA TCACTGGGAA ATCATTCACTT AGCAGTCAAA AGAAAATTTG CCAGTTAAA AGAAAATTTAC TTTAAAGAT TAATGCAACAA ACAGTACAA ACAGTACAA ACAGTACAA TCTTGTTACA TTTGTTACAA	120 180 240 300 360 420 480 660 720 840 900 900 1020
50 55 60 65	Seq ID NO: Nucleic Ac Coding seq  Coding seq  CACACATACG CAAAAAAAA CGGCGAGGGG CAGCTCCTCTTGTTGAGG AAATATCCAA CAACTTAATG AACACATTCA GTAGCGGAA GAAAAGGGA AAATGCAATA GAGATGCAATA AGAGTTACAT AATGCTCAT AATGCTCAT ACAGTTAGAC TTCGTTATG TTCTCTAGAAC AGTTCAGAAAA AGTTCAGAAAA	574 DNA secid Accession dence: 148 11   CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGATA TCATAACAC GAGTTTAAG TCTACTGAT AGTTAAGAGC CGATTATGA TCATACTGT TGACATCTCT TGACATCTCT AGTTATGAT TCATACTGTT TGACATCTCT AGGTGTTTCCAGAAAGT TCATACTGAT AGGTGTTTCCAGAAAGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAAATGT TCTCAGAGTGT	Quence n #: Eos ser 4518  21   CTCACTTCGA CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA AAAGATTAAA TGGGAAACA AATGGTGTT TGGATCGGAC TTTATCCATT TGGATCGGAC GACCTTCTG GCACTACAC GCACTTGCC GGACTACTTA CTCATACACT TCAGGCTGAC TTAGGATTAC	TUENCE  31    TCTATACACT CCGATCCACTC CCGATCCTACA GCTAATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAGG AGTTTTCAG GACACAGTTG GCAAACTCAA GACACAGTTG CCAAACAATT GGAAAGGAAC CCAGAGAATT ATGATTAGAG CCAGAGAATT ATGATTAGAGA	GGAGGATTAA TGAGAAGCAG AGCATTCCT ACTACAGACA ATCARAAAAA ATATTGATGA AGGATAAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAAAA CTTGGACAGA CTGACAGAA CTGACAAGTA ACTGATTCTTAC ACTGATTATA ACTTGATTAC ACTGATTATAC ACTGATTACAGA AGATTCATGA ATACCAGCCT AGGTTTGAGGA ATACCAGCT AGTTTTGAGGA ATACCAGCT AGTTTTGAGGA ATACCAGCT AGTTTTGAGGA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAA ATCATTGGAA TCACTGGGAA TCACTGGGAA ATCATTCACTT AGCAGTCAAA AGAAAATTTG CCAGTTAAA AGAAAATTTAC TTTAAAGAT TAATGCAACAA ACAGTACAA ACAGTACAA ACAGTACAA TCTTGTTACA TTTGTTACAA	120 180 240 300 360 420 480 540 660 720 780 900 960 1020 1080 1140
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAC CAGCTCCTCT CTTGTTGAGA AAATACAA CAAGTAAATG AACACATTCA ACACATACAA GAGATCCAAT AATGCAATA AATGCAATA AATGCAATA AATGCTCAT AACAGTTAAAG TTAGATCCAT ACAGTTAGAT ACAGTTAGAT TCTCTCAGAC TCTCTCTAGAAC TCTCTCTAGAAC TCTCTCTAGAAC TCTCTCTAGAAC TCTCTCTAGAAC CAGTTCAGAAC	574 DNA secid Accession dence: 146 11   CACGCACGAT ATTTCTTCG CCGCAGACCG GTGTTTGCCG AGATTGCTG TGAATACAGA TGTCATACAGA TGTCATCAGA TGTACTGGATTAGAGAGCATACTGAT TGACATCTCC TCTCTGAAAG TCATACTGAT AGGTGTTTTC CCAGAAAATGT CTCAGAGCACACATCATACTGT TTCACACTCCC TCTCTGAAAG TCAATACTGT TGACATCTCC TCTCTGAAAG TCAATACTGT TGACATCTCC TCTCTGAAAG TCAATACTGT TCAGAGAGACACA TCAATACTGT TAGATCTCC TCTCTGAAAG TCAAGAGACCA TCAATACTGT TCAGAGAGACA TCAATACTTATTTATTTATTTATTTATTTATTTATT	quence n #: Eos sec 4518  21   CTCACTTCGA CTCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA AATGGTGTT TGGATCAGAG GAACCTTCAG GAACCTTCAG TCCTGCACA CCAGTTGGCT TCGCACA CCAGTTGGCT TCAGCGTGACA CCAGTTGGCT TCAGCGTGACA CTATACACT TCAGCGTGACA CTATACACT TCAGCGTGACA CACCAAGCAT ACCCAAGCAT ACCCAAGCAT ACCCAAGCAT ACCCAAGCAT GCTACCCAAT	JUENCE  JI  TCTATACACT CCGAATCCTAA GCTRATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAATTTAG CAATTTTCAG AGTGTTTGAG AGTGTTTGAG AGTGTTAGT CCAAACTCAA GACACACTCAA GACACACTCA GATACTTTTTGTG GAAAACAATT GGAAACGAAT ATGATTGAGA AGAATTTTGAG AGATTTGAGG AGATTTTGAGG AGATTTTTAG GAAAACAATT ATGATTGAGA AGAATTTTGAGA ATGATTTGAGA	GAGGATTAA TGAGAAGAA ATCATACAGACA ATCATGATGA ATATTGATGA ATATTGATGA ATATTGATGA AGATAACTT AAGGACAAAA ATTTTGAGGA GTTTTGAGGA GTTTTGAGAA GTTTTGAGAA ACTGGATTGT AAGTTCTTAC TCGAGAAGTA ACTGGATTGT AAGTTCTTAC TCGAGAGCA AGATTCATGA AGATTCATGA ATACCAGCCT AGTTTGCAGAT ATTCTTCAGAT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTACA TTACATTTACA TTATAAAGAT AATGCAACAA ACAGTACAAA ACAGTACAAA ACAGTACAAA TCTTTAAA	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1200
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA GTCAGCGGAG AAATACCAA GTCAGCGGAG AAATCCAATAC GTCAGCGGAG AAATCCAATA GAGATCCAATA AATGCAATA AATGCTAATA ACACTTAGAC TTAGATCCAT AATGGCTCAT ACACTTAGAC TCTCTTAGAC TCTCTTAGAC TCTCTTAGAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC AGTTCAGAAC CGGTAAAGAC CAGTTGGATGG GTGCTTATC	574 DNA secid Accession dence: 148 11   CACGCACGAT ATTTCCTTCG CCGCAGACCG GTGTTTGCCG AGATTGGCTG GAGTTTCATAACAC GAGTTTCAGA TCTACTGAT TCTACTGAT TCTACTGAT TCATACTGT TGACATCTCC TCTCTGAAG TCATGCTGAT AGGTGTTTTC CAGAAAATGT CTCAGATCGT GAGAGACACAT GAGAGACCAT CAATAATTTG	quence n #: Eos ser 4518  21   CTCACTTCGA CTCGCATCGG TCTGGAAATG CCTGGATTGG GTCCTATACA AATGGTGTT TGGATCAGAG TTATCAAT TGGATCAGAG GAACCTTCTG GACTCAT GAACCATTTACCATT TCCATTCTG TCCTGCACA CCAGTTGGT GGACTACTTA CTCATACACT TCAGTCGAC TTATCATAT CTCATACACT TCAGTCGAC TCATACACT TCAGTCGAC ACCAGTGAC AACCAAGCAT GCTACCAAAG AACCAAGCAT AAAATACAGC	TUENCE  31  TCTATACACT CCGATCCTAA GCTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTAG AGTTTCAGG GTTTTCAGG GATTTTCAG GACACAGTA CCAAACTCAA GACACAGTA GACACAGTA CCAAACTAG GACACAGTT GGAAAGGAA TTGTTGGG CCAGAAATT ATGATTGAG AAACAATT GGAAAGGAA GACATTTTGAG AAACAATT ATGATTGAGA GACAATTTAGA GACAACTGA	GGAGGATTAA TGAGAAGAA ATATTGATGA AGGATAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAAA GTTTTGAGGA GTTTTGAGGA ACTGGACAAGTA ACTGGATTATTCACAAAA ACTGGATTGTTCAGAAA ACTGGATTGTTCAGAAA ACTGGATTGTTCAGAAAAA ATACCAGCT AGGTTTGCAGAT ATTCTTCAGGT AGTTTTCAGGT ATTCTTCAGAT TTCTTCAGATT TTCTTCAGATT TTCTTCAGAT	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAA TTGGGGAAA TGACTACCGT TCACTGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTAC TTTACAGTTAAC TTTACATTTAC TTTTAAAGAT ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAG TCTTTACAGTTAC TTTTTACAGTTACA TCTTGTTACCAG TCAAGACTTG AGTAGCAAT GCCTACTGAT	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1140 1260 1260 1320 1380
50 55 60 65	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CARARARAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG ARATACAA ACATTCAA GTCAGCGGAG ARATCCAAT GAGATCAAT GAGATCAAT ACAGTTCAAG GTTAGATCCAT ACAGTTCAAC TTCGTTATG TTCTTTGGAC AGTTCAGAAC AG	574 DNA secid Accession ac	Quence n #: Eos sec 4518  21   CTCACTTCGA CTCCCCTCC TCTGGAAATG CCTGGATTGGA GCTAACAA CCCAAAACAA AATGGTGTT TGGATCAGAG TGATCGGAC TCTACCACT TCCCTGCACA CCAGTTGGCT TCCCTGCACA CCAGTTGGCT TCAGGCTGACA CTCATACACT TCAGGCTGACA CTATACACT CTACACACT TCAGGCTGACA CTATACACT CTACAAGCAT GCTACCAAGCAT GCTACCAATACAAC CCCCGAATTA	31  TCTATACACT CTATACACT CTATCACTC CGAATCCTAA GGTAATGGAT TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA AAAGCAAGCA CATAGTTTAG CGATTTTGAG AGTCTTTGAG GACACAGTT GGAAACTCA TTTTTGTG CAAAACAATT ATGAATTAGAA CAAGTTG AGAATTTTTGAG AAATTTTTGAG AAACAATT GGAAACGAATT ATGATTGAGA AAACTATTTGAGA AAACCAACTTG AAATTTTTGAGA AAACCAACTTG AAATTTTGAGA AAACCAACTTG AAACCAACTTG AAACCAACTTG AAACCAACTTG AAACCAACTTG AAACCAACTTG AATTGGAACTG AATTGGAACTG	GGAGGATTAA TGAGAAGCA AGCATTTCCT ACTACAGACA ATCAGACAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA TTGGGACAGAA CTTGAATAAC CTGACAAGTA ACTTGATTAC TTCGAGAGCA AGATTCTTAC AGTTTTGAGGA AGATTCATGA TTCGAGAGCA AGATTCATGA TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTCTTCAGAT TTGTTCAGAT TTGTTCAGAT TTGTTCAGAT	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TCACTGGGA ATCATTGGAA TCACTGGGA AGAACTTAC TTCACTGTA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAG ACAGTTAGT TCTTGTTAC TCTTGTTACAG TCAAGACTTG AGTAGCATTG AGTAGCATTG AGTAGCATTG AGTAGCATTG AGTAGCATTG AGTAGCATTG AGTAGCATTG AGTAGCATTG AGTAGCATAC TCAAGACTTG AGTAGCATAC CAAGACGAG	120 180 240 300 360 480 540 660 720 780 900 960 1020 1140 1200 1200
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAAC CAGCIAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTACA GTCAGCGGAG AAATGCAATA GAGATCCAAT AATGCTATA AATGCTATA AATGCTAT AATGGCTCAT ACAGTTAGAC TTCTCTAGAC TCTCTGTTATG TTCTCTAGAC CAGTTCAGAAC CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT AATCCTAAAC GGTGCTTATTC TGCACTAATG AATCCTGAAC CAGAGGGGAA	574 DNA secid Accession ac	Quence n #: Eos sec 4518  21   CTCACTTCGA CTCCCCCTCC TCTGGAAATG GCTCACTTACA CCCAAAACAA TGGGAAAACA TGGGAAAACA TGGATCAGA GAACTTCTG GTCCTCCACA CCAGTTGGT TCAGGTCGACA CCAGTTGGCT TCAGGCTGAC TCATACACT TCAGGCTGAC ACCAAGCAT AAAATACAGC CCCTGAATT AGAAGGCGT	JUENCE  J1  TCTATACACT CTCTCCACTC CGAATCCTAA GCTRATGGAT TCTCCTATCA TTTCAGGGTT GTGGAATTA AAAGCAAGCA CATAGTTTGA CGATTTTCAA GCTTTTGAGG AGTGTTAGTC CCAAACTCAA GACACAGTTG GTTTTTTGTG GGAAAGAAT ATGATTGAGA AGACACAGAA ATTGATTGAGA ATTGATTAGA ATTGAATCGAACTGA ATTGGAACTGA ATTGGAACTGA ATTGGAACTG	GAGGATTAA TGAGAAGAA ATATTGATGA AGCATTACATAA ATATTGATGA AGCATAAAAA ATATTGATGA AGCACAAAA ATTTTGAGACAAA ATTTTGAGACAAGA ATTTTGAGAA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA TTCAGAGCA ATACCAGCT AGTTTCAGA TTCTCAGAT TTGTCAGAT TTGTCAGAT AGAATAAT TTGTCAACAAT AAGAATAAT TTGTCAACAAT AAGAATAAT TTGTCAACAAT AAGAATAAT CTGGTAGAGAA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCATCAGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA ACAAATTTCCACTT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAA ACAGTACTACA TTCGTACTACA TCAAGACTTGAT ACAGGAAGAAGAA CAAGGAAGGAAG	120 180 240 300 360 420 660 660 720 780 840 900 960 1020 1140 1260 1260 1320 1380
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAAC CAGCIAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AACACATTACA GTCAGCGGAG AAATGCAATA GAGATCCAAT AATGCTATA AATGCTATA AATGCTAT AATGGCTCAT ACAGTTAGAC TTCTCTAGAC TCTCTGTTATG TTCTCTAGAC CAGTTCAGAAC CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT CAGTTCAGAT AATCCTAAAC GGTGCTTATTC TGCACTAATG AATCCTGAAC CAGAGGGGAA	574 DNA secid Accession ac	Quence n #: Eos sec 4518  21   CTCACTTCGA CTCCCCCTCC TCTGGAAATG GCTCACTTACA CCCAAAACAA TGGGAAAACA TGGGAAAACA TGGATCAGA GAACTTCTG GTCCTCCACA CCAGTTGGT TCAGGTCGACA CCAGTTGGCT TCAGGCTGAC TCATACACT TCAGGCTGAC ACCAAGCAT AAAATACAGC CCCTGAATT AGAAGGCGT	JUENCE  J1  TCTATACACT CTCTCCACTC CGAATCCTAA GCTRATGGAT TCTCCTATCA TTTCAGGGTT GTGGAATTA AAAGCAAGCA CATAGTTTGA CGATTTTCAA GCTTTTGAGG AGTGTTAGTC CCAAACTCAA GACACAGTTG GTTTTTTGTG GGAAAGAAT ATGATTGAGA AGACACAGAA ATTGATTGAGA ATTGATTAGA ATTGAATCGAACTGA ATTGGAACTGA ATTGGAACTGA ATTGGAACTG	GAGGATTAA TGAGAAGAA ATATTGATGA AGCATTACATAA ATATTGATGA AGCATAAAAA ATATTGATGA AGCACAAAA ATTTTGAGACAAA ATTTTGAGACAAGA ATTTTGAGAA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA ACTGACAAGTA TTCAGAGCA ATACCAGCT AGTTTCAGA TTCTCAGAT TTGTCAGAT TTGTCAGAT AGAATAAT TTGTCAACAAT AAGAATAAT TTGTCAACAAT AAGAATAAT TTGTCAACAAT AAGAATAAT CTGGTAGAGAA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCATCAGT TCACTGGGGA ATTTCCACTT AGCAGTCAAA ACAAATTTCCACTT TTACATTTAC TTTTAAAGAT AATGCAACAA ACAGTACAAA ACAGTACTACA TTCGTACTACA TCAAGACTTGAT ACAGGAAGAAGAA CAAGGAAGGAAG	120 180 240 360 420 480 540 660 720 780 900 900 1020 1180 11200 1260 1320 1380 1440
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CARARARAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG RARTATCCAA GACATTCA GTCAGCGGAG GATTCAATG GAATGCAATA GAGATGCAATA GAGATGCAATA ACGGTTAGCA TTAGATCCAT ACTGGTTATG TTCTTTGGTATG TTCTTTGGTATG TTCTTTGGTAT CAGTTCAGAC GGTAGAGAC CAGTTGGATG GGTGCTTATTG GGTCTTATTG GATCCTAATG GAAGAGGGAA AACCAAATAC ACCAAATAC ACCAACT ACCAACT ACCAACT ACCAACT ACCAACT ACCAACT ACCAACT ACCAACT ACCA	574 DNA secid Accession ac	quence n #: Eos sec 4518  21   CTCACTTCGA CTCCCCCTCC TCTGGAAATG CCTGGATTGGA GCTAACAA GGAAACTA TGGGATCAGAG TGATCGGAC TTTATCCATT TGGACTCAGA GAACCTTCTG GCCTGCACA CCAGTTGGAT GGACTACTA GGACTACTA GAACTACTA CTCATACACT TCAGGCTGAC CAACTACTA CTCATACACT TCAGGCTGAC TTATGATACACT TCAGGCTGAC ACCAAGCAT AAAATACAGC CCCTGAATTA AGAAGGCGCT ACCCCAAACTA AGAAGGCGCT ACCCCAACTTA AGAAGGCGCT ACCCCAACTTA AGAAGGCGCT ACCCCAACTTA ACCCCCAACTTA ACCCCAACTTA ACCCCCAACTTA ACCCCAACTTA ACCCCCAACTTA ACCCCAACTTA ACCCCCAACTTA ACCCCCAACTTA ACCCCAACTTA A	JI  TCTATACACT  CTATCCACTC  CGAATCCTAA  GCTAATGGAT  TCTCCTATCA  TCTCCTATCA  TCTCCTATCA  TCTCCTATCA  TCTCCTATCA  TCTCCTATCA  TTTCAGGGTT  ANAGCAAGCA  CATAGTTTAG  GATTTTCAG  GTTTTTGTG  GTTTTTTGTG  GTTTTTTGTG  GTAATCAATT  GGAAACAATT  ATGAATAGAA  AATGGAATT  ATGATTAGA  AATGGAACTGA  ATTGGAACTGA  ATTGGAACTGA  ATTGTGAACTG  ATTGTGAACTG  ATTGTGAACTG  ATTGTGAACTG  ATTGTGAACTC  TCTACCACAA	GGAGGATTAA TGAGAAGAA AGCATTCCT ACTACAGACA ATCARARARA ATATTGATGA GGGATARAC ATCTCACTAA AGATAACTTT ARGACAAAA GTTTTGAGGA TTGGGACAAGA CTGACAAGTA ACTGATTTAC ACTGATTAC ACTGATTAC AGTTTTAC AGTTCTTAC AGTTTTCAGGA ATACCAGCCT AGGTTCTAGAT TTCTCAGAT TTCTCAGAT TTCTCAGAT TTCTCAGAT TTCTCAGAT TTCTCAGAT CAGATGGCTA AGATACATAC CAGATGGCTA CAGATGGCTA CAGATGGCTA CAGATGGCTA CAGATGACAG CACACTACAG CACACTACAG GAGGAAGTGA	ACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TCACTGGGA ATCATCACT AGCAGTCAAA AGAAAATTTG CCACTT AGCAGTCAAA AGAAAATTTAC TTTAAAGAT TAATGCAACAA ACAGTACAAG ACAGTTCTAC TTTGTTACA TTTGTTACA TTTGTTACCAC TCAAGACTTG AGTAGCATA AGCAGTTTG AGTAGCATA AGCAGTTTG TCATGGCATA CAAGACTTG AGTAGCATA CAAGACGAG TCAAGAGAGA CAATGCTACA TCAAGAGAGAG TCACATAGGG ATTCTCTGGA	120 180 240 300 360 480 540 660 720 780 960 1080 1140 1260 1320 1380 1340 1500
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAAC CAGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATATCCAA CAAGTAAATG AGTCAGCGGAG AAATGCAATA GAGATCAATA GAGATCAATA AGGAATCAAT AATGCTCATA ACAGTTAGA TTACATCAAG TTCTCTAGAC TCTCGTTATG TTCTCTAGAC ACGTTAGAT CAGTTCAGAAC CGGTAGATC GGTGCTATTC GGCACTAATG AATCCTGAAC AAGGGGAAATACA AAGGGAAATCA AAGGGAAATCA AAGGGAAATCA AAGGGAAATCA AAGGGAAATCA	574 DNA secid Accession ac	Quence n #: Eos sec 4518  21	JUENCE  JI  TCTATACACT CTCTCCACTC CGAATCCTAA GCTRATGGAT TCTCCTATCA TTTCAGGGTT GTGGAATTTA ARACCAGCA CATAGTTTAG CGATTTTCA GGTTTTGAG AGTGTTAGA TTGTTTAGAG AGCACAGAT GCAAACTCA CARAACAATT GGAAAGTAG CCAGAGAATT ATGATTGAG ATTGATTAGA ATTGATTAGA ATTGAATTGA ATTGAACTGA ATTGAACTGA ATTGAACTG ATTGAACTG ATTGAACTG ATTGAACTG ATTGCACACA TCCCCCAACAA TCCCCCACAA	GAGGATTAA TGAGAAAAA ATATTGATGA GGGATAAAAC ATCACAAAAAA ATATTGATGA GGGATAAACC ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA GTTTTGAGAA ACTGATATACTTT CAGAAGTTA ACTGATTACAGT ATACCAGCCT AGTTTCATGA ATACCAGCCT AGTTTCAGAT TTGTCAGAT TTGTCAGAT TTGTCAGAT TTGTCAGAT TTGTCAGAT TTGTCAGAT AGAATAAT CAGATAATAA CAGACTTAAAGAAAAAAAAAA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCATCAG ATCATTGGAA ATCATTGGAA ATTACCATT AGCAGTCAAA ACAAATTTC GCAGGCTGCT TTACATTTAA ACAATACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACCAA TCTGTTTACA TTGTACCAG TCAGGACTTGA TCAGGAGGAGGAG CAGTGCTACT CGCATAGGG ATTCTCTGGA TAAATTAGCC	120 180 240 300 360 480 540 600 720 780 900 960 1020 1140 1200 1320 1380 1440 1500
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAC CAGCIAGGGG CAGCTCCTCT CTTGTTGAAG AAATACCAA CAAGTAAATG AACACATTCAA GACACATTCAA GACACATTCAA GACACATACAG ATTCCAAAG TAGGATCCAT AATGCTCAT ACAGTTAGAC TCTCTCTAGAC TCTCTCTAGAC AGTTCAGAAC TGGAAAGAGGAA AGCAAATCA AACGAAATCA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGGTTAATG AACGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA	574 DNA secid Accession ac	quence n #: Eos sec 4518  21    CTCACTTCGA CTCACCTCGA CTCGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGATCAGAG TTATCCATT TGGATCAGAG TCATCAGT TCAGATCGAC CCAGTTGGCT GGACTACTAC CTCATACACT TCAGGCTGAC CCAGTTGGCT AGACCAAGCAT AAAATACAGC CCCTGAATTA AGAAGGCGCT ACCCCAATTA AGAAGGCGCT GCCTACACCGA ATCTTTAAACT GCTTACCGA TTATGATACCC AACCAATTA AGAAGGCGCT ACCCCAGATTA AGAAGGCGCT GCCTAACCGA ATCTTTAAAT GCATTCTCAG	JUENCE  JI  TCTATACACT CCGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAATTTAG CATAGTTTAG CATAGTTTAG CATAGTTTAG CATAGTTTAG GCAAACTAA GACACAGTA GACACAGTT GGAAACAAT GGAAACAAT GGAAACAAT ATGATTGGA ATTGATTAG ATTGATTAG ATTGATTAG ATTGATTAG ATTGATTAG ATTGATTAG ATTGATTAG ATTGACTAG ATTGCACTAC ATTGCACTAC ACTGTCACTG	GAGGATTAA TGAGAAGAA ATATTGATGA AGATTACATAA ATATTGATGA GGATAAACA ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA ACTGGATTGTTTCACAAGTA ACTGGATTGT AAGTTCTTAC TCGAGAGTA ACTGGATTGT AAGTTCTTAC TCGAGAGCA AGATTCATGA ATACCAGCCT AGTTTGCAGT TTGTCGACAT TTGTCGACAT AAGAATTAAT TCTGTAGAG CACACTACAA GAGAAAGTAA AACCAGTCACAA CACCACCACACACACACACAACAACAACACACACACACAC	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATTGGAA ATCATTGGAC ATTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGAACAA ACAGTACAAA ACAGATACAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA TTGTACAG TCAAGACTTG AGTTAGACAGA CCAGTCTGAT CAAGAGAGAGA CCAGTGCTACA CCAGCTTACA TCACATACAGA TCAAGACTTGAT CAAGACTTGAT CAAGACTTACA TCACAGATACAGA TCAAGACTTACA TCACATAGAGAAA ACAGTACAGA TCAAGACTTACA TCACATTAGAC TCACATTAGAC TCACACTGTG	120 180 240 360 420 480 540 660 720 780 900 900 1020 11200 1260 1320 1380 1440 1560 1620
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAC CAGCIAGGGG CAGCTCCTCT CTTGTTGAAG AAATACCAA CAAGTAAATG AACACATTCAA GACACATTCAA GACACATTCAA GACACATACAG ATTCCAAAG TAGGATCCAT AATGCTCAT ACAGTTAGAC TCTCTCTAGAC TCTCTCTAGAC AGTTCAGAAC TGGAAAGAGGAA AGCAAATCA AACGAAATCA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGGTTAATG AACGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA AAGGAAATACA	574 DNA secid Accession ac	quence n #: Eos sec 4518  21    CTCACTTCGA CTCACCTCGA CTCGGAAATG CCTGGATTGG GTCCTATACA CCCAAAACAA GAAACTTAAA TGGGATCAGAG TTATCCATT TGGATCAGAG TCATCAGT TCAGATCGAC CCAGTTGGCT GGACTACTAC CTCATACACT TCAGGCTGAC CCAGTTGGCT AGACCAAGCAT AAAATACAGC CCCTGAATTA AGAAGGCGCT ACCCCAATTA AGAAGGCGCT GCCTACACCGA ATCTTTAAACT GCTTACCGA TTATGATACCC AACCAATTA AGAAGGCGCT ACCCCAGATTA AGAAGGCGCT GCCTAACCGA ATCTTTAAAT GCATTCTCAG	JUENCE  JI  TCTATACACT CCGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TTTCAGGGTT GTGGAATTTAG CATAGTTTAG CATAGTTTAG CATAGTTTAG CATAGTTTAG GCAAACTAA GACACAGTA GACACAGTT GGAAACAAT GGAAACAAT GGAAACAAT ATGATTGGA ATTGATTAG ATTGATTAG ATTGATTAG ATTGATTAG ATTGATTAG ATTGATTAG ATTGATTAG ATTGACTAG ATTGCACTAC ATTGCACTAC ACTGTCACTG	GAGGATTAA TGAGAAGAA ATATTGATGA AGATTACATAA ATATTGATGA GGATAAACA ATCTCACTAA AGATAACTTT AAGGACAAAA GTTTTGAGGA GTTTTGAGGA ACTGGATTGTTTCACAAGTA ACTGGATTGT AAGTTCTTAC TCGAGAGTA ACTGGATTGT AAGTTCTTAC TCGAGAGCA AGATTCATGA ATACCAGCCT AGTTTGCAGT TTGTCGACAT TTGTCGACAT AAGAATTAAT TCTGTAGAG CACACTACAA GAGAAAGTAA AACCAGTCACAA CACCACCACACACACACACAACAACAACACACACACACAC	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCATTGGAA ATCATTGGAC ATTCCACTT AGCAGTCAAA AGAAAATTTG GCAGGCTGCT TTACATTTAC TTTTAAAGAT AATGAACAA ACAGTACAAA ACAGATACAA ACAGTACAAG AGCAGTTTGT TCTTGTTACA TTGTACAG TCAAGACTTG AGTTAGACAGA CCAGTCTACA CCAGTACTGAT CAAGACTTG CAAGACTTG CAAGACTTG CATCACTGAT CAAGACTACAA CAAGTACAGA TCAAGACTTACA TCACAGACTTACA TCACAGACTTACA TCACATAGGA ATTCTCTGGA ATTATTAGCC TCACACTGTG	120 180 240 300 360 480 540 660 720 780 900 960 1080 1140 1260 1320 1320 1440 1500 1560 1680
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CABABABAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG ABATATCCAA CAAGTABATG AGTCAGCGGAG AAATGCAATA GAGATGCAAT ACAGTTCAAAG TTAGATCCAT ACTGGTTAGA TCTTGGTTAGA TCTTGGTTAGA TCTTGGATTAGAC TCTGGTTATG TTCTCTAGAC TGGGAAAGAC CAGTTGGAT ACAGTTAGAT ACAGTTAGAT AATGCTTATAG AATCCTAAAC AGAAATCA AACGGTATTAGAAC AACGGAATACA AACGGTAATCA ACGAAATCA ACAGAAAAAGGGAAAAAGGGAAAAAGGGAAAAAGGGAAAAAGGGAAAA	574 DNA secid Accession ac	quence n #: Eos sec 4518  21	JUENCE  JI  TCTATACACT CTCTCCACTC CGAATCCTAA GCTTAATGGAT TCTCCTATCA TTTCAGGGTT GTGGAAATTAGA ARACCAAGCA CATAGTTTAG CGATTTTGAG AGTGTTAGAC GTTTTTGAG GTTTTTGAG GTTTTTGAG GTTTTTGAG GTTTTTGAG ACAGACTCA ATGATTAGA ATGATTAGA ATGATTAGA ATTGATAGA ATTGAACAC ATTGAACCA ATTGAACCA ATTGAACCA ATTGAACCA ATTGAACCA ATTGAACCA ATTGAACCA ATTGAACCA ATTGAACCA ATCACACA TCCCCAACAA TCCCCAACAA TCCCCAACAA TCCCAACAA ATCACTTCCC ACTGTGACTG ACAGTTCTA	GAGGATTAA TGAGAGAA AGATTGATGA AGATTAAAAAA ATATTGATGA AGATAAAAA ATATTGATGA AGATAAACTTT AAGGACAAAA CTGACAGAA ACTGACAGA GTTTTGAGGA CTGACAGTA ACTGACAGTA ACTGACAGTA ACTGACAGTA ATACTCTTAC TTCGAGAGC TTCTTAGAGT TTGTCGACAT TTGTCGACAT TTGTCGACAT TTGTCGACAT TTGTCGACAT TTGTCGACAT TTGTCGACAT TTGTCGACAT AGAATAAAAAAAAAA	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCATCAG ATCATTGGAA ATCATTGGAA ATTACCATT AGCAGTCAAA AGAAATTTG GCAGGCTGCT TTACATTTAA ATTACATTTAC ATTGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAA ACAGTACAAC TCTTGTACA TTTGTACCAG TCAGGACTTGT TCATGTACA TCTTGTACCAG AGTAGCAG ATTCTCTGGA ATTACTCTGCA TCAGCATAGGG ATTCTCTGGA TAAAATTAGCC TCACACTGTG TCACACTGTG TCACACTGTG TCACACTGTG TCACACTGTG TCACACTGTG TCACACTGTG TCACACTGTG	120 180 240 300 360 480 540 660 720 780 960 1020 1140 1260 1320 1380 1440 1560 1560 1680 1740
50 55 60 65 70 75	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAC CAGCIAGGGG CAGCTCCTCT CTIGTTGAGA CAAGTAAATG AACACATICA ACACATACA GACACATACA GACACATACA GACACATACA GACACATACA GACACATACA GACACATACA GACACATACA ACGACATACA TCACACAAA ACGACATACA ACGACATACA CAGTTCAGAC TCTCTCTCAGAC TCTCTCTCAGAC TCTCTCTAGAC TCGCTATAC TCGCTATAC TCGCTATAC ACGTTAGATC AATCCTAAAC AAGGACAAATCA AACGAAATACA AAGGATAATCA AAGGATAATCA AAGGATAATCA AAGGATATCA AAGGATATCA AAGGATATCA AAGGATACA AAGGATATCA AAGGATATCA AAGGATATCA AAGGATATCA AAGGATATCA AAGGATATCA AAGGATATCA AAGGATATCA AAGGATATTCAGAC GAAGATAAAG GAAGGTTACTT AACTTCTCGG	574 DNA secid Accession ac	quence n #: Eos sec 4518  21	JUENCE  JI  TCTATACACT CCGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCAGGCT GGAGCACTGA ACTCCTATCA TTTCAGGGTT GTGGAATTTAG CAATTTTCAG ACTGTTTGAG ACTGTTTGAG ACTGTTTGAG ACTGTTAGT CCAAACCAAT GCAACACTGA ATTGTAGAG GAATTTTTGA GGACAGAAT ATGATTAGG AAACCAAT ATGATTAGG ATTGTAACTG ATTGCACACA ATTGCACACA ATTGCACACA ATCCCCAACAA TCCCCAACAA TCCCCAACAA TCCACTTCCC ACTGTGACTG TCTAAAACTG ACTGTGACTG TCTAAAACTG ACTGTGACTG TCTAAAACTG ACAGTTTCTA ACAGTTCTAA ACAGTTTCTA ACAGTTCTAA ACAGTTTCTA ACAGTTCTAA ACAG	GAGGATTAA TGAGAAAAA ATATTGATGA AGGATAAACA ATCACAAAAAA ATATTGATGA AGGACAAAAA ATATTGAGGA ATCACTAA AGGACAAAA ATTTTGAGGA GTTTTGAGGA GTTTTGAGGA ACTGGATTGT AAGTTCTTAC TCGAGAGCA AGATTCATGA AGATTCATGA ATTCTTCAGGA TTCTTCAGGA TTCTTCAGGA TTCTTCAGAT AGATTGAT AAGATTCATA AGAATTAA TTCTTCAGAT CAGAATGAT AAGAATGAT AAGAATGAT AAGAATGAT AAGAATGACA AACTGCCACC TCTTAGATC TTACAGAC TTACAGAC TTACAGAC TTACAGACT TAACAGAATTAA AACCAGTCAC TCTTTAGATC TAACAGAATTAA AACCAGTCAC TCTTTAGATC	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAATTTG GCAGGCTGCT TTACATTTACA TTACATTTACA TTACATTTACA TTACATTTACA ATCAGTACAAA ACAGTACAAA TTCTTTACA TTCTTTACA TTCTTTACA TTCTTTACA TTCTTTACA TCAGTACATAC CAGTGCTACA TCACATATGG TCACACTTGTG TCACACTTGTG TCACACTTGTG TCACACTTGTG TCACACTTGTG TCACACTTGTG TCACACTTGTG TGAGGAGGAG CTCCAGGTCCC	120 180 240 360 420 480 540 660 720 780 900 900 1020 11200 1260 1320 1440 1560 1560 1620 1620 1620
50 55 60 65 70 75	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CAAAAAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG AAATACCAA CAAGTAAATG AACACATTCAA GATAGCGGAG AAATGCAATA GAGATGCAATA GAGATGCAATA AGGATCCAT AATGCTCAT ACTTCAGAG TTCAGAGGGA ACTTCAGAG CAGTTCAGAC CGGAAAGGGA AGTTCAGAAC AGGTGCTATTG AATCCTGAAC GAAGAGGAAA AACCAAATCA AAGGGTAATG AACGAAATCA AAGGGTAATG AACGAAATCA AAGGGTAATG AACTTGTCGG AGTTTATGCG AGTTTATGCG AGGTTATTG AACTTGTCGG AGTTTATG ACTTGTCGG AGTTTATG ACTTGTCGG AGTTTATG ACTTGTCGG AGTTTATG ACTTGTCGG AGTTTATG ACTTGTCGG AGTTTATG ACTTGTCGG AGTTTATTG ACTTGTCGG AGTTATTTG ACTTGTCGG AGTTTATTG ACTTGTCGG AGTTCTTG ACTTGTCGG AGTTTATTG ACTTGTCGG AGTTTATTG ACTTGTCGG AGTTTATTG ACTTGTCGG AGTTTATTG ACTTGTCGG AGTTTATTG ACTTGTCGG AGTTCTTG ACTTGTCGG AGTTCTG ACTTGTCGG AGTTCTG ACTTGTCGG AGTTCTG ACTTGTCGG AGTTCATTG ACTTGTCGG AGTTCTG ACTTGTCGG ACTTCTG ACTTCTG ACTTGTCGG ACTTCTG ACT	574 DNA secid Accession ac	quence n #: Eos sec 4518  21  CTCACTTCGA CTCCCCCTCC TCTGGAAATG CCTGGATTGG GTCCTATACA GAACTTAAA GAACTTAAA GAACTTAAA TGGGATCGGAC TTATCCATT TGGATCGGAC TTATCCATT TGGATCGGAC GACCTACTA GAACCATGGCTGACA ACCAGGTGGT TCATGCTAC ACCAGATT AGAAGGGGCT AAAATACAGG CCCTGAATTA AGAAGGGGCT ACCCCAGATT AGCATTAAAT GCTACCGA ATCTTTAAAT GCTTCTCAG AATCTTTAAAT GACTTCTCAG AATCTTAAAT CCCTTAAAT CCCTTAAAT CCCTTAAAT CCCTTAAAT CCTTTAAAT CCTTTTAAAT CCTTTTAAT CCTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTAAT CCTTTTTAAT CCTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CCTTTTTAAT CTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTAAT CTTTTTTTT	TUENCE  31  TCTATACACT CCGAATCCTAA GCTAATGGAT TCTCTCACTCA GCTAATGGAT TCTCGGGTT GTGGAAATTA AAAGCAAGCA CATAGTTTAG CAATTTCAG ACTTTCAGG ACTTTTGAGG AGTATTGAG ACACACTTG GCAAACAATT GGAAAGAATT ATGATTGAG ATTGTTAGAG AATTTTAG ATTGTTAGAG ATTGTTAGAG ATTGTTAGAG ATTGTTAGAG ATTGTTAGAG ATTGTGAATC TCCCCAACAA TCCCCAACAA TCCCCTCCC ACTGTGACTG ACTGTGACTG ACTGTGACTG ACAGTTTCTG ACAGTTTCTA	GGAGGATTAA TGAGAAGAA ATATTGATGA AGGATAAAAA ATATTGATGA GGGATAAAAA ATATTGATGA GGGATAAAAC ATCTCACTAA AGGACAAAA ATTTTGAGGA ATTTTGAGGA ATTTGAGGAA ATTGATGATGA ACTGGATTGT AAGTTCTTAC TTCGAGAGCA AGATTCTTAC ATTCTCAGGAT TTCTTCAGGAT TTCTTCAGAT TTGTGGACAT AGGATGCTA AGGAATGCTA AGGAATGCTA AGGAATGCTA AGGAATGCTA AGGAATGCTA AGGAATGCTA AGGAATGCTA AGGAATGCTA AGGAATGCTA AGGAATGCAC CACACTACAA GAGGAAGTGA AACTGCACC TTCTTAGATC TAACAGAATA ATTCTTCAGAT TAACAGAATA ATTCTTCAGAT AATTCTTCAGA	ACAAACAAA AGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA TGACTACAT TCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAAATTTG CCAGGTGCT TTACATTTACA TTTAAAGAT AATGACAAA ACAGTACAA ACAGTACAA ACAGTACAA TCATGTACA TCATGTACA TCATGTACA TCATGTACA TCATGTACA TCATGTACA TCATGTACA TCAAGACTTG AGCTACATGAT CAAGACTGTG TCACATGTGT TCACATTGTACA TCACATGTG TCACACTGTG TCACACTGTCC ATTTTCCTCCC	120 180 240 300 360 420 540 660 720 780 900 900 1020 1140 1260 1320 1380 1500 1560 1680 1740 1680 1740 1860
50 55 60 65 70	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CABABABAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG ABATACAA CAAGTABATA GAACATTCA GTCAGCGGAG GAATGCAATA GGAABAAGGGA GATTCAAAG TTAGATCCAT ACAGTTAGAC ACGTTAGTA ACGGTAATA CAGTTAGAC TCTGGTTATG ACTTCAGAC AGGTAATAC AGGAAAAGAC CAGTTGATTC GAACTTATTC AACGAATACA AAGGGTAATC AACGAATACA AAGGAATACA AAGGGTAATG AAGGAATACA AAGGGTAATG AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATTCTTCTGGACTTCTTCTGCACTTCTTCTGAAC AGGTTATTCTTCTGGAAAACCCAATTCAACTGTTCTGGAAAACCCAATTCAACTGTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCAACTTCTTGGAAAACCCAATTCTTCTGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTAACTTTCTTGGAAAACCCAATTCTTCTGAAAAACCCAATTCTTCTGGAAAACCCAATTCTTGAAAAACCCAAGGAAAAAACCCAAGGAAAAAACCCAAGGAAAAAA	574 DNA secid Accession ac	Quence n #: Eos sec 4518  21	31  TCTATACACT CGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA ARAGCAAGCA CATAGTTTAG CGATTTTCAG GTTTTTGAGG AGTGTTAGAC GTTTTTGAGG GTTTTTGAG GTTTTTGAG ACACAGTTG GAAAAGAAAT ACAACTGAA ATTGGAAACTGAA ATTGGAAACTGAA ATTGGAACTG ATTGTGAACTG ATTGTGAACTG ATTGTGAACTG ATTGTGAACTG ACTGTCACCAA TCCCCAACAA TCCCCAACAA TCCACTTCCC ACTGTCACTG CTTAAAACTG ACAGTTCTA GGAGCTGAAGG ACAGTTCTAA GGAGCTGAAGG ACAGTTCTAA	GAGGATTAA TGAGAGA AGCGTTTCCT ACTACAGACA ATCANANAA ATATTGATGA GGGATANACC ATCTCACTAA AGATAACTTT AAGGACANAA CTTGAGGA GTTTTGAGGA GTTTTGAGGA CTGACAGTA ACTGATTTAC AGTTTCACAGT AAGTTCATAA AGATTCATGA ATACCAGCCT AGTTTGAGAT TTGTGAGAT TTGTCAGAT AACAGTCAC AACTGCCAC TTCTTAGAT ATTCTTCAGAT ATT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAA ATCATTGGAA TTGACTGGGGA ATTTCCACTT TACACTTTA AGAGATAAT AGAGATCAAA ACAGTCCAAA ACAGTCCAAA ACAGTCCAAA ACAGTACAAG AGCAGTTTGT TTTTTAACATTAC TTTTTAACAAT AATGCAACAA ACAGTACAAG AGCAGTTTGT TCCTGTTACA TCTGTTACA TTTGTACCAG TCAGAGGGGG ATTCTCTGGA TAAATTAGC TCACACTGGG TCACACTTGG TCACACTGGG TCACACTGGG TCACACTGGG TCCACACTAGGGAGAGGAG CTCCAGTCCC ATTCTCTCCAAATGCTTCCCC AAATGCTTCCC	120 180 240 300 360 480 540 660 720 780 960 1020 1140 1260 1320 1380 1440 1560 1560 1680 1740 1860 1920
50 55 60 65 70 75	Seq ID NO: Nucleic Ac Coding seq  1   CACACATACG CABABABAAAC CGGCGAGGGG CAGCTCCTCT CTTGTTGAAG ABATACAA CAAGTABATA GAACATTCA GTCAGCGGAG GAATGCAATA GGAABAAGGGA GATTCAAAG TTAGATCCAT ACAGTTAGAC ACGTTAGTA ACGGTAATA CAGTTAGAC TCTGGTTATG ACTTCAGAC AGGTAATAC AGGAAAAGAC CAGTTGATTC GAACTTATTC AACGAATACA AAGGGTAATC AACGAATACA AAGGAATACA AAGGGTAATG AAGGAATACA AAGGGTAATG AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATACA AAGGAATTCTTCTGGACTTCTTCTGCACTTCTTCTGAAC AGGTTATTCTTCTGGAAAACCCAATTCAACTGTTCTGGAAAACCCAATTCAACTGTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTGGAAAACCCAATTCAACTTCTTGGAAAACCCAATTCTTCTGAAAACCCAATTCTTCTGGAAAACCCAATTCTTCTAACTTTCTTGGAAAACCCAATTCTTCTGAAAAACCCAATTCTTCTGGAAAACCCAATTCTTGAAAAACCCAAGGAAAAAACCCAAGGAAAAAACCCAAGGAAAAAA	574 DNA secid Accession ac	Quence n #: Eos sec 4518  21	31  TCTATACACT CGAATCCTAA GCTAATGGAT TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA TCTCCTATCA ARAGCAAGCA CATAGTTTAG CGATTTTCAG GTTTTTGAGG AGTGTTAGAC GTTTTTGAGG GTTTTTGAG GTTTTTGAG ACACAGTTG GAAAAGAAAT ACAACTGAA ATTGGAAACTGAA ATTGGAAACTGAA ATTGGAACTG ATTGTGAACTG ATTGTGAACTG ATTGTGAACTG ATTGTGAACTG ACTGTCACCAA TCCCCAACAA TCCCCAACAA TCCACTTCCC ACTGTCACTG CTTAAAACTG ACAGTTCTA GGAGCTGAAGG ACAGTTCTAA GGAGCTGAAGG ACAGTTCTAA	GAGGATTAA TGAGAGA AGCGTTTCCT ACTACAGACA ATCANANAA ATATTGATGA GGGATANACC ATCTCACTAA AGATAACTTT AAGGACANAA CTTGAGGA GTTTTGAGGA GTTTTGAGGA CTGACAGTA ACTGATTTAC AGTTTCACAGT AAGTTCATAA AGATTCATGA ATACCAGCCT AGTTTGAGAT TTGTGAGAT TTGTCAGAT AACAGTCAC AACTGCCAC TTCTTAGAT ATTCTTCAGAT ATT	AACAAACAAA AGGAGCCGCA CGCTTGCATT ACAGAGAAAA TTGGGGAAAG AGATCTTACA ATCATTGGAA ATCACTGGGGA ATTTCCACTT AGCAGTCAAA AGAAATTTG GCAGGCTGCT TTACATTTACA TTACATTTACA TTACATTTACA TTACATTTACA ATCAGTACAAA ACAGTACAAA TTCTTTACA TTCTTTACA TTCTTTACA TTCTTTACA TTCTTTACA TCAGTACATAC CAGTGCTACA TCACATATGG TCACACTTGTG TCACACTTGTG TCACACTTGTG TCACACTTGTG TCACACTTGTG TCACACTTGTG TCACACTTGTG TGAGGAGGAG CTCCAGGTCCC	120 180 240 300 360 480 540 600 720 780 900 960 1020 1140 1200 1320 1380 1440 1560 1620 1620 1740 1800 1900

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                                                                                                     5100
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                                                                                                     5340
55
          AAAAAA AAAAAAAA AAAAAAAA
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#### Seq ID NO: 575 Protein sequence: Protein Accession #: Eos sequence

60	Protein Acc	cession #: F	son medinence	=			
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	MRILKRFLAC	IQLLCVCRLD	WANGYYRQQR	KLVEEIGWSY	TGALNQKNWG	KKYPTCNSPK	60
	OSPINIDEDL	TOVNVNLKKL	KFQGWDKTSL	ENTFIHNTGK	TVEINLTNDY	RVSGGVSEMV	120
65	PKASKITPHW	GKCNMSSDGS	EHSLEGOKFP	LEMQIYCFDA	DRFSSFEEAV	KGKGKLRALS	180
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	TGKEEIHEAV	CSSEPENVQA	DPENYTSLLV	TWERPRVVYD	TMIEKFAVLY	QQLDGEDQTK	360
	HEFLTDGYOD	LGAILNNLLP	NMSYVLQIVA	ICTNGLYGKY	SDQLIVDMPT	DNPELDLFPE	420
70	LIGTERIIKE	ERECKDIEEG	AIVNPGRDSA	TNQIRKKEPQ	ISTTTHYNRI	GTKYNBAKTN	480
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	GSKTVLRSPH	MNLSGTAESL	NTVSITEYEE	ESLLTSFKLD	TGAEDSSGSS	PATSAIPFIS	600
	ENISQGYIFS	SENPETITYD	VLIPESARNA	SEDSTSSGSE	ESLKDPSMEG	NVWFPSSTDI	660
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75	TEVTPHAFTP	SSROODLVST	VNVVYSQTTQ	PVYNAEASNS	SHESRIGLAE	GLESEKKAVI	780
	PLVIVSALTP	ICLVVLVGIL	IYWRKCFQTA	HFYLEDSTSP	RVISTPPTPI	FPISDDVGAI	840
	PIKHFPKHVA	DLHASSGFTE	EFETLKEFYQ	EVQSCTVDLG	ITADSSNHPD	NKHKNRYINI	900
	VAYDHSRVKL	AQLAEKDGKL	TDYINANYVD	GYNRPKAYIA	AQGPLKSTAE	DEWRMIWEHN	960
	VEALAWILNT	VEKGRRKCDQ	YWPADGSEEY	<b>GNFLVTQKSV</b>	QVLAYYTVRN	PTLRNTKIKK	1020
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	TGTYIVLDSM	LQQIQHEGTV	NIFGFLKHIR	SQRNYLVQTE	EQYVFIHDTL	VRAILSKETE	1140
	VLDSHIHAYV	NALLIPGPAG	KTKLEKQFQL	LSQSNIQQSD	YSAALKQCNR	EKNRTSSIIP	1200
	VERSRVGISS	LSGEGTDYIN	ASYIMGYYQS	NEFIITOHPL	LHTIKDFWRM	IMDHNAQLVV	1260
0.5	MIPDGQNMAE	DEFVYWPNKD	EPINCESFKV	TLMAEEHKCL	SNEEKTIIOD	FILEATODDY	1320
85	VLEVRHFQCP	KWPNPDSPIS	KTFELISVIK	EEAANRDGPM	IVHDEHGGVT	AGTFCALTTL	1380
		DVYQVAKMIN	LMRPGVFADI	EGAĞLLAKAI	LSLVSTRQEE	NPSTSLDSNG	1440
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# WO 02/086443

Seq ID NO: 576 DNA sequence Nucleic Acid Accession #: EOS sequence Coding sequence: 148-4494

5	Coding sequence: 148-4494						
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13	GTCAGCGGAG	GAGTTTCAGA	AATGGTGTTT	AAAGCAAGCA	AGATAACTTT	TCACTGGGGA	540
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	AATCCTGAAC	TTGATCTTTT	CCCTGAATTA	ATTGGAACTG	AAGAAATAAT	CAAGGAGGAG	1440
	GAAGAGGGAA	AAGACATTGA	AGAAGGCGCT	ATTGTGAATC	CTGGTAGAGA	CAGTGCTACA	1500 1560
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	GAAGGTACTT	CAGCCTCTTT GGACTGCAGA	AAATGATGGC	TCTAAAACTG	TTCTTAGATC	TCCACATATG	1800 1860
	እርምምየአ ተፕሮርል	CCACTTTCAA	GCTTGATACT	GGAGCTGAAG	ATTCTTCAGG	CTCCAGTCCC	1920
40	CCDACTTCTG	CTATCCCATT	CATCTCTGAG	AACATATCCC	AAGGGTATAT	ATTTTCCTCC	1980
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	GAAGATICAA	CTTCATCAGG CTAGCTCTAC	TTCAGAAGAA	GCACTAAAGG	ATGTTGGATC	AGGCAGAGAG	2160
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45	ALCOUNTAINED CALC	CAGGCCCCAGT	GATGTCACAG	GGTCCCTCAG	TTACAGATCT	GGAAATGCCA	2280
	CATTATTCTA	CCTTTGCCTA AGGATTTGGT	CTTCCCAACT	GAGGTAACAC	ACTOGORAGE ACTOGORAGE	AACCCCATCC	2340 2400
	CTATACAATG	ACCCCAGTAA	TAGTAGCCAT	GAGTCTCGTA	TTGGTCTAGC	TGAGGGGTTG	2460
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	ATGATTGTTC	ATGATGAGCA	TGGAGGAGTG	ACGGCAGGAA	CTTTCTGTGC	TCTGACAACC CAAGATGATC	4320
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	ATCCTCAGCC	TTGTGAGCAC	AAGGCAGGA	GAGAATCCAT	CCACCTCTC	GGACAGTAAT	4440
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85	CCATTCTCC	CCCAAATTTA	TATCATTAAC	AATGTGTGC	: TTTTTGCAAC	ACTTGTAATT	4680
	<b>ጥልርጥጥልጥጥል</b> ገ	מדייות באריוים יו	AAATGATTG	ATTTTACAGT	: ATTTCTAAG	A ATGGAATTGT	4740
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                                                                                                  360
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        5460
        Α ΑΑΑΑΑΑΑΑ ΑΑΑΑΑΑΑΑΑ
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85	AARAACACTC	TICCHIMIGA	THITCHNONIA	CALTICALISATION OF THE PARTY OF THE	CATGGACCAA	ATTTATATTT	7620
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        7920
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WO 02/086443

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## WO 02/086443

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TAA

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PCT/US02/12476

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CTGCTGCGTG CCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT
                                                                                           900
        GTCGCTCCAG ACCTATGATG ACTTGTTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT
                                                                                           960
        GGTCCTTCCA CTGTGCACCT GCGCGGGGGA GGCGACCTCA GTTGTCCTGC CCTGTGGAAT GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG
70
                                                                                         1080
        TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGA ACTGTGTATT TATTTAAAAC TCTGGTGATA AAAATAAAGC TGTCTGAACT GTTAAAAAAA
                                                                                         1140
75
        Seq ID NO: 685 Protein sequence
        Protein Accession #: NP_004855.1
                                                                           51
80
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         EDLLTRLRAN QSWEDSNIDL VPAPAVRILI PEVRLGSGGH LHLRISRAAL PEGLPEASRL
                                                                                           120
        HRALFRLSPT ASSEMDUTRP LERQLSLARP QAPALHLRLS PPPSQSDQLL ASSSSARPQL
ELHLRPQAAR GRRRARARNG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC
                                                                                           180
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85
         LAKDCHCI
```

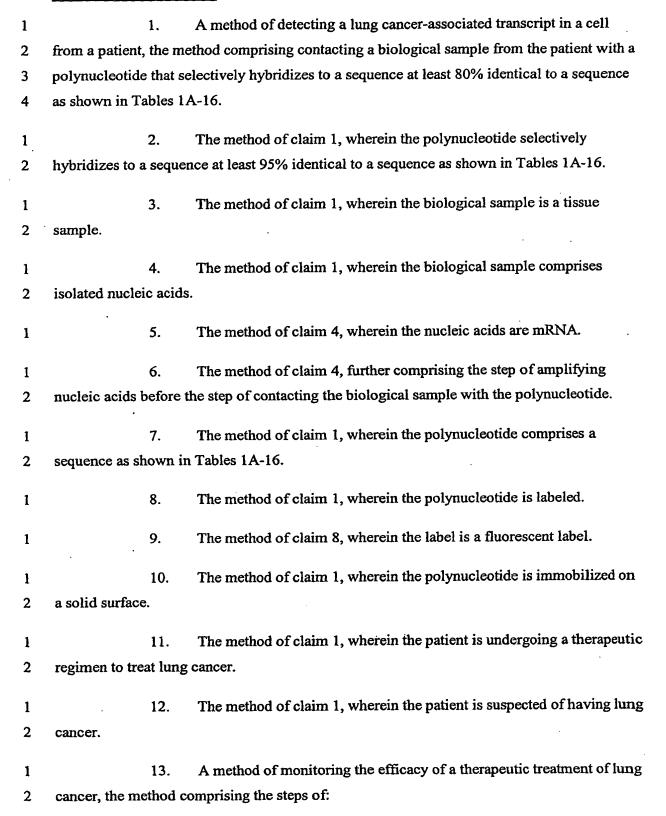
Seq ID NO: 686 DNA sequence

Nucleic Acid Accession #: NM_002423.2 Coding sequence: 48..851

```
41
                                                                      51
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        TGCTGTGTGC TGTGTGCCTG CTGCCTGGCA GCCTGGCCCT GCCGCTGCCT CAGGAGGCGG
                                                                                     120
        GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT
                                                                                     180
        ATGACTCAGA AACAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAT
                                                                                     240
10
        TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCCGCGT CATAGAAATA ATGCAGAAGC
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                                                                                     360
        CTTCCAAAGT GGTCACCTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG
                                                                                     420
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                                                                                     480
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        ACTCCTACCC ATTTGATGGG CCAGGAAACA CGCTGGCTCA TGCCTTTGCG CCTGGGACAG
                                                                                     600
       GTCTCGGAGG AGATGCTCAC TTCGATGAGG ATGAACGCTG GACGGATGGT AGCAGTCTAG
GGATTAACTT CCTGTATGCT GCAACTCATG AACTTGGCCA TTCTTTGGGT ATGGGACATT
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                                                                                     780
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20
        GAAAGAAATA GAAACTTCAG GCAGAACATC CATTCATTCA TTCATTGGAT TGTATATCAT
                                                                                     900
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CTTTTTTATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACTCCTTT
                                                                                     960
                                                                                   1020
        ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGCGCGTAG ATGTCAATAA
                                                                                   1080
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                                                          41
                                                                      51
30
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                                                                                      60
        EMQKFFGLPI TGMLNSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL
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                                                                                     180
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35
        PONFKLSODD IKGIOKLYGK RSNSRKK
        Seq ID NO: 688 DNA sequence
        Nucleic Acid Accession #: NM 005221.3
        Coding sequence: 1..870
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                                                          41
                                                                      51
                                             31
                                 21
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                                                                                      60
        TTCCAGACGT CCGCAGCTAT GCACCATCCG TCTCAGGAAT CGCCAACTTT GCCCGAGTCT
                                                                                     120
45
        TCAGCTACCG ATTCTGACTA CTACAGCCCT ACGGGGGGAG CCCCGCACGG CTACTGCTCT
                                                                                     180
        CCTACCTCGG CTTCCTATGG CAAAGCTCTC AACCCCTACC AGTATCAGTA TCACGGCGTG
                                                                                     240
        AACGGCTCCG CCGGGAGCTA CCCAGCCAAA GCTTATGCCG ACTATAGCTA CGCTAGCTCC
TACCACCAGT ACGGCGCGC CTACAACCGC GTCCCAAGCG CCACCAACCA GCCAGAGAAA
                                                                                     300
        GAAGTGACCG AGCCCGAGGT GAGAATGGTG AATGGCAAAC CAAAGAAAGT TCGTAAACCC
                                                                                     420
50
        AGGACTATTT ATTCCAGCTT TCAGCTGGCC GCATTACAGA GAAGGTTTCA GAAGACTCAG
TACCTCGCCT TGCCGGAACG CGCCGAGCTG GCCGCCTCGC TGGGATTGAC ACAAACACAG
                                                                                     480
        GTGAAAATCT GGTTTCAGAA CAAAAGATCC AAGATCAAGA AGATCATGAA AAACGGGGAG
                                                                                     600
        ATECCCCCG AGCACAGTCC CAGCTCCAGC GACCCAATGG CGTGTAACTC GCCGCAGTCT CCAGCGGTGT GGGAGCCCCA GGGCTCGTCC CGCTCGCTCA GCCACCACCC TCATGCCCAC
                                                                                     660
55
        CCTCCGACCT CCAACCAGTC CCCAGCGTCC AGCTACCTGG AGAACTCTGC ATCCTGGTAC
                                                                                     780
        ACAAGTGCAG CCAGCTCAAT CAATTCCCAC CTGCCGCCGC CGGGCTCCTT ACAGCACCCG
                                                                                     840
        CTGGCGCTGG CCTCCGGGAC ACTCTATTAG
        Seq ID NO: 689 Protein sequence
60
        Protein Accession #: NP_005212.1
                                             31
                                                          41
                                                                      51
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                                                                                      60
65
        PTSASYGKAL NPYQYQYHGV NGSAGSYPAK AYADYSYASS YHQYGGAYNR VPSATNQPEK
                                                                                     120
        EVTEPEVRMV NGKPKKVRKP RTIYSSFQLA ALQRRFQKTQ YLALPERAEL AASLGLTQTQ
                                                                                     180
        VKIWFONKRS KIKKIMKNGE MPPEHSPSSS DPMACNSPQS PAVWEPQGSS RSLSHHPHAH
        PPTSNQSPAS SYLENSASWY TSAASSINSH LPPPGSLQHP LALASGTLY
```

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein neorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

#### WHAT IS CLAIMED IS:



3	WO 02/086443 PCT/US02/12476  (i) providing a biological sample from a patient undergoing the therapeutic
4	treatment; and
5	(ii) determining the level of a lung cancer-associated transcript in the
6	biological sample by contacting the biological sample with a polynucleotide that selectively
7	hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16,
, 8	thereby monitoring the efficacy of the therapy.
0	thereby monitoring the emeacy of the therapy.
1	14. The method of claim 13, further comprising the step of: (iii) comparing
2	the level of the lung cancer-associated transcript to a level of the lung cancer-associated
3	transcript in a biological sample from the patient prior to, or earlier in, the therapeutic
4	treatment.
1	15. The method of claim 13, wherein the patient is a human.
1	16. A method of monitoring the efficacy of a therapeutic treatment of lung
2	cancer, the method comprising the steps of:
3	(i) providing a biological sample from a patient undergoing the therapeutic
4	treatment; and
5	(ii) determining the level of a lung cancer-associated antibody in the biologic
6	sample by contacting the biological sample with a polypeptide encoded by a polynucleotide
7	that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in
8	Tables 1A-16, wherein the polypeptide specifically binds to the lung cancer-associated
9	antibody, thereby monitoring the efficacy of the therapy.
1	17. The method of claim 16, further comprising the step of: (iii) comparing
2	the level of the lung cancer-associated antibody to a level of the lung cancer-associated
3	antibody in a biological sample from the patient prior to, or earlier in, the therapeutic
4	treatment.
1	18. The method of claim 16, wherein the patient is a human.
1	19. A method of monitoring the efficacy of a therapeutic treatment of lun
2	cancer, the method comprising the steps of:
3	(i) providing a biological sample from a patient undergoing the therapeutic

treatment; and

5	(ii) determining the level of a lung cancer-associated polypeptide in the			
6	biological sample by contacting the biological sample with an antibody, wherein the antibody			
7	specifically binds to a polypeptide encoded by a polynucleotide that selectively hybridizes to			
8	a sequence at least 80	0% identical to a sequence as shown in Tables 1A-16, thereby		
9	monitoring the effica	cy of the therapy.		
		m 4 5 1 10 5 d		
1	20.	The method of claim 19, further comprising the step of: (iii) comparing		
2	-	cancer-associated polypeptide to a level of the lung cancer-associated		
3	polypeptide in a biol	ogical sample from the patient prior to, or earlier in, the therapeutic		
4	treatment.			
1	21.	The method of claim 19, wherein the patient is a human.		
1	22.	An isolated nucleic acid molecule consisting of a polynucleotide		
2	sequence as shown in Tables 1A-16.			
1	23.	The nucleic acid molecule of claim 22, which is labeled.		
1	24.	The nucleic acid of claim 23, wherein the label is a fluorescent label		
1	25.	An expression vector comprising the nucleic acid of claim 22.		
1	26.	A host cell comprising the expression vector of claim 25.		
1	27.	An isolated polypeptide which is encoded by a nucleic acid molecule		
2	having polynucleotic	le sequence as shown in Tables 1A-16.		
1	28.	An antibody that specifically binds a polypeptide of claim 27.		
1	29.	The antibody of claim 28, further conjugated to an effector component.		
1	30.	The antibody of claim 29, wherein the effector component is a		
2	fluorescent label.			
1	31.	The antibody of claim 29, wherein the effector component is a		
2	radioisotope or a cyl	totoxic chemical.		
1	32.	The antibody of claim 29, which is an antibody fragment.		

3	33.	The antibody of claim 29, which is a humanized antibody	
3	34.	A method of detecting a lung cancer cell in a biological sample from a	
patient, the met	hod c	omprising contacting the biological sample with an antibody of claim	
28.			
3	35.	The method of claim 34, wherein the antibody is further conjugated to	
•	36	The method of claim 35, wherein the effector component is a	
		The memor of claim 33, wherein the effector compensation	
nuorescent labe	71.		
3	37.	A method of detecting antibodies specific to lung cancer in a patient,	
the method con	ıprisir	ng contacting a biological sample from the patient with a polypeptide	
encoded by a nucleic acid comprises a sequence from Tables 1A-16.			
:	38.	A method for identifying a compound that modulates a lung cancer-	
associated polypeptide, the method comprising the steps of:			
(i) contacting the compound with a lung cancer-associated polypeptide, the			
polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least			
		quence as shown in Tables 1A-16; and	
		termining the functional effect of the compound upon the polypeptide.	
:	39.	The method of claim 38, wherein the functional effect is a physical	
effect.		• • • • • • • • • • • • • • • • • • • •	
	40	The method of claim 38, wherein the functional effect is a chemical	
	<del></del>	The memor of claim 50, wherein the rancolonia extension is a constant	
enect.		· ·	
	41.	The method of claim 38, wherein the polypeptide is expressed in a	
eukaryotic host	cell c	or cell membrane.	
	42.	The method of claim 38, wherein the functional effect is determined by	
measuring ligar	nd bin	ding to the polypeptide.	
		The method of claim 38, wherein the polypeptide is recombinant.	
	patient, the met 28.  an effector come fluorescent laber the method come encoded by a measure associated poly polypeptide encoded by a feet to be feet.  effect.	28.  35. an effector componer  36. fluorescent label.  37. the method comprising encoded by a nucleic (i) compolypeptide encoded 80% identical to a second (ii) decompolypeptide encoded (iii) decompolypeptide encoded 80% identical to a second (iiii) decompolypeptide encoded 80% identical to a second (iiii) decompolypeptide encoded 80%	

1	44. A method of inhibiting proliferation of a lung cancer-associated cell to			
2	treat lung cancer in a patient, the method comprising the step of administering to the subject a			
3	therapeutically effective amount of a compound identified using the method of claim 38.			
1	45. The method of claim 44, wherein the compound is an antibody.			
1	46. The method of claim 45, wherein the patient is a human.			
1	47. A drug screening assay comprising the steps of			
2	(i) administering a test compound to a mammal having lung cancer or a cell			
3	isolated therefrom;			
4	(ii) comparing the level of gene expression of a polynucleotide that selectively			
5	hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-16 in a			
6	treated cell or mammal with the level of gene expression of the polynucleotide in a control			
7	cell or mammal, wherein a test compound that modulates the level of expression of the			
8	polynucleotide is a candidate for the treatment of lung cancer.			
1	48. The assay of claim 47, wherein the control is a mammal with lung			
2	cancer or a cell therefrom that has not been treated with the test compound.			
1	49. The assay of claim 47, wherein the control is a normal cell or mammal			
1	50. A method for treating a mammal having lung cancer comprising			
2	administering a compound identified by the assay of claim 47.			
1	51. A pharmaceutiPcal composition for treating a mammal having lung			
2	cancer, the composition comprising a compound identified by the assay of claim 47 and a			
3	physiologically acceptable excipient			

### REVISED VERSION

# (19) World Intellectual Property Organization

International Bureau





(43) International Publication Date 31 October 2002 (31.10.2002)

PCT

(10) International Publication Number WO 2002/086443 A2

(51) International Patent Classification⁷: C 21/04, C12Q 1/68

C07H 21/02,

(21) International Application Number:

PCT/US2002/012476

(22) International Filing Date: 18 April 2002 (18.04.2002)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

18 April 2001 (18.04.2001) US 60/284,770 60/290,492 10 May 2001 (10.05.2001) US 60/339,245 9 November 2001 (09.11.2001) US 13 November 2001 (13.11.2001) US 60/350,666 60/334,370 29 November 2001 (29.11.2001) US 12 April 2002 (12.04.2002) 60/372,246

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- (74) Agent: HALLUIN, Albert, P.; HOWREY SIMON ARNOLD & WHITE LLP, 301 Ravenswood Avenue, Box 34, Menlo Park, CA 94025 (US).

- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

#### Declaration under Rule 4.17:

of inventorship (Rule 4.17(iv)) for US only

#### Published:

- with declaration under Article 17(2)(a); without abstract;
   title not checked by the International Searching Authority
- (48) Date of publication of this revised version: 17 June 2004
- (15) Information about Correction: see PCT Gazette No. 25/2004 of 17 June 2004, Section II

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

'O 2002/086443 A2 ||||||||||||||||

## PATENT COOPERATION TREATY

## **PCT**

## DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13ter.1(c) and 39)

Applicant's or agent's file reference		· · · · · · · · · · · · · · · · · · ·	5-1		
Applicant s of agent s the reference	IMPORTANT DECLARATION		Date of mailing (day/month/year)		
18501-15-3PC			TO HOR SOUT		
International application No.	International filing date (day/mo.	date (day/month/year) (Earliest) Priority date (			
PCT/US02/12476	18 April 2002 (18.04.2002)	f :	i0 May 2001 (10.05.2001)		
International Patent Classification (IPC)	or both national classification and	IPC			
TBCCD+ CD7U 21/02 21/04- C120 1/69	and \$10 Cl . 426/6 526/02 1 22	•			
IPC(7): C07H 21/02, 21/04; C12Q 1/68 Applicant	and US Ci.: 433/0, 330/23.1, 23.	J			
••					
EOS BIOTECHNOLOGY, INC					
This International Searching Authority has will be established on the international and	ereby declares, according to Article application for the reasons indicate articles are to:	e 17(2)(a), that no	International search report		
a. scientific theories.	rnational application relates to.				
b. mathematical theories.	lan.				
F-4	cs .				
c. plant varieties.					
d. animal varieties.					
e essential biological and the products of		ints and animals, o	other than microbiological processes		
.	ethods of doing business.				
g. schemes, rules or n					
. 🗂					
i methods for treatme	ent of the human body by surgery	or therapy.			
j methods for treatme	ent of the animal body by surgery	or therapy.	•		
k. diagnostic methods practised on the human or animal body.					
i. mere presentations					
m. computer programs	for which this International Search	ning Authority is n	ot equipped to search prior art.		
2. The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:  the description the claims the drawings					
in accordance	the ciding	<u> </u>	iic drawings		
The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:  the written form has not been furnished or does not comply with the standard.  the computer readable form has not been furnished or does not comply with the standard.					
4. Further comments:					
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Name and mailing address of the ISA/US  Authorized officer  Co Co Co Co					
Mail Stop PCT, Atm: ISA/US Commissioner for Patents Carlo Misera Carlo Misera Carlo Misera					
P.O. Box 1450 PRIMARY EXAMINER					
Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230 Telephone No. 703-308-0196					
Form PCT/ISA/203 (July 1998)					

#### PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To: TOWNSEND AND TOWNSEND AND CREW LLP TWO EMBARCADERO CENTER	PCT					
EIGHTH FLOOR SAN FRANCISCO, CA 94111-3834	NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL SEARCH REPORT OR THE DECLARATION					
	(PCT Rule 44.1)					
	Date of Mailing (day/month/year) 15 AUG 2003					
Applicant's or agent's file reference 18501-15-3PC	FOR FURTHER ACTION See paragraphs 1 and 4 below					
International application No. PCT/US02/12476	International filing date (day/month/year)  18 April 2002 (18.04.2002)					
Applicant EOS BIOTECHNOLOGY, INC	,					
The applicant is hereby notified that the international search.	ch report has been established and is transmitted horewith.					
Filing of amendments and statement under Article 19: The applicant is entitled, if he so wishes, to amend the cla	ims of the international application (see Rule 46):					
When? The time limit for filing such amendments is international search report.	When? The time limit for filing such amendments is normally two months from the date of transmittal of the					
	Where? Directly to the International Bureau of WIPO, 34, chemia des Colombettes 1211 Geneva 20, Switzerland, Facsimile No.: (41-22) 740.14.35					
For more detailed instructions, see the notes on the accompanying sheet.						
<ol> <li>The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.</li> </ol>						
3. With regard to the protest against payment of (an) additi	ional fee(s) under Rule 40.2, the applicant is notified that:					
the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.						
no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.						
4. Reminders	·					
Shortly after 18 months from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in Rules 90 bis.1 and 90 bis.3, respectively, before the completion of the technical preparations for international publication.						
Within 19 months from the priority date, but only in respect of some designated Offices, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase until 30 months from the priority date (in some Offices even later); otherwise the applicant must, within 20 months from the priority date, perform the prescribed acts for entry into the national phase before those designated Offices.						
In respect of other designated Offices, the time limit of 30 months (or later) will apply even if no demand is filed within 19 months.						
See the Annex to Form PCT/IB/301 and, for details about the applicable time limits, Office by Office, see the PCT Applicant's Guide, Volume II, National Chapters and the WIPO Internet site.						
Name and mailing address of the ISA/US  Mail Stop PCT, Attn: ISA/US  Commissioner for Patents	Authorized officer Carla Myers TUBELL Harris for					
P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703)305-3230	Telephone No. 703-308-0196					
Form PCT/ISA/220 (April 2002)	(See notes on accompanying sheet)					